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# OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 04:22:08 ; Search time 4768.86 Seconds  
(without alignments)  
10661.374 Million cell updates/sec

Title: US-09-804-014A-7  
Perfect score: 1747  
Sequence: 1 gaagcctgattctgacgaaa.....agttctgcagcactcacac 1747

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

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- 2: gb\_hlg:\*
- 3: gb\_in:\*
- 4: gb\_ov:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_scs:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
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- 39: em\_hlgo\_hum:\*
- 40: em\_hlgo\_mus:\*
- 41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1747	100.0	1747	6	AX268121
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3	1408.2	80.6	1447	9	AF315818
4	1321.6	75.6	1341	6	AX352535
5	1069	61.2	1599	6	126643
6	1065.8	61.0	1599	10	AF032099
7	844.2	48.3	15763	9	AC008687
8	658.2	37.7	1551	4	OCU38240
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12	639	36.6	1836	9	HUMPOCH
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## ALIGNMENTS

RESULT 1  
LOCUS AX268121 1747 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 7 from Patent WO0168651.  
ACCESSION AX268121  
VERSION AX268121.1 GI:16516622  
KEYWORDS  
SOURCE  
ORGANISM human.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 Padigaru,M., Vernet,C.A., Fernandes,E., Shinkets,R.A.,  
Spaderna,S.K., Majumder,K. and Li,L.  
TITLE Polypeptides and nucleic acids encoding same

JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;  
 FEATURES Curagen Corporation (US)  
 Location/Qualifiers  
 source 1.1747  
 /organism="Homo sapiens"  
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 BASE COUNT 255 a 582 c 375 g 335 t  
 ORIGIN

Query Match 100.0%; Score 1747; DB 6; Length 1747;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-230;  
 Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 GCGGGGCGGACGCTGGGCGCGCTTCGCGGACACGTCGTAGGGGACCGACGCGCGCG 480
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QY 1681 GGCACCCCGGCAAGAACCTGGTCCAGCAAGTGTGGAAGAGTGTAGGTCTGCGACAGAC 1740
DB 1681 GGCACCCCGGCAAGAACCTGGTCCAGCAAGTGTGGAAGAGTGTAGGTCTGCGACAGAC 1740
QY 1741 CTTACAC 1747
DB 1741 CTTACAC 1747

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RESULT 2  
 HSA310479  
 LOCUS  
 DEFINITION  
 Homo sapiens mRNA for potassium voltage-gated channel,  
 Shaker-related subfamily, member 7 (KCNM7 gene).  
 ACCESSION  
 AJ310479.1 GI:12830376  
 VERSION  
 KCN7 gene; KVI.7 gene; potassium voltage-gated channel,  
 shaker-related subfamily, member\*.  
 KEYWORDS  
 human.  
 SOURCE  
 Homo sapiens  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	(bases 1 to 4372)		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
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Q	y	826	CTTGAGACGCTGCTGACTTCTCGGACGACGCGAGCGGAGGGGCTTGTGCTGCAGC	885
D	b	839	CTTGAGACGCTGCTGACTTCTCGGACGACGCGAGCGGAGGGGCTTGTGCTGCAGC	898
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D	b	899	CGCAGCGCGCGCGCGGTGTTCGCCGCTCCGCTGAATGGCTCTACGCAATGCTGGAATCC	955
Q	y	946	ACCCGCGCTGCGCTTCAATACCCGTTCTTCGGGGAGAGCGGTGATTTGTTGGTT	1005
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QY	1486	TCGGGGCGTGTGACTATTTTCCTCCAGATGCGCCGTCAATGTCTCCAAATTTTCAGTACTT	1545
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DB	1736	TSAGGCTGTGACAGACTTCACAC	1757
RESULT 3	AF315818	1447 bp	mRNA
LOCUS	AF315818		
DEFINITION	Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete cds.		
ACCESSION	AF315818		
VERSION	AF315818.1	GI:14485554	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 1447)		
TITLE	Bardien-Kruger, S., Wulff, H., Arleff, Z., Brink, P., Chandý, K.G. and Corfield, V.		
JOURNAL	Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI) Unpublished		
REFERENCE	2 (bases 1 to 1447)		
AUTHORS	Bardien-Kruger, S., Wulff, H., Arleff, Z., Brink, P., Chandý, K.G. and Corfield, V.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7535, South Africa		
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	WFSEELLVRLVCPSSKAIFEFKNWNLLIDFVALIFVALIGTELAROGQOAMSLAI		
	LRLVRLVRRPRIFRLSRKSLQTLQGLTLARSMELDLIFLELIGVLRSSANYFAR		
	VDRVDSHTSLIPESFMVAIVYMTVTGTGDAPVTVGGKIVGSLCAIGVLTLSLPVV		
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	HLTVEV"		
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ORIGIN			312 t
Query Match	80.6%	Score 1408.2;	DB 9, Length 1447;
Best Local Similarity	99.4%;	Pred. No. 3.5e-184;	

	Matches	1435	Conservative	0	Mismatches	3	Indels	5	Gaps	2
OY	305	ACACGCTGGTTTCGGGGGTGCGGGGGCTGCGCGCCATGAGCGCGGTGCGCCGCC	364							
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OY	365	CCGTGCGGCTGCTGGGAGCGGCTGGTGCTCAACGTGCGCGGCTGCGCTTCAGACGGCG	424							
Db	59	CCGTGCGGCTGCTGGGAGCGGCTGGTGCTCAACGTGCGCGGCTGCGCTTCAGACGGCG	118							
OY	425	GGCGCAGCGCTGGGCGGCTTCCGGACACTGCTAGGGAGACCAGCGCGCGCGGCGC	484							
Db	119	GGCGCAGCGCTGGGCGGCTTCCGGACACTGCTAGGGAGACCAGCGCGCGCGGCGC	178							
OY	485	TTCTACGACGACGCGCGCGAGATTATTCTTCGACCGGACCGGCCACGCTTCGACGCC	544							
Db	179	TTCTACGACGACGCGCGCGAGATTATTCTTCGACCGGACCGGCCACGCTTCGACGCC	238							
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REFERENCE  
1 Curtis, R.A.  
52906, 33408, and 12189, potassium channel family members and uses  
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JOURNAL Millennium Pharmaceuticals, Inc. (US)  
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 Kalkan, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandry, G.,  
 Husted, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M.,  
 Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandry, K.G.  
 Genomic organization, chromosomal localization, tissue  
 distribution, and biophysical characterization of a novel mammalian  
 Shaker-related voltage-gated potassium channel, Kv1.7  
 J. Biol. Chem. 273 (10), 5851-5857 (1998)  
 MEDLINE 98157988  
 PUBMED 9488722  
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 Kalkan, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandry, G.,  
 Husted, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M.,  
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 Direct Submission  
 Submitted (30-OCT-1997) Physiology and Biophysics, University of  
 California at Irvine, Irvine, CA 92697, USA  
 JOURNAL Location/Qualifiers  
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AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submission
JOURNAL	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	3 (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	4 (bases 1 to 157633)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Oct 3, 2001 this sequence version replaced gi:10312243.

Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
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OY	1671	CTCCACTGTGGGCAACCCCAAGGAAACCTGTGTACCGAACTGTGAGAGACAGTTGAGG	1730
Db	81417	CTCCACTGTGGGCAACCCCAAGGAAACCTGTGTACCGAACTGTGAGAGACAGTTGAGG	81358
OY	1731	TCTGTGAGGACCTGCACAC	1747
Db	81357	TCTGTGAGGACCTGCACAC	81341

RESULT 8					
OCU38240					
LOCUS	OCU38240	1551 bp	DNA	linear	MAM 30-JUN-1999
DEFINITION	Oryctolagus cuniculus glibenclamide-sensitive voltage-gated potassium channel (Kv1.3-glib) gene, complete cds.				

ACCESSION U38240  
 VERSION 038240.1 GI:3264840  
 KEYWORDS Oryctolagus cuniculus.  
 SOURCE Oryctolagus cuniculus.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 REFERENCE 1 (bases 1 to 1551)  
 YAO, X., CHANG, A.Y., BOUIPAEP, E.L., SEGAL, A.S. and DESIR, G.V. Molecular cloning of a glibenclamide-sensitive, voltage-gated potassium channel expressed in rabbit kidney  
 J. Clin. Invest. 97 (11), 2525-2533 (1996)  
 JOURNAL 96249424  
 MEDLINE 8647945  
 PUBMED 2 (bases 1 to 1551)  
 REFERENCE Desir, G.  
 AUTHORS Direct Submission  
 TITLE Submitted (10-Oct-1995) Gary Desir, Medicine, Yale, 2074 LMP 333  
 JOURNAL Cedar Street, New Haven, CT 06510, USA  
 COMMENT On Jun 29, 1998 this sequence version replaced gi:1033191.  
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 VWLLEYPSSPARGIAIVSLVILISIVILFLEPREDKDYPAAPSDVVEA  
 NGTSGAPAGASSPDPFEVETLCIIWSEFLAFPCAPSKATFSNIMLIDIVA  
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 SMRDVGLIFPLFIVYILFSSAVYFAEDDPTSGSSIPDAFWMAVVTMTVIGDMM  
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 BASE COUNT 279 a 504 c 460 g 308 t  
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 Best Local Similarity 69.7%; Pred. No. 2.8e-81;  
 Matches 913; Conservative 0; Mismatches 378; Indels 18; Gaps 1;

Db 340 GTCAACGTCCCATCGACATCTTCTCCGAGAGATCCGTTTACAGCTGGGCGAGAG 399  
 QY 647 GCCGTGCACAGCCTGCGCGAGAGAGAGGCTGCGCGGTCGCGCGAGCGCCCTGCGC 706  
 Db 400 GCCATGAGAGATTCGCGCGAGAGAGAGGCTTCTGCGGAGAGAGAGCGCGCTGCCC 459  
 QY 707 CGCGCGGCTTCCGCGCGAGAGAGGCTTCTGCGAGTTTCCGAGAGACTTCAGGCC 766  
 Db 460 CGCGCGAGCTTCCAGCGCGAGAGAGGCTGCTCTTGAGAGTACCTGAGACTCTCGGGCCG 519  
 QY 767 GCGCGGCTGCGCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826  
 Db 520 GCGCGGAGATCCCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 579  
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 Db 580 CTCGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639  
 QY 887 GCAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 946  
 Db 640 GTGCTGAGGCGCGCGCGAGAGAGGCTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 692  
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 Db 742 TCCCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801  
 QY 1067 GTGATGAACCTCATGATTTTGGTATCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1126  
 Db 802 ATGATGAACCTCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 861  
 QY 1127 CTGCGCGCGAGAGAGGCTGCGCGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1186  
 Db 862 CTGCGCGAGAGAGAGGCTGCGCGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921  
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 LOCUS AL513469 90458 bp DNA linear HTG 13-JUN-2001  
 DEFINITION Homo sapiens chromosome 1 clone RP1-183f4 map p13.3-21.2, \*\*\*  
 SEQUENCING IN PROGRESS \*\*\*, 4 unordered pieces.  
 ACCESSION AL513469

VERSION AL513469.1 GI:12733823  
KEYWORDS HTG: HTGS\_PHASE1; HTGS\_CANCELLED.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 90458)  
AUTHORS Plumb,B.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone  
requests: clonerequest@sanger.ac.uk  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: dj183f4  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 89137 bases at least Q40  
Consensus quality: 89533 bases at least Q30  
Consensus quality: 89799 bases at least Q20  
Insert size: 90158; sum-of-contigs  
Insert size: 113871; 11.8% error; agarose-fp  
Quality coverage: 5.37x in Q20 bases; sum-of-contigs quality  
coverage: 4.35x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 23486: contig of 23486 bp in length  
\* 23487 23586: gap of 100 bp  
\* 23587 52350: contig of 28764 bp in length  
\* 52351 52450: gap of 100 bp  
\* 52451 55763: contig of 3313 bp in length  
\* 55764 55863: gap of 100 bp  
\* 55864 90458: contig of 34595 bp in length.  
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Best Local Similarity 66.3%; Pred. No. 1.5e-79;  
Matches 983; Conservative 0; Mismatches 473; Indels 26; Gaps 3;

QY 120 GCGGGCGGGGCGGGCGGGGCGAGGGCGGGCGTCCGGCAGAGGGCGGGCGT 179  
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QY 180 GCCCTGTGCGCTCCCGCGCGCGGGGTCAAGTGGCCCGTCCCTGCGGCGTAAAGCCGC 239  
DB 1138 GTGAACACGCGCTAAGGCGAGCCCGCGAGCGCCGACGCTGCGCCGCAATGACCTGT 1197  
QY 240 CTGCGCGCTATTCTTACGCGCGAGACACCGGACACCGGCGTGGGGCGGGCGTGC 299  
DB 1198 GTGCGCGGGGA--CCACTGTGTGAGCGCGAGTGGCGGATGGTGGAGGGCGCCCGCTC 1255  
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DB 1256 AAGCGCGCTGTGGGGGCGGGGCGCGCCACCGCTACGAGCGCGCTCCCTCATGTGCGG 1315  
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DB 2018 ACCGATCGATTTGTGTGCGCATCATTCCTTATTAACATCTGTGGTACGAGCTGGCG 2077  
QY 1134 GCGAGCGAGGGGTGGCGCAGCGCATGTCACTGAGCGCATGTGAGTATCGATTCGAT 1193  
DB 2078 AACGACAGGGCAATGACAGCAGAGCCATGTCTGTGCGCATCTGAGGCTATCGCGCTG 2137  
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RESULT 13  
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 LOCUS HUMKCHAN H.sapiens K+ channel protein (HLK3) complete cds.  
 ACCESSION M85217.1 GI:186664  
 VERSION M85217.1 GI:186664  
 KEYWORDS K+ channel protein; voltage dependent potassium channel.  
 SOURCE Homo sapiens cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3004)  
 AUTHORS Attali,B., Romey,G., Honore,E., Schmid-Alliana,A., Mattei,M.G.,  
 Lesage,F., Ricard,P., Barhanin,J. and Lazdunski,M.  
 TITLE Cloning, functional expression, and regulation of two K+ channels  
 in human T lymphocytes  
 JOURNAL J. Biol. Chem. 267 (12), 8650-8657 (1992)  
 MEDLINE 92235098  
 PUBMED 1373731  
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 Best Local Similarity 70.4%; Pred. No. 1.8e-78;  
 Matches 876; Conservative 0; Mismatches 351; Indels 18; Gaps 1;

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 QY 1011 TTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070  
 Db 850 TCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909  
 QY 1071 TGAACCTGATGATTTTGTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1130  
 Db 910 TGAACCTGATGATTTGCTGCTATCTTATTTATCATCTCTGCGTACCGAGCTGG 969

QY	1131	CCCCGACGAGGGGTGGGGCCAGAGGCGCATGTACGTACGTGGCCATCCGTAGAGATCCGAT	1190
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QY	1191	TGTGTCCGTCTTCCGCACTTTCAAAGCTGTCCCGCACTCAAGAGGCCCTGGCAAAATCTTGG	1250
Db	1030	TGTTAAGGGTCTTCGCGCATCTTCAAGCTGTTCGCGCCACTCCAAAGGGGCTGCAGATCTCG	1089
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QY	1311	GTCGTGCTCTCTTTTCCAGCGCCCGCTCACTTATGGCGAAGTTGACGCGGGGTGACCTCCCAT	1370
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QY	1371	TCATAGCATCTCCGTGAGTCTCTTGTGTGGCGGATGATACCATGCTACAGTTGGCTATG	1430
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QY	1431	GAGACATGTGGCACCCGTCACCTGTGGGTGGGACAGATAGTGGGCTCTCTGTGTCGCATTTGGG	1490
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	RESULT 14
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DEFINITION	Human potassium channel protein (HPCN3) gene, complete cds.
ACCESSION	M5515
VERSION	M5515.1 GI:189672
KEYWORDS	potassium channel protein.
SOURCE	Human DNA.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Phillipson,L.H., Lamendola,J., Bell,G.I. and Steiner,D.F. Genomic sequence of a human potassium channel related to RCK3 1 (sites) 2 (bases 1 to 1820)
AUTHORS	Phillipson,L.H., Hice,R.E., Schaefer,K., Lamendola,J., Bell,G.I., Nelson,D.J. and Steiner,D.F.
JOURNAL	Sequence and functional expression in Xenopus oocytes of a human insulinoma and islet potassium channel
TITLE	Pfroc.Natl. Acad. Sci. U.S.A. 88 (1), 53-57 (1991)
REFERENCE	91095456 1986382
JOURNAL MEDLINE	
PUBMED	
FEATURES	
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gene	
CDS	

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Db	250	CGGGCGGGGGGAGAGAGACTGCTCCGGGGAGCGCGTGTCATCAACATCTCCGGGGCTGC	309		
QY	411	GCTTCGAGACGGCGGGCGGCGACGCTGGGGCCGCTCCCGGACACTGCTGATAGGGACCCAG	470		
Db	310	GCTTCGAGACGACGAGTGAAGACCCCTTTCGCCAGTTCGCCGAGACGCTGCTGGCGGACCCCA	369		
QY	471	CGCGCCCGGGCGCGCTTCACAGCAGCGCGCGCGCGCATATTTCTTCACCGGACCGGAC	530		
Db	370	AGCGGGCGCATAGAGTACTTCGACCCCGTCGCCACAGAGTACTTCTTCACCCGCAACCGGC	429		
QY	531	CCAGCTTCGACGCGCGCTCTACTACTACCAAGTCCGATCGGCGCGCTGCGCGCGCGCGGC	590		
Db	430	CCAGCTTCGACGCGCATCTCTACTACTATCAATGATCCCGGGGGCGCATCCGCGCGCGGTCA	489		
QY	591	ACGTGCGCGCTGAGCTCTCTCTGAGAAAGGTGCGCTTACGCGGCTGGGGCGCGCGCGCC	650		
Db	490	ACGTGCCCATGAGACATTTTCTCCGAGGAGATCCGCTTCTACAGCTGGGCGAGGAGGCCA	549		
QY	651	TGGCAGCGCTCGCGGAGAGAGAGGAGCTCCCGGATCCCGCGAGGCGCCCGTGGCGCGGC	710		
Db	550	TGGAGAACTTCGCGGAGAGACAGAGGCTCTCTGCGGAGAGAGAGCGCGCTTGCGCCCGCC	609		
QY	711	GCGCGCTTCGCGCGCAGCTGTGGCGGCTTTTCGATTTTCCGAGAGCTCTGAGCGCGCGC	770		
Db	610	GCGACTTCAGCGCGAGGTGTGGCGGCTTCGAGTACCCGAGAGCTCCGGGGCGCGGCC	669		
QY	771	GCGTGTGCGCGCTGAGTCTCGCTGCTGATCTCTGCTCATCGTCTCTTCTGCGCTCG	830		
Db	670	GGGGCATCTCGCATGCTGTCTCGCTGCGATCTCATCTGATCTGATCTTCTGCGCTCG	729		
QY	831	AGAGCGCTGCGGACTCCCGGAGACAGCGCGAGCGGAGCGGCGCTTCTCTGACGCGGAG	890		
Db	730	AGAGCGCTGCGGAGTTCGCGGAGACAGAGAGACTACCCCGCTCGACGTCGAGAGACTAT	789		
QY	891	CCGGCGCGGCTTTCGCCGCTCCGCGATGTGACTCCAGCAATGCGCTGGAATCCACGCC	950		
Db	790	TGCAAGGAG-----CCGGCAGCAGCTGGGGGTCCCGCGGAGAG	831		
QY	951	GCTGCGCTTCATGACCCGCTTCTGCTGTGTGAGAGCGCTGTGATTTGTTGGTCTCT	1010		
Db	832	CCCTCAGCTTCTCCGATCCCTTCTCGGTGAGAGACGCTGCAATCATCTGCTTCTCT	891		
QY	1011	TTGAGCTGCTGTGATGCGCTCTGCTGTCTCCAGCAGAGGCTATCTTCTTCAAGAACGTGA	1070		
Db	892	TGCAAGCTGCTGTGTGCGGCTTCTCTCGTGTCTTAGGAAGGACCACTCTTCGAGGAACATCA	951		
QY	1071	TGAACCTCATGATTTTGTGTGCTATCTCTCCCTACTTTGTGTGACACTGGGACCGGAGCTGG	1130		
Db	952	TGAACCTCATGATTTGTGGCATCTCTTATTTTATCACTCTGGGTCCGAGCTGG	1011		
QY	1131	CCCGGACGAGGGGTGGCGAGCAGGCGCATGTCACTGTGCGCATCTTGAAGTCAATCCGAT	1190		
Db	1012	CGGAACGACAGGGGCAATGAGACAGCAGGCGCATGTCTGTGCGCATCTGTGAGGTCATCCGCC	1071		
QY	1191	TGTGTGCTGTCTTCCGATCTTCAAGCTGTCCCGGACTCAAGAGGCGCTGCAATCTTGG	1250		
Db	1072	TGTGTAGGCTTTCGATCTTCAAGCTGTGTGGCGCATTCGAAAGGCGCTGAGATCTCG	1131		



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Db 71511 CTAACTTTAGCTACTTTTACCAACGGGAGACAGAGGGCGAAGAGGCAGGGATGTACAGCC 71452
QY 1590 ATGTGGACATGCAGCCTTGTGSCCACTGGAGGCAAGGCCAATGGGGGCTGTGGACG 1649
    ||||| |||| |||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71451 ATGTGGACACACAGCCCTGGGCTACCTGGAGGCAAGGCTAATGGGGGCTGTGGACT 71392
QY 1650 GGGAGGTACCTGAGCTACCACTCTCACTCTGGGCACCCCGAGGGAACACCTGGTCACCG 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71391 CTGAGGTGCTGAACCTCTCCACACACTCTGGCCCCCTGCAGGGAACACATGTTGACTG 71332
QY 1710 AAGTGTGAGGAACAGTTGAGGTCTGCAGG 1738
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Db 71331 AGGTGTGAGGGTCAACTGGGGTCTCCAGG 71303

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Search completed: February 20, 2003, 09:59:47  
 Job time : 5512.86 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 : Search time 418.075 Seconds  
(without alignments)  
9410.374 Million cell updates/sec

Title: US-09-804-014a-7

Perfect score: 1747

Sequence: 1 gaagcctgattctgacgaaa.....agctctgacgagccacacac 1747

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_101002:\*  
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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1747	100.0	1747	22	AAS13338	Human cDNA encoding
2	1420.2	81.3	1792	24	AAD37899	Human ion channel
3	1333.6	76.3	1686	23	ABL78540	DNA encoding novel
4	1321.6	75.6	1341	24	ABL57038	Human potassium ch
5	1068	61.1	1598	16	AAT04953	Mouse Kv1.7 voltag
6	601.4	34.4	691	24	AAD28734	Human ion channel
7	596.2	34.1	2867	24	ABN95856	Gene #2354 used to
8	596.2	34.1	2867	24	ABL65917	Lung cancer relate
9	588.2	33.7	1836	22	AAH21452	Human Kv1.5 DNA.

10	546	31.3	3147	24	AB199654	Mouse ischaemic co
11	508.6	29.1	994	24	AB019704	Oligonucleotide fo
12	508.6	29.1	994	24	AB019705	Oligonucleotide fo
13	506.6	29.0	994	24	AB019702	Oligonucleotide fo
14	506.6	29.0	994	24	AB019703	Oligonucleotide fo
15	367.4	21.0	7642	24	AB133117	Human immune syste
16	348.2	19.5	7642	24	AB133116	Human immune syste
17	340.4	19.5	8758	24	AB133119	Human immune syste
18	311.4	17.8	2157	22	AAS29512	Human endocrine po
19	311.4	17.8	2159	23	ABR43428	DNA encoding novel
20	303.4	17.4	2237	23	AB113285	Drosophila melanog
21	296.6	17.0	7488	24	AB133113	Human immune syste
22	291.4	16.7	7488	24	AB133112	Human immune syste
23	262.8	15.0	8758	24	AB133118	Human immune syste
24	233.8	13.4	492	22	ABR06356	Human cDNA seq ID
25	233.8	13.4	492	22	AAS28936	cDNA encoding for
26	233.8	13.4	492	22	AAS29636	DNA encoding rena
27	233.8	13.4	492	22	AAS30165	DNA encoding novel
28	233.8	13.4	492	23	ABK43751	Human immune syste
29	228.8	13.1	7500	24	AB133114	Human immune syste
30	215.6	12.3	2064	24	ABR84401	Human Kv4.3 potass
31	215.6	12.3	2072	19	AAV61572	Human Kv potassium
32	215.6	12.3	2104	19	AAV61571	Human Kv potassium
33	215.6	12.3	2121	24	ABR84400	Human Kv4.3 potass
34	213.6	12.2	2578	22	AAH99538	Human protein enco
35	213.6	12.2	2711	22	AAH21246	Human Kv4.1 cDNA.
36	213.2	12.2	3424	20	AAZ11901	Human potassium ch
37	212.4	12.2	2104	19	AAV61573	Human Kv potassium
38	205.2	11.7	1521	24	ABQ49288	Oligonucleotide fo
39	205.2	11.7	1521	24	ABQ49289	Oligonucleotide fo
40	191	10.9	998	22	ABR43164	Human breast cell
41	191	10.9	998	22	ABA53583	Human foetal liver
42	191	10.9	998	22	ABR23338	Human foetal liver
43	191	10.9	998	22	AAK01849	Probe #1804 for ge
44	191	10.9	998	22	AAK27308	Human brain expres
45	191	10.9	998	22	AA111882	Human bone marrow Probe #1815 for ge

#### ALIGNMENTS

RESULT 1	
AAS13338	
ID	AAS13338 standard; cDNA: 1747 BP.
AC	AAS13338;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA encoding NOV4 protein.
XX	
KW	Human: NOV4; ss; cytosolic; neurotrophic; neuroprotective; vulnary;
KW	cerebroprotective; antiparkinsonian; hypotensive; antisthmatic;
KW	antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW	antiatherosclerotic; dermatological; cancer; neurological disorder;
KW	Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW	immune disorder; autoimmune disease; respiratory disorder;
KW	bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW	cell growth regulation disorder; lesional psoriatic skin;
XX	atherosclerosis; abdominal aortic aneurysm.
OS	Homo sapiens.
XX	
FT	key
FT	5'UTR
FT	1..37
FT	Location/Qualifiers
FT	/*tag= a
FT	38..1717
FT	/*tag= b
FT	/*product= "NOV4"
FT	1718..1747
FT	/*tag= c
PN	WO200168851-A2.





Db 1261 TCGGGCTCCATGCGTACGCTGGGCTCCCTCATCTTTTCTCTTCATGCGTGTGCTCT 1320  
QY 1321 CTTTTCACGCGCGCTACTTTGCGAGTTGACGGGGGAGTCCCATTTGCTAGCAT 1380  
Db 1321 CTTTTCACGCGCGCTACTTTGCGAGTTGACGGGGGAGTCCCATTTGCTAGCAT 1380  
QY 1381 CCTGAGTCTTGTGTGGGCGGTAGTACATGACTAGATTTGGCTATGAGACATGGC 1440  
Db 1381 CCTGAGTCTTGTGTGGGCGGTAGTACATGACTAGATTTGGCTATGAGACATGGC 1440  
QY 1441 ACCCGTCACTGTGGGTGGGCAAGATAGTGGGCTCTGTGTGCTCATTTGGCGGCTGCTGAC 1500  
Db 1441 ACCCGTCACTGTGGGTGGGCAAGATAGTGGGCTCTGTGTGCTCATTTGGCGGCTGCTGAC 1500  
QY 1501 TATTTCCCTGCGACGTGCGCTGATTTCTCAATTTACGTAATTTATCACCGGAGAC 1560  
Db 1501 TATTTCCCTGCGACGTGCGCTGATTTCTCAATTTACGTAATTTATCACCGGAGAC 1560  
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Db 1561 AGAGGGCGAAGAGCGTGGGATGTTTCAGCATGTGACATGACGCTTGTGGCCACTGGA 1620  
QY 1621 GGGCAAGGCGCATGGGGGCTGTGTGACGGGAGGTAAGTACCTGACCTTCCACTCTG 1680  
Db 1621 GGGCAAGGCGCATGGGGGCTGTGTGACGGGAGGTAAGTACCTGACCTTCCACTCTG 1680  
QY 1681 GGCACCGCCCGAGGAGACCTGTGTGACGGAAGTGTGAGGAACGTTGAGGTGTGACGAGAC 1740  
Db 1681 GGCACCGCCCGAGGAGACCTGTGTGACGGAAGTGTGAGGAACGTTGAGGTGTGACGAGAC 1740  
QY 1741 CTCACAC 1747  
Db 1741 CTCACAC 1747

## RESULT 2

AAD37899 AAD37899 standard; cDNA; 1792 BP.

AC AAD37899;

DT 10-SEP-2002 (first entry)

DE Human ion channel protein encoding cDNA.

XX Human: novel human protein; NHP; ion channel protein; forensic biology;

KM pharmacogenomic; drug screening; mental disorder; biological disorder;

KM symptomatic manifestation; phenotypic manifestation; medical disorder;

OS gene: ss.

XX Homo sapiens.

FH Key

FT CDS

FT 93..1463

FT /tag= a

FT /product= "Human ion channel protein"

FT /note= "This region is specifically claimed as

FT SEQ ID NO: 1 in claim 1 of the specification"

XX WO200231150-A2.

XX 18-APR-2002.

XX 10-OCT-2001; 2001WO-US31900.

XX 10-OCT-2000; 2000US-239623P.

XX (LEXI-) LEXICON GENETICS INC.

XX Friiddle CJ, Hilbun E, Gerhardt B, Turner CA;

XX WPI; 2002-452348/48.

XX P-PSDB; AAE23655.

DR

XX Novel human ion channel polynucleotide encoding protein sharing  
PT structural similarity with mammalian ion channel proteins, e.g.  
PT potassium channels useful in therapeutic, diagnostic and  
PT pharmacogenomic applications.  
XX  
XX Disclosure; Page 36; 36pp; English.  
XX  
XX The present invention relates to novel human proteins (NHPs), human ion  
CC channel proteins and polynucleotides encoding such proteins. Sequences of  
CC the invention are useful in therapeutic, diagnostic and pharmacogenomic  
CC applications. They are useful for the identification of protein coding  
CC sequences, for mapping a unique gene to a particular chromosome, as  
CC additional DNA markers for restriction fragment length polymorphism  
CC (RFLP) analysis and in forensic biology, for screening libraries,  
CC isolating clones, preparing templates for cloning and sequencing, as  
CC hybridization probes, in microarrays or other assay formats, to screen  
CC collections of genetic material from patients who have a particular  
CC medical condition, to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay. NHPs are useful  
CC for the detection of mutant human proteins or inappropriately expressed  
CC proteins for the diagnosis of disease, for the generation of antibodies,  
CC for screening for drugs effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of the  
CC protein in the body, for identification of other cellular gene products  
CC related to the protein and as reagents in assays for screening for  
CC compounds that can be used as pharmaceutical agents in the therapeutic  
CC treatment of mental, biological or medical disorders and diseases. The  
CC present sequence is a cDNA encoding human ion channel protein.  
XX  
SQ Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other;

Query Match 81.3%; Score 1420.2; DB 24; Length 1792;

Best Local Similarity 99.1%; Pred. No. 3.3e-252;

Matches 1450; Conservative 0; Mismatches 8; Indels 5; Gaps 2;

QY 285 CTGGGGCGGCGGTGCGGGGCGACAGTGTGCTGCGGGTCCCGGGGCTGGCGGCATG 344  
Db 36 CGGGGCGGGGCGTCCGGGCGACACGTGTGCGGGTCCCGGGGCTGGCGGCATG 95  
QY 345 GAGCGGGGTGCGCGCGCGCGCGGTGCGGTGCGGAGGCGGTGCGGAGCGTGGCCG 404  
Db 96 GAGCGGGGTGCGCGCGCGCGCGGTGCGGTGCGGAGGCGGTGCGGAGCGTGGCCG 153  
QY 405 GGCTGGGCTTGCAGACGCGGGGCGCGAGCTGTGGGCGCTTCCGGACACTCTTAGGG 464  
Db 154 GGCTGGGCTTGCAGACGCGGGGCGCGAGCTGTGGGCGCTTCCGGACACTCTTAGGG 213  
QY 465 ACCCAGCGCGCGCGCGCGCTTACGACGAGCGCGCGCGAGTATTTCTTGACCGGC 524  
Db 214 ACCCAGCGCGCGCGCGCGCTTACGACGAGCGCGCGCGAGTATTTCTTGACCGGC 273  
QY 525 ACCGCGCCAGCTTGCAGCGCGCGCTCTACTACAGTCCGGTGGGCGCGCGCGGC 584  
Db 274 ACCGCGCCAGCTTGCAGCGCGCGCTCTACTACAGTCCGGTGGGCGCGCGCGGC 333  
QY 585 CGCGCGACGTGCGCGCGCGCTTCTGAGTGAAGTGGGCTTCTAGAGGCTGGGCGG 644  
Db 334 CGCGCGACGTGCGCGCGCGCTTCTGAGTGAAGTGGGCTTCTAGAGGCTGGGCGG 393  
QY 645 CGGCGCTGGCAGCGCTGCGCGGAGGAGGAGGCTGCGCGCGCGCGCGCGCGCGGC 704  
Db 394 CGGCGCTGGCAGCGCTGCGCGGAGGAGGAGGCTGCGCGCGCGCGCGCGCGCGGC 453  
QY 705 CGGCGCGCGCTTGCAGCGCGCGAGTGTGCTTTTGAATTTCCGAGAGCTCAGG 764  
Db 454 CGGCGCGCGCTTGCAGCGCGCGAGTGTGCTTTTGAATTTCCGAGAGCTCAGG 513  
QY 765 CGGCGCGCGCTGCGCGCGAGTGTGCTGCTGATCTCTGCTGCTGCTGCTCTTCT 824  
Db 514 CGGCGCGCGCTGCGCGCGAGTGTGCTGCTGATCTCTGCTGCTGCTGCTCTTCT 573  
QY 825 GCTCGAGAGCTGTGCTGCTGCTGCGAGACCGCGGCGAGCGGCGCTGCTGCGAG 884

D	574	GCCTGAGAGAGCTGCTGAGCTTCGCGAGACACCGGACCGGAGCGGGGCTTGGTGTGCTGACG	633
Q	885	CCGCAAGCCGGCCGGGTGTTCCCGGCTCCGCTGAATGGCTCCAGCCAAATGCTCGAATC	944
D	634	CCGGACGGCGGGCC---GTTCCCGGCTGCGGTGAATGGCTCCAGCCAAATGCGCTGGAAATC	690
Q	945	CACCCGCGCTCCCTTCGAATGACCCGCTTCGAGGGGAGGAGCGTGTGATTTGTTGGT	1004
D	631	CACCCCGCTCCCTTCGAATGACCCGCTTCGAGGGGAGGAGCGTGTGATTTGTTGGT	750
Q	1005	TCTCCTTTGAGCTCTGTGTAGCGCTCCGTGCTGTGTCCAAAGACGCTATCTTTCACAA	1064
D	751	TCTCCTTTGAGCTCTGTGTAGCGCTCCGTGCTGTGTCCAAAGACGCTATCTTTCACAA	810
Q	1065	ACGTGATGAACTTATGATTTTGTGGCTATCCTTCCCTACTTTGTGGCACTGGCACCG	1122
D	811	ACGTGATGAACTTATGATTTTGTGGCTATCCTTCCCTACTTTGTGGCACTGGCACCG	870
Q	1125	AGCTGGCCCGGACAGAGGGGTGGGCGACAGGACCAATGTACTAGGGCACTCTGAGAGTCA	1184
D	871	AGCTGGCCCGGACAGAGGGGTGGGCGACAGGACCAATGTACTAGGGCACTCTGAGAGTCA	930
Q	1185	TCCGATTTGTCGTGTCTTCCGACTCTTCAAGCTGTCCGGCACTCAAAAGGCGTGCAAA	1244
D	931	TCCGATTTGTCGTGTCTTCCGACTCTTCAAGCTGTCCGGCACTCAAAAGGCGTGCAAA	990
Q	1245	TCTTGGGGCAGACGCTTCGGGCGCTCCATGGGTGAGGTGGGCGCTCCCATCTTTTCTCT	1304
D	991	TCTTGGGGCAGACGCTTCGGGCGCTCCATGGGTGAGGTGGGCGCTCCCATCTTTTCTCT	1050
Q	1305	TCATGCGTGTGTCTCTTTTCCAGCGCGCTCTACTTTTGGCGAAGTTGACCGGGGTGACT	1364
D	1051	TCATGCGTGTGTCTCTTTTCCAGCGCGCTCTACTTTTGGCGAAGTTGACCGGGGTGACT	1110
Q	1365	CCCATTTTCATGAGATCCCTGAGTCCCTTGTGGGGCGGTAGTACACATGACTACAGTTGG	1422
D	1111	CCCATTTTCATGAGATCCCTGAGTCCCTTGTGGGGCGGTAGTACACATGACTACAGTTGG	1170
Q	1425	GCTATGAGAGATGGACCCGCTCACTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCCA	1484
D	1171	GCTATGAGAGATGGACCCGCTCACTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCCA	1230
Q	1485	TTTGGGGGCTGTACTATTTTCCCTGCGCATGCGCCGCTCATTTGTCTCCAAATTCAGCTACT	1544
D	1231	TTTGGGGGCTGTACTATTTTCCCTGCGCATGCGCCGCTCATTTGTCTCCAAATTCAGCTACT	1290
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D	1291	TTTATACACCGGGAAGACAGAGGGCGCAAGAGCTGGAGTTTCACCACTATGTGACATGCACG	1350
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Q	1665	TACACGCTCCACTGTGGGCAACCCCGGAGAAACCTGGGCAACCGAAGTGTAGGAAACG	1724
D	1411	TACACGCTCCACTGTGGGCAACCCCGGAGAAACCTGGGCAACCGAAGTGTAGGAAACG	1470
Q	1725	TTTGAAGTCTGCAGGACCTCACAC	1747
D	1471	TTTGAAGTCTGCAGGACCTCACAC	1493
RESULT 3			
AAS78540			
ID	AAS78540 standard; cDNA; 1686 BP.		
XX	AAS78540;		
XX	13-FEB-2002 (first entry)		
DE	DNA encoding novel human diagnostic protein #14344.		

QY 525 ACCGCCCCAGCTTGGAGCGCGCTGCTACTACTACCAAGTCGCGGTGGCGGCTGGCGGC 584  
 DB 560 ACCGCCACAGCTTGGAGCGCGCTGCTACTACTACCAAGTCGCGGTGGCGGCTGGCGGC 619  
 QY 585 GCGCGACAGCTGCGCGCTGAGCTCTCTGGAAGAGTGGCTTCTACGGCTGGCGCGG 644  
 DB 620 GCGCGACAGCTGCGCGCTGAGCTCTCTGGAAGAGTGGCTTCTACGGCTGGCGCGG 679  
 QY 645 GCGCGCTGGAGCGCTGCGCGGAGAGAGGGCTGCGCGGTGGCGCGCGCGCGCTGC 704  
 DB 680 GCGCGCTGGAGCGCTGCGCGGAGAGAGGGCTGCGCGGTGGCGCGCGCGCGCTGC 739  
 QY 705 CCGCGCGCGCTTGGCGCGCGAGCTGAGCTGCTCTTTCGAGTTTCCGAGAGCTTTCAGG 764  
 DB 740 CCGCGCGCGCTTGGCGCGCGAGCTGAGCTGCTCTTTCGAGTTTCCGAGAGCTTTCAGG 799  
 QY 765 CCGCGCGCGCTGCGCGCTGAGCTCTCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 824  
 DB 800 CCGCGCGCGCTGCGCGCTGAGCTCTCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 859  
 QY 825 GCTTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884  
 DB 860 GCTTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 919  
 QY 885 CCGCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944  
 DB 920 CCGCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 976  
 QY 945 CACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004  
 DB 977 CACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1036  
 QY 1005 TCTCTTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064  
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 QY 1065 ACCTGATGAACCTCATGATTTTGTGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1124  
 DB 1097 ACCTGATGAACCTCATGATTTTGTGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1156  
 QY 1125 AGCTGGCGCGCGAGCGAGGGGTGGCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1184  
 DB 1157 AGCTGGCGCGCGAGCGAGGGGTGGCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216  
 QY 1185 TCGGATTTGGGTGGGTCT 1244  
 DB 1217 TCGGATTTGGGTGGGTCT 1276  
 QY 1245 TCTTGGGCGAGAGCTTGGCGCTTCCATGAGCTGAGCTGGGCTCTCTCTCTCTCTCTCTCT 1304  
 DB 1277 TCTTGGGCGAGAGCTTGGCGCTTCCATGAGCTGAGCTGGGCTCTCTCTCTCTCTCTCTCT 1336  
 QY 1305 TCATCGGTGTGCT 1364  
 DB 1337 TCATCGGTGTGCT 1396  
 QY 1365 CCGATTTCACTACATCCCTGAGTCTCTCTGCTGGGAGTACCATACATACATG 1424  
 DB 1397 CCGATTTCACTACATCCCTGAGTCTCTCTGCTGGGAGTACCATACATACATG 1456  
 QY 1425 GCTATGAGAGCATGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1484  
 DB 1457 GCTATGAGAGCATGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1516  
 QY 1485 TTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1544  
 DB 1517 TTTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1576  
 QY 1545 TTTATACCGGAG 1604  
 DB 1577 TTTATACCGGAG 1636  
 QY 1605 CTGTGTGCCACATGAGAGGAGGCAATGGGGGCTGTGTGAGAGGGAG 1654

DB 1637 CTTGTGCGCCACATGAGAGGAGGCAATGGGGGCTGTGTGAGAGGGAG 1686  
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 ID ABL57038 standard; cDNA; 1341 BP.  
 AC ABL57038;  
 DT 22-JUL-2002 (first entry)  
 DE Human potassium channel 12189 partial cDNA.  
 XX  
 KW potassium channel; ion transport; 12189; nootropic; anticonvulsant;  
 KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;  
 KW antidepressant; antimanic; tranquilizer; anorectic; antimigraine;  
 KW antiarteriosclerotic; vasotropic; vulnery; antiarrhythmic;  
 KW cardiatic; antiinflammatory; cytosatic; osteopathic; hepatotropic;  
 KW antidiabetic; immunosuppressive; antiarthritic; antirheumatic;  
 KW antipsoriatic; antihypertoid; antilucer; dermatological; antianemic;  
 KW antistimatic; antiallergic; ophthalmological; immunomodulator;  
 KW analgesic; virucide; human; gene therapy; gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key location/Qualifiers  
 FT 1..1341  
 FT /\*tag- a  
 FT /product- "12189"  
 FT /partial  
 FT /note= "The CDS does not include a start codon"  
 XX  
 PN W0200194390-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PE 06-JUN-2001; 2001MO-US18340.  
 XX  
 PR 06-JUN-2000; 2000US-209845P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Curtis RAJ;  
 DR WPI; 2002-401589/43.  
 DR P-PDB; ABB76166.  
 XX  
 PT New potassium channel family member polypeptide and polynucleotide,  
 PT useful for diagnosing, treating viral diseases, neurological, cardiac,  
 PT cellular proliferative or differentiative, bone, immune, liver and  
 PT metabolic disorders -  
 XX  
 PS Claim 1; Page 135-136; 158pp; English.  
 XX  
 CC The present sequence is that of a partial cDNA for human 12189  
 CC (see ABB76166), a novel potassium channel family member. 12189  
 CC contains a potassium channel tetramerisation domain, an ion  
 CC transport protein domain and a core membrane region including 6  
 CC transmembrane domains. The invention provides human potassium  
 CC channel 52906, 33408 and 12189 nucleic acids and proteins, as well  
 CC as antisense nucleic acid molecules, recombinant expression vectors,  
 CC host cells, transgenic animals, fusion proteins, antigenic peptides,  
 CC and antibodies. Also claimed are: a method for detecting the  
 CC presence of a 52906, 33408 or 12189 nucleic acid; a method for  
 CC modulating the activity of a 52906, 33408 or 12189 polypeptide using  
 CC a compound that binds the polypeptide; a method for identifying a  
 CC compound which modulates the activity of the polypeptide; a method  
 CC of treating or preventing an ion flux-related disorder using an  
 CC agent that modulates the activity or expression of a 52906 or  
 CC 12189 polypeptide or nucleic acid, especially a peptide,  
 CC phosphopeptide, small molecule, antibody, antisense molecule,  
 CC ribozyme, a triple helix molecule, or a 52906 or 12189 nucleic

acid. The ion flux-related disorders include: potassium channel associated disorders, such as neurological disorders and central nervous system disorders such as cognitive and neurodegenerative disorders e.g. Alzheimer's disease, Parkinson's disease, senile dementia, Huntington's disease, Gilles de la Tourette's syndrome, multiple sclerosis, progressive supranuclear palsy, epilepsy, Jacob-Creutzfeldt disease, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders such as depression, schizophrenia, mania, anxiety disorders or phobic memory loss, learning or memory disorders, amnesia or age-related memory loss, attention deficit disorder, obsessive-compulsive disorder, migraine or obesity; cardiac-related disorders such as arteriosclerosis, ischemia reperfusion injury, restenosis, arterial inflammation, tachycardia, congestive heart failure, myocardial infarction and arrhythmia. The polypeptides and nucleic acids are also useful as diagnostic targets and therapeutic agents for: controlling cellular proliferative and/or differentiative disorders e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma; disorders associated with bone metabolism such as osteoporosis, rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic hypercalcaemia; immune disorders such as autoimmune disorders, diabetes mellitus, arthritis, including rheumatoid arthritis, osteoarthritis and psoriatic arthritis, multiple sclerosis, myasthenia gravis, autoimmune thyroiditis, ulcerative colitis, psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma, allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease, chronic active hepatitis, autoimmune uveitis, scleroderma; liver disorders including storage disorders such as Gaucher's disease, glycogen storage disease, haemochromatosis and porphyria; disorders; viral diseases; pain; or metabolic disorders such as obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.

Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Query Match 75.6%; Score 1321.6; DB 24; Length 1341;

Best Local Similarity 99.5%; Pred. No. 4.3e-234; Matches 1337; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

374 TGTGCGAGCGGCTGTGCTCAACGTGGCCGCGCTTTCGAGACGGGCGGACG 433  
 1 TGTGCGAGCGGCTGTGCTCAACGTGGCCGCGCTTTCGAGACGGGCGGACG 60  
 434 CTGGGGCGCTTCCCGGACACTCTGTAGGAGCCAGCGCGCGCGCTTCTACAC 493  
 61 CTGGGGCGCTTCCCGGACACTCTGTAGGAGCCAGCGCGCGCGCTTCTACAC 120  
 494 GACCGCGCGCGAGTATTTCTTGACCGGACCGCCACCTTGAGCGCGCTGTAC 553  
 121 GACCGCGCGCGAGTATTTCTTGACCGGACCGCCACCTTGAGCGCGCTGTAC 180  
 554 TACTACAGTCCGCTGGGCGGCTGGCGCGCGGCGACGTCGCGCTTCTCTG 613  
 181 TACTACAGTCCGCTGGGCGGCTGGCGCGCGGCGACGTCGCGCTTCTCTG 240  
 614 GAAAGGTGGCTTCTACGGGCTGGGCGCGCGGCGCTGGGACGCTTCGCGAGAGAG 673  
 241 GAAAGGTGGCTTCTACGGGCTGGGCGCGCGGCGCTGGGACGCTTCGCGAGAGAG 300  
 674 GCGTGGCGGCGAGTGG 733  
 301 GCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTGG 360  
 734 CTGCTTTTCAGTTTCCCGAGAGCTCTACGCGCGCGCGCTGCGCGTATCTCCGTG 793  
 361 CTGCTTTTCAGTTTCCCGAGAGCTCTACGCGCGCGCGCTGCGCGTATCTCCGTG 420  
 794 CTGCTTTTCAGTTTCCCGAGAGCTCTACGCGCGCGCGCTGCGCGTATCTCCGTG 853  
 421 CTGCTTTTCAGTTTCCCGAGAGCTCTACGCGCGCGCGCTGCGCGTATCTCCGTG 480  
 854 GACCGCGCGCGAGGCGCTGCTGCGACGCGCGCGCGCGCGCGCGCGCGCGTCCGCG 913  
 481 GACCGCGCGCGAGGCGCTGCTGCGACGCGCGCGCGCGCGCGCGCGCGCGTCCGCG 537

914 CTGAATGGCTCCAGCAAAATGCTGGAATCCACCCGCTGCCCTTCATGACCCGCTTC 973  
 538 CTGAATGGCTCCAGCAAAATGCTGGAATCCACCCGCTGCCCTTCATGACCCGCTTC 597  
 974 TTGCTGTGGAGAGCGCTGTATTTGTTGGTTCCTTTGAGCTGCTGTACGCTCTG 1033  
 598 TTGCTGTGGAGAGCGCTGTATTTGTTGGTTCCTTTGAGCTGCTGTACGCTCTG 657  
 1034 GTCTGTCCCAACCAAGGCTATTTCTTCAGAACGATGATGATGATTTGTGGCT 1093  
 658 GTCTGTCCCAACCAAGGCTATTTCTTCAGAACGATGATGATGATTTGTGGCT 717  
 1094 ATCTTCCCTACTTTTGGGCACTGGGACCGAGCTGGCCGCGAGGAGGCTGGCCAG 1153  
 718 ATCTTCCCTACTTTTGGGCACTGGGACCGAGCTGGCCGCGAGGAGGCTGGCCAG 777  
 1154 CAGGCAATGTACTGTGGCATCTCTGAGAGTATCCGATTTGGTGTCTTCCGATCTTC 1213  
 778 CAGGCAATGTACTGTGGCATCTCTGAGAGTATCCGATTTGGTGTCTTCCGATCTTC 837  
 1214 AAGCTGTCCGCGCACTCAAAAGGCGCTGGAATCTTGGGCGAGAGCTTGGGCGCTCATG 1273  
 838 AAGCTGTCCGCGCACTCAAAAGGCGCTGGAATCTTGGGCGAGAGCTTGGGCGCTCATG 897  
 1274 CGTAGGCTGGGCTCTCATCTTTTCTCTTCATCGGTGTGTCTTCTTTCAGAGCGCC 1333  
 898 CGTAGGCTGGGCTCTCATCTTTTCTCTTCATCGGTGTGTCTTCTTTCAGAGCGCC 957  
 1334 GTCTACTTTCGCGAAGTTGACCGGGGTGAGCTCCCATTTACATACCTCCGATCTCTG 1393  
 958 GTCTACTTTCGCGAAGTTGACCGGGGTGAGCTCCCATTTACATACCTCCGATCTCTG 1017  
 1394 TGTGTGGCGGTAGTCACCATGATGATGATGATGATGATGATGATGATGATGATGATG 1453  
 1018 TGTGTGGCGGTAGTCACCATGATGATGATGATGATGATGATGATGATGATGATGATG 1077  
 1454 GGTGTGCAAGATATGAGGCTCTGTGTGTCATGTCGCGGCGGTGACTATTTCCCTGCA 1513  
 1078 GGTGTGCAAGATATGAGGCTCTGTGTGTCATGTCGCGGCGGTGACTATTTCCCTGCA 1137  
 1514 GTGCGCGCTGATTTCTCCAAATTTGACGTAATTTATACCGGGAGACAGAGGGGAAAG 1573  
 1138 GTGCGCGCTGATTTCTCCAAATTTGACGTAATTTATACCGGGAGACAGAGGGGAAAG 1197  
 1574 GCTGGGATGTTCAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1633  
 1198 GCTGGGATGTTCAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257  
 1634 GGGGGGCTGTGTGACGGGAGGTAAGTACCTGACCTTCCATCTGTGGGACACCCCAAG 1693  
 1258 GGGGGGCTGTGTGACGGGAGGTAAGTACCTGACCTTCCATCTGTGGGACACCCCAAG 1317  
 1694 GAACACCTGTGTACCGAAGTGA 1717  
 1318 AACACCTGTGTACCGAAGTGA 1341

# RESULT 5

AAT04953 standard; cDNA; 1598 BP.

AAT04953;

11-Apr-1996 (first entry)

Mouse Kv1.7 voltage-gated potassium channel coding sequence.

Mouse Kv1.7 voltage-gated potassium channel; insulin antagonist drug screening; insulin agonist drug screening;

non-insulin-dependent diabetes mellitus; ds.

Mus musculus.

XX	Key	Location/Qualifiers
FH	CDS	1..1598
FT		/*tag= a
FT		/note="specification states sequence is 1599.
FT		Incomplete stop codon given"
XX		
PN	MO9523858.A1.	
XX		
PD	08-SEP-1995.	
XX		
PE	23-FEB-1995; 95MO-US02221.	
XX		
DR	WPI: 1995-320573/41.	
DR	P-PSDB: AAR82937.	
XX		
PT	New voltage-gated potassium channel gene - used to identify	
PT	material(s) which can increase insulin release e.g. for treating	
PT	non-insulin dependent diabetes mellitus.	
XX		
PS	Claim 1; Page 22-23; 38pp; English.	
XX		
CC	The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-	
CC	gated potassium channel. It may be used in drug screening for	
CC	identification of therapeutics which modulate the channel and,	
CC	therefore, modulate insulin secretion. Selective antagonists	
CC	increase insulin release and thereby reduce hyperglycaemia	
CC	associated with non-insulin-dependent diabetes mellitus.	
XX		
SQ	Sequence 1598 BP: 232 A; 521 C; 502 G; 343 T; 0 other;	
	Query Match 61.1%; Score 1068; DB 16; Length 1598;	
	Best Local Similarity 81.5%; Pred. No. 1.8e-187;	
	Matches 1288; Conservative 0; Mismatches 280; Indels 12; Gaps	
QY	137 CGGGGCAAGGCGAGGGGCGCTCCGGGAGAGGCGCGCGTCCCTGTGCGCCCTCCGC	196
DB	31 CGGAAAGCGCGGTGGCAGTGTTCACAGAGTGGAAAGGAGGCGCCCTAGC	90
QY	197 CCGCGGGGGTTCACAGTGCCTCCCTCCCTCCGCGCTAGCGCCCTGCGCGGCTATTATTC	256
DB	91 CCGCGGGGGTTCACAGTGCCTCCCTCCCTCCGCGCTAGCGCCCTGCGCGGCTATTATTC	150
QY	257 GCGCGAGACCGGAGACCGGAGACCGGCGCTGGGGGCGGGGAGCCACAGTGGTTC	316
DB	151 ACCCGCGACACCGGAGACCGGAGACCGGCGCTGGGGGCGGGGAGCCACAGTGGTTC	210
QY	317 GCGGGTGCAGGGGGCTGGCGCGCCATGAGAGCGCGGTCGCCGCCCTGCGCGTGC	376
DB	211 ACCGGTGCAGGGGGCTGGCGCGCCATGAGAGCGGTCGCCGCCCTGCGCGTGC	267
QY	377 TGGCAGCGGGTGTGCTCAACGTGGCGCGGCTGTGCTTGAACCGGCGCGGACGCTG	436
DB	268 TGGCAGCGGGTGTGCTCAACGTGGCGCGGCTGTGCTTGAACCGGCGCGGACGCTG	327
QY	437 GCGCGCTTCGCGGACACTGTCTAGGGGAGCCAGGCGCGCGCGCGGCTTACGACGAC	496
DB	328 GCGCGCTTCGCGGACACTGTCTAGGGGAGCCAGGCGCGCGCGGCTTACGACGAC	387
QY	497 GCGCGCGCGAGTATTCTTCGACCGGAGACCGGCGCGGCTTACGACGCGGCTTACTAC	556
DB	388 GCGCGCGCGAGTATTCTTCGACCGGAGACCGGCGCGGCTTACGACGCGGCTTACTAC	447
QY	557 TACCAAGTCCGGTGGGCGGCTGGCGGGCGCGGCGGACGTCCGCTGAGCTCTTCTGAA	616
DB	448 TACCAAGTCCGGTGGGCGGCTGGAGCGCGCGGCGGACGTCCGCTGAGCTCTTCTGAG	507

[illegible]







PN W0200194629-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 30-MAY-2001; 2001MO-US10638.  
 XX  
 PR 05-JUN-2000; 2000US-209473P.  
 PR 05-JUN-2000; 2000US-209531P.  
 PR 18-SEP-2000; 2000US-23133P.  
 PR 18-SEP-2000; 2000US-233617P.  
 PR 20-SEP-2000; 2000US-234009P.  
 PR 20-SEP-2000; 2000US-234034P.  
 PR 20-SEP-2000; 2000US-234052P.  
 PR 22-SEP-2000; 2000US-234509P.  
 PR 22-SEP-2000; 2000US-234567P.  
 PR 25-SEP-2000; 2000US-234923P.  
 PR 25-SEP-2000; 2000US-234924P.  
 PR 25-SEP-2000; 2000US-235077P.  
 PR 25-SEP-2000; 2000US-235082P.  
 PR 25-SEP-2000; 2000US-235134P.  
 PR 25-SEP-2000; 2000US-235280P.  
 PR 26-SEP-2000; 2000US-235637P.  
 PR 26-SEP-2000; 2000US-235638P.  
 PR 27-SEP-2000; 2000US-235711P.  
 PR 27-SEP-2000; 2000US-235720P.  
 PR 27-SEP-2000; 2000US-235840P.  
 PR 27-SEP-2000; 2000US-235863P.  
 PR 28-SEP-2000; 2000US-236028P.  
 PR 28-SEP-2000; 2000US-236032P.  
 PR 28-SEP-2000; 2000US-236033P.  
 PR 28-SEP-2000; 2000US-236034P.  
 PR 28-SEP-2000; 2000US-236109P.  
 PR 28-SEP-2000; 2000US-236111P.  
 PR 29-SEP-2000; 2000US-236842P.  
 PR 29-SEP-2000; 2000US-236891P.  
 PR 02-OCT-2000; 2000US-237112P.  
 PR 02-OCT-2000; 2000US-237113P.  
 PR 02-OCT-2000; 2000US-237278P.  
 PR 02-OCT-2000; 2000US-237294P.  
 PR 02-OCT-2000; 2000US-237295P.  
 PR 02-OCT-2000; 2000US-237316P.  
 PR 02-OCT-2000; 2000US-237425P.  
 PR 03-OCT-2000; 2000US-237588P.  
 PR 03-OCT-2000; 2000US-237604P.  
 PR 03-OCT-2000; 2000US-237606P.  
 PR 03-OCT-2000; 2000US-237608P.  
 PR 01-NOV-2000; 2000US-244867P.  
 PR 01-NOV-2000; 2000US-245084P.  
 XX  
 PA (AVAL-) AVALON PHARM.  
 XX  
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Sopet DR, Weaver Z;  
 XX  
 DR WPI; 2002-188264/24.  
 XX  
 PT Screening for anti-neoplastic agent involves exposing cells to a  
 PT chemical agent to be tested for anti-neoplastic activity, and  
 PT determining a change in expression of a gene of a signature gene set -  
 XX  
 PS Claim 1; SEQ ID 4254; 44pp; English.  
 XX  
 CC The present invention describes a method (M1) for screening for an  
 CC anti-neoplastic agent. The method involves exposing cells to a chemical  
 CC agent to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening  
 CC an anti-neoplastic agent, and can be used for producing a product which  
 CC is the data collected with respect to the anti-neoplastic agent as a  
 CC result of M1, and the data is sufficient to convey the chemical

CC structure and/or properties of the agent. M1 can be used in the  
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 CC carcinoma, papillary carcinoma and Wilms' tumour.  
 XX  
 SQ Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;  
 Query Match 34.1%; Score 596.2; DB 24; Length 2867;  
 Best Local Similarity 68.6%; Pred. No. 9,7e-101;  
 Matches 873; Conservative 0; Mismatches 358; Indels 42; Gaps 2;  
 QY 347 GCCGCGGTGCCCGCCCGCCGCTGCTGCGAGCGCTGTCTCAACGTCGGG 406  
 DB 553 GACCAGGCTCTGGGACGCGGCTCCCTGACACACAGCGGCGTCACATCAATCTCCGG 612  
 QY 407 CTGGCTTCGAGACGGGGGCGGACCGCTGGCGCTCCCGGACACTCTGCTAGGAG 466  
 DB 613 CTGGCTTTTGAAGCAGCTGGGACCCAGCGAGTTCCCAACACACTCTGGGGG 672  
 QY 467 CCAGCGCGCGCGCGCGCTTCTACGACGAGCGCGCGGAGTATTTCTTGACCGGAC 526  
 DB 673 CCCGCAAGCGCGCTGCGCTACTTGACCCCTGAGAACGAGTACTTTCGACCGCAC 732  
 QY 527 CGGCGCAGCTTCGACGCGGCTGCTACTACTACAGTCCGGTGGCGGCGGCGCG 586  
 DB 733 CGGCCAGCTTCGACGAGTATCTCTACTACTACAGTCCGGGGCGCGCTGCGGAGCGG 792  
 QY 587 GCGCAGCTGCGCTGACGCTCTCTCTGGAAGAGTGGCTTTCTTACGAGGCTGGCGG 646  
 DB 793 GTCAACGCTTCCCTGAGAGGTTCTGCGAGAGTATCTTACGAGTGGGGAGAG 852  
 QY 647 GCCCTGCGACGCGCTGCGCGAGAGAGAGGCGCGCGCTGCGCGCGCGCGCGCTGCC 706  
 DB 853 GCCATGAGCGCGCTTGGCGGAGATGAGAGGCTTCACTTAAGAAAGAGAGAGCCCTGTC 912  
 QY 707 CGCGCGCTTTCGCGCGCGCAGCTGTGCTCTTTCAGATTTCCGAGAGCTCTCAGGCC 766  
 DB 913 CGCAACGAGTTCCAGCGCGCAGGTGTGCTTATCTTTCAGATTCGAGAGCTCTGCGTGC 972  
 QY 767 GCGCGCTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826  
 DB 973 GCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032  
 QY 827 CTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886  
 DB 1033 TTGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092  
 QY 887 GCAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925  
 DB 1093 CACGAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 1152  
 QY 926 AGCCAAATGCTGGAATTCACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985  
 DB 1153 GGCCTACGGTGGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212  
 QY 986 ACGCTGTATTTTGGTCTCTCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045  
 DB 1213 ACCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272  
 QY 1046 AAGCTATCTTCTTCAAGAACGTGATGACCTGATTTTGGCTATCTTCCCTAC 1105  
 DB 1273 AAGCAGAGGTTCTCCGAGACATCATGATATCATGATGAGGCTGCTGCTGCTGCTGCTG 1332  
 QY 1106 TTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150  
 DB 1333 TTCAATCCCTTGGGACCGAAGTGGAGAGCAGAGCAGGAGGAGGAGGAGGAGGAGGAGG 1392  
 QY 1151 -----CAGCAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204  
 DB 1393 AATGGGACGAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452







Db 2398 CCGGGGACAGACCCCTAAAGCTATGAGGGAGTGGGCTGCATCTTTTCCCTT 2457  
 QY 1306 CACGGTGTGCTCTTTTCCAGGCCGCTACTTTGCCAGTTGACCGGTGACATC 1365  
 Db 2458 CATTGGGTCATCTTTTTCAGCCAGTACTTGGGAGCGGAGAACCTACTATC 2517  
 QY 1366 CCATTTCATGACATCCCTGAGTCTTGTGGGCGGTAGTACCATGACTACATGG 1425  
 Db 2518 GCACCTCTCCAGTATCCCGATCTTGTGGGCGGTGTCCATGACCATGTTGG 2577  
 QY 1426 CTATGGAGCATGACCCCTGACTGTGGGTGCAAGATAGTGGCTCTGTGTCCAT 1485  
 Db 2578 ATACGGTGAATGATCCCTGTGACATTTGAGGCAAGATCGTGGCTCTGTGTCCAT 2637  
 QY 1486 CGCTGGTGTGCTGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545  
 Db 2638 CGCTGGTGTGCTGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2697  
 QY 1546 TTATCACCGGAGACAGAGGCGGAGAGGCTGGATGTTTCAAGCATGT 1593  
 Db 2698 CTACCCAGAGAACTGAGGGGAGAGAGGCTGCTGCTGCTGCTGCT 2745  
 RESULT 11  
 ID ABQ19704 standard; DNA; 994 BP.  
 XX ABQ19704;  
 AC ABQ19704;  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.  
 XX  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PE 01-SEP-2001; 2001WO-EP10074.  
 XX  
 PR 01-SEP-2000; 2000DE-1043826.  
 PR 05-SEP-2000; 2000DE-1044543.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Plepenbrock C, Berlin K, Guelzig D;  
 DR WPI; 2002-371829/40.  
 PT Determining the degree of cytosine methylation in genomic DNA, useful  
 PT for diagnosis and prognosis, comprises selective hybridization of  
 PT amplicons from chemically treated DNA  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
 XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one  
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
 CC and the degree of hybridisation to both classes is determined from the  
 CC label on the amplicon. From the ratio of labels hybridised to the two  
 CC classes of oligomers, the degree of methylation is calculated. The method  
 CC is used: (i) for diagnosis and/or prognosis of side effects of

CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
 CC systems etc., particularly by detecting mutations or single nucleotide  
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue  
 CC types and for investigating cell differentiation. The method allows the  
 CC methylation status of many C residues to be determined simultaneously.  
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
 CC method for determining the degree of cytosine methylation described in  
 CC the disclosure of the invention.  
 XX  
 SQ Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;  
 Query Match 29.1%; Score 508.6; DB 24; Length 994;  
 Best Local Similarity 74.3%; Pred. No. 1.2e-84;  
 Matches 705; Conservative 0; Mismatches 194; Indels 50; Gaps 3;  
 QY 1 GAAGCTGATTTGACGAAACACACGACGCAAGAAATGAGAGACGACAGCATC 60  
 Db 33 GAAGTTGATTTTACGAAATATACGATATACGAAATTTGAGAGACGATGATGAT 92  
 QY 61 CCGGCGGCAAG 120  
 Db 93 TCGGCGGTAG 152  
 QY 121 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 Db 153 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212  
 QY 181 CCCTGTGCGCCCTCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 Db 213 TTTTGTGCTTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 272  
 QY 241 TCGCGGCGCTA-TTTTACGCGCGGAGACCGGACCGGACCGGCGGCGGCGGCGG 295  
 Db 273 TGTGCGGTATTTTACGCGCGGAGATATCGATATCGGATATCGGATATCGGAT 332  
 QY 296 -----GTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 312  
 Db 333 CCGGCGGTCAGAGCGGTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392  
 QY 313 GTTTCGGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372  
 Db 393 GTTTCGGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG -TCGTCG 450  
 QY 373 CTCTCTGCGAGCGGCTGCTCAACGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 432  
 Db 451 TTGTTTCGAGCGGCTGCTTAAACGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 510  
 QY 433 GCTGGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 492  
 Db 511 GTTGGGCGGTTTTCGATATTTTGTAGGGGATTTAGCGCGGCGGCGGCGGCGGCGG 570  
 QY 493 CGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 552  
 Db 571 CGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 630  
 QY 553 CTACTACAGTCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 612  
 Db 631 TTATTTATTTAGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 690  
 QY 613 GGAAGAGGTGGCTTCTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 672  
 Db 691 GGAAGAGGTGGTTTTCAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750  
 QY 673 GGGCTCCCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732  
 Db 751 GGGTTGTTGGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 810  
 QY 733 GCTGCTTTTCGATTTTCGAGAGCTCAGAGCGGCGGCGGCGGCGGCGGCGGCGG 792  
 Db 811 GTTGTTCGATTTTCGAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAG 870  
 QY 793 GCTGTATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 852





PR 05-SEP-2000; 2000DE-1044543.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

Sequence 994 BP; 359 A; 354 C; 152 G; 129 T; 0 other;

Query Match	29.08%	Score 506.6;	DB 24;	Length 994;
Best Local Similarity	74.28%	Pred. No. 2.7e-84;		
Matches 703; Conservative	0;	Mismatches 194;	Indels 50;	Gaps 3

[illegible]

OY	434	CTGGGCGCTTCCGGACACTCTCTAGGGAGCCAGCGCGCGCCCTTCTACGAC	499
Db	512	CTAAACCCCTTCCGGACACTCTCTAAAAAACCCAAAGCGCGCGCTTCTACGAC	571
OY	494	GACGGCGCGCGAGATATTTCTTGACCGGACCGGCCAGCTTGCAGCGCTCTAC	555
Db	572	GACCGCGCGCGAGATATTTCTTGACCGGACCGGCCAGCTTGCAGCGCTCTAC	631
OY	554	TACTACAGTCCGGATGGGGCGCTCGCGCGCGCGCGACGCGCGCTGCGAGCTTCTG	613
Db	632	TACTACCAATCCGATTAAACGACTACGACGACCGACGCACTACCGCTCTGAGCTTCTTA	691
OY	614	GAAGAGTGCGCTTCTAAGGCGCTGGGCGCGCGCCCTTGACGCGCTGCGAGAGAG	673
Db	692	AAAAAATAACCTTCTAAGAGACTAAAGCGCGACGACCTTAACAGCGCTACGCGAAAAAGAA	751
OY	674	GCGTGCCTGGTCCGCGCGCGAGCGCGCCCTGCGCGCGCGCTTGGCGCGCGCACTGG	733
Db	752	AACATACCGGATACCGCGCGAGACGCGCCCTTACCGCGCGCGCTTGGCGCGCAACTATYAA	811
OY	734	CTGCTTTTCGATTCCCGAGAGCTCTCAGGCGCGCGCGGCTCGCGCTAGTCTCCGTG	793
Db	812	CTACTTTTCGAAATTTCCCGAAACTCTCAAAACGCGCGCGTACTCGCGGTAATCTCGTA	871
OY	794	CTGCTCATCTCGTCTCCATCGTCTTCTGCTCGAGAGCGTCTGACTTCCGCGAC	853
Db	872	CTAATCATCCCTCGTCTCCATCGTCTTCTCACTCGAAGACGCTACTTCTCCGCGAC	931
OY	854	GACCGCGAGCGAGGGGCTGTGTGACACCGCCAGCGCGGCGGT 900	
Db	932	GACCGCGAGCGAGAACTTACTACTACAGCGCAACCGACCGCCGAT 978	

## RESULT 15

ABL3311/c  
ID ABL33117 standard; DNA; 7642 BP

AC	ABL33117;
XX	
DT	26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 1090.

KW Human: immune system disease; cytosine methylation; antileukemic  
KW antiarteriosclerotic; antianemic; cystostatic; neutropic;  
KW neuroprotective; anti-HIV; anticoagulant; ophthalmological;  
KW antithematic; antithritic; antididiabetic; antipsoriatic;  
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease  
KW gene; ds.

05 Homo sapiens

PN WO200200928-A2

PD 03-JAN-2002

PF 02-JUL-2001; 2001WO-EP07537.

PR 30-JUN-2000; 2000DE-1032529.

XX  
XX

XX  
2  
1  
3  
1  
1  
2

**XX**

XX

PT Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -

PS Claim 1; SEQ ID NO 1090; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, CC rheumatoid arthritis, psoriasis and inflammatory/intestinal bowel diseases. The present sequence is a gene of the invention.

XX Sequence 7642 BP; 1881 A; 279 C; 1925 G; 3557 T; 0 other;

Query Match 21.0%; Score 367.4; DB 24; Length 7642;

Best Local Similarity 57.8%; Pred. No. 1.2e-58; Matches 684; Conservative 0; Mismatches 481; Indels 18; Gaps 1;

QY 381 AGCGCTGTGCTCAACGTCGGCGGCTGCGCTTCGAGACGCGGGCGGCGACGCTGGGCC 440  
 DB 2401 AAGCGCTAATCATCAACATCTCCGAACTACGCTTCGAAACGCACTAATAAACCTTTACC 2342  
 QY 441 GCTTCCGGACACTGTGTAGGGGACCCGCGCGCGCGCTTCTACGACGACGCGC 500  
 DB 2341 AATTCCCGAAACGCTACTAAGACGACCCCAAGACGACATMAAACTCTTCGACCCGCTCC 2282  
 QY 501 GCCGCGAGTATTTCTGACACGCGCGCGCGCTTCGACGCGCGCTTCTACTACAC 560  
 DB 2281 GCACGAAATATCTTCTGACCGACCGACCGCACTTCGACGCGCTTCTACTATATC 2222  
 QY 561 AGTCGGGTGGGCGGTGCGCGCGCGCGACGTCGCGCTGACGTCCTTCTGGAAAGG 620  
 DB 2221 AATCCGAAACCGCATCTCCGCGACGATCAACGATACCATTCGATTCGCAAAAAA 2162  
 QY 621 TGCGCTTCAAGGGCGGGCGCGCGCGCTGCGACGCGCGCGGAGACGAGGCGC 680  
 DB 2161 TCGGCTTCAACCACTAAGCAAAAAACCAATAAAATTCGCGGAAACGAAACCTTCC 2102  
 QY 681 CGGTGCGCGCGCGCGCGCGCGCGCTTCGCGCGCGCTTCGCGCGCTTCTGCTT 740  
 DB 2101 TACGAAAAAAGCAACGACCTTACCGCGCGCGCTTCGACGCGCAATTAATTAATCT 2042  
 QY 741 TCGAGTTTCCGAGAGCTCTCAGGCGCGCGCGCTGCTCGCGCTGCTCGCTGCTG 800  
 DB 2041 TCGAATATCCCGGAAACCTCGAAGCGAGCAACATCGCATGATTCGCTATATCA 1982  
 QY 801 TCGTGTTCGACATGCTGCTTCTGCTGCGAGACGCTGCTGCTGCTGCGGAGACGCG 860  
 DB 1981 TCGTCAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1922  
 QY 861 ACGGCAAGGGGCTTGTGCTGACGCGCGCGCGCGGCTTCGCGCGCTTCGCTGATG 920  
 DB 1921 ACTACCGCGCTTCGAGCTGCGAATACTCATTCGAAACACCGCAACACACGTCGAAAT 1862  
 QY 921 GCTCAGCAAAATGCTGGAATCAACCGCGCTTCGCTTCAAATGACCGCTTCGCTG 980  
 DB 1861 CCGCGCAAAAA-----CTCCAACTTCGCGATTCCTTCTTGTA 1820  
 QY 981 TGGAGACGCTGTGATTTGTGCTTCTGCTTGTAGCTGCTGCTGCTGCTGCTGCTG 1040  
 DB 1819 TAAAAAGCTATACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1760  
 QY 1041 CAAGCAAGCTATCTTCTCAAGAACGTATGAACTCATGATTTTGTGGCTATGCTTC 1100  
 DB 1759 CTAAACAAACGACCTTCTGCGAATCATTAACCTTAATCGACATTAATTAACCATTC 1700  
 QY 1101 CCTACTTGTGGCACTGGGACGAGCTGCGCGCGAGGAGGGGTGGGCGACAGGCCA 1160  
 DB 1699 CTATATTTATCACTTAATTAACGACATTAACGACAAACAAATTAACAAACAAACA 1640  
 QY 1161 TGTCAATGGCAATCCGAGAGATCATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220  
 DB 1639 TATCTTAACCAATCAAAAAATCATCCGCTTAATAAAAAATCTTCGATCTTCAAACTAT 1580

QY 1221 CCGGCACTCAAGAGGCGCTGCAAAATCTTGGGCCAGACGCTTCGGGCTCCATGCTGAGC 1280  
 DB 1579 CGGCGCACTCAAAAAAATCTCAAAATCTCTCGAACAAGGCTTAAAAAGCTACGAAAC 1520  
 QY 1281 TGGGCGCTCTCACTCTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1340  
 DB 1519 TAAATTAATCAATCT 1460  
 QY 1341 TTGCGCAAGTGGACCGGCTGAGCTCCCATTTCTACTAGCATCCCTGAGCTCTTGAGG 1400  
 DB 1459 TTACCGCAACAAAGACCGCCCATCTCAATTTCAACAAATTCGGAATACCTTCAATAA 1400  
 QY 1401 CGGTAGTCAACATGATCACTAGTTGGCTATGAGACATGGCACCGCTGCTGAGTGGCA 1460  
 DB 1399 CAATTAATACATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1340  
 QY 1461 AGATAGTGGGCT 1520  
 DB 1339 AATTAATTAATCT 1280  
 QY 1521 TCAATGCTCAATTTTCACTACTTTTATACCGGAGACAGA 1563  
 DB 1279 TAAATTTTCAACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1237

Search completed: February 20, 2003, 06:32:00  
 Job time : 456.075 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 02:24:22 ; Search time 71.815 Seconds  
(without alignments)  
7460.705 Million cell updates/sec

Title: US-09-804-014A-7  
Perfect score: 1747  
Sequence: 1 gaagcgtatctgcagcaaa.....agctctgcagcactcacac 1747

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1069	61.2	1599	1	US-08-288-405A-9
2	614.2	35.2	1994	1	US-08-527-152-1
3	215.6	12.3	2064	1	US-09-178-109-3
4	215.6	12.3	2072	4	US-09-142-791A-3
5	215.6	12.3	2104	4	US-09-142-791A-1
6	215.6	12.3	2121	4	US-09-178-109-1
7	213.2	12.2	3424	4	US-09-336-643A-9
8	212.4	12.2	2104	4	US-09-142-791A-5
9	212	12.1	271	1	US-08-288-405A-19
10	187.4	10.7	696	1	US-07-955-916-5
11	173.8	9.9	1805	1	US-07-955-916-6
12	161	9.2	2127	1	US-08-464-340A-1
13	161	9.2	2127	5	PCT-US94-08449A-1
14	152.8	8.7	2483	1	US-08-464-340A-3
15	152.8	8.7	2483	5	PCT-US94-08449A-3
16	132.6	7.6	2293	4	US-09-336-643A-5
17	130.8	7.5	196	1	US-08-288-405A-18
18	128.4	7.3	1927	4	US-09-336-643A-3
19	128	7.3	3102	4	US-09-336-643A-17
20	106.4	6.1	3080	4	US-09-336-643A-7
21	97.4	5.6	139	1	US-07-961-268-3
22	97.4	5.6	139	1	US-07-961-268-4
23	79.4	4.5	896	4	US-09-105-058C-1
24	68.2	3.9	1926	4	US-09-249-585A-4
25	68.2	3.9	1931	2	US-09-130-114-2
26	63.4	3.6	2353	5	PCT-US92-06840-1
27	62.8	3.6	8438	1	US-07-945-283-1

28	62.6	3.6	4257	2	US-08-690-473-1	Sequence 1, Appli
29	62.6	3.6	4257	4	US-09-259-821A-1	Sequence 1, Appli
30	62.6	3.6	4257	4	US-08-843-659-1	Sequence 1, Appli
31	62	3.5	12001	1	US-08-458-568A-11	Sequence 11, Appli
32	61.8	3.5	44377	2	US-08-804-227C-7	Sequence 7, Appli
33	61.8	3.5	44377	2	US-08-804-198-1	Sequence 1, Appli
34	61.2	3.5	2721	6	5215881-2	Patent No. 5215881
35	60.6	3.5	2150	2	US-08-318-837-1	Sequence 1, Appli
36	60.4	3.5	1312	5	PCT-US94-02389-1	Sequence 1, Appli
37	60.4	3.5	1312	5	US-08-205-506A-1	Sequence 1, Appli
38	60.2	3.4	2028	4	US-09-634-920-1	Sequence 1, Appli
39	60.2	3.4	2734	3	US-09-135-021-79	Sequence 79, Appli
40	60.2	3.4	2821	4	US-09-135-010A-115	Sequence 115, App
41	60.2	3.4	2821	4	US-09-597-735-115	Sequence 115, App
42	60.2	3.4	2821	4	US-09-597-733-115	Sequence 115, App
43	60.2	3.4	3181	3	US-09-135-021-1	Sequence 1, Appli
44	60.2	3.4	3181	4	US-09-135-020-1	Sequence 1, Appli
45	60.2	3.4	3181	4	US-09-135-010A-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-288-405A-9  
Sequence 9, Application US/08288405A  
Patent No. 5559009  
GENERAL INFORMATION:  
APPLICANT: Chandry, Kanianthara G.  
APPLICANT: Kalman, Katalin  
APPLICANT: Gutsch, Gritsch  
APPLICANT: Gutman, George A.  
TITLE OF INVENTION: A No. 5559009ei Voltage-Gated Potassium Channel  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
ADDRESSEE: Attn: Walter H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,405A  
FILING DATE: 10-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,431  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-59844-1/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1599 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1599  
US-08-288-405A-9

Query Match	61.2%	Score 1069;	DB 1;	Length 1599;
Best Local Similarity	81.5%;	Pred. No. 1.2e-199;		
Matches 1289; Conservative	0;	Mismatches 280;	Indels 12;	Gaps 4

QY	137	CGGGGACAGGGAGGGGGGGGCTCCGGGACAAGAGGGGCGGGGCGTGGCCCTGTGGCCCTCCCGC	196
Db	31	CGGAAAAGCGCGGGGTGGCAGTGTTCACAGSTGTGGGAACGGACAGAGGGGCCCTCTAC	90
QY	197	CCGCGCGGGGTACACAGTGGCCCTCCCTCGCGCCCTAGCCGCCCTGGCCGGGCTATTATTAC	256
Db	91	CCCCGGGGGGAACACGCGGCCCTCCCGCGCCCTGGCCGACCTTTCATGCTATTATT	150
QY	257	CGCGGGACACCGGACACCGGACACCGGGCTGGGGGGCGCGCTGGGGCCACACGTGGTTG	316
Db	151	ACCGCGCGACACCGGAACCCGACGTGGGGGGGTGGGGGGCCAGCGCTGGTC	210
QY	317	CGGGGTGGCGGGGCTCGCGCGCCATGAGAGCGCGGGTCCCGCGCCCTGCGGGAGTGC	376
Db	211	ACCGGTGGCCCGGGCTGTGGCGCCCATGAGACCAAGGTGCCCGCCCGT---GGTGC	267
QY	377	TGCGAGCGGGTGGTGTCTCAACGTGGCGCGGCTGCGTTCGAAGACGGCGGGCGCGACGTG	436
Db	268	TGCGAGGGGGTGGTGTCTCAACGTGGCGGGTTCGCTTGAAGACCGCGCGCGCACGCTC	327
QY	437	GGCGCTTCCCGGACACTTGTGAAGGGAAACCGAGCGCGCGGGCGGCGCTTACAGACGC	496
Db	328	GGCGGCTTCCCGGACACGCTGTGGGGAGACCCGGTGGCGCGACCGGCTTCTACAGACGGC	387
QY	497	GGCGCGCGGAGTATTCTTCGACCGGGACACCGGCCACGTTGACAGCCGTGCTACTAC	556
Db	388	GGCGCGCGGAGTATTCTTCGACCGACACCGGCCACGTTGAGATGGGGTGTCTACTAC	447
QY	557	TACCACTCGGTGGGGGGGCTGGGGGGCGGGCGACAGTGGCGGTGAGCTTCTCTGAA	616
Db	448	TACCACTCGGGGGCGCGGAGACCGCGGGCGACAGTGGCGCTTCTCTGAG	507
QY	617	GAGTGGGCTTCTACGGGCTGGGGCGGGCGGCGCTGGACGGCTGGCGAGAGACAGGAGC	676
Db	508	GAGTGGCTTCTACAGGGGCTGGG---CGGGGGCTGGCGGGCTGGGAGAGACAGAGGC	564
QY	677	TGCGGGTGGCGCGGACGCGCCCGTGGCCCGCGCGCGCTTGGCCCGCCAGCTGGAGCTG	736
Db	565	TGCGGGT---CGCGGAGCGGGCGGCTGGCCCGC---CCTTGGGGGTAGCTTGGGCTG	618
QY	737	CTTTTCAGTTCCTCCGAGACCTCTCAAGCGCGCGGGGTGCTGGCGGTATCTCGTGTG	796
Db	619	CTTTTCAGATTCCTGTGAGACTCTGCAAGGCTGGCGCGGCTGCTGGCGGTGCTCGTACTC	678
QY	797	GTCATCTGCTCTCCACAGCTGCTTCTGCTCTGAAACGCTGCTCTGACTTCCGACAGC	856
Db	679	GTCATCTGGGTCTCCACGTGGGTCTTTTGGCTTGAACACTGCAAGACTTCCGACAGC	738
QY	857	CGCGAGGACAGGGGCTTGGTCTGTGCAAGCGGACGCCGGCGGGGTTCGCCGCTCGCTG	916
Db	739	CGCATATACCGGGGGCTCGCGCGGAGAGCGGGCTGACTGAGCTCTCTCGCTCGGCTC	798
QY	917	AATGGCTCCAGCCAAATAGCCCTGGAAATPCACACCCCGCTGCGCTCAATGACCGGTTTC	976
Db	799	AATGGCTCCAGTCCCATGAGGAGGCCCTCCCGGACGCCCTTCAAGATCATATTCTTT	858
QY	977	GTTGGTGAAGCGCTGTGTATTGTGGTTCCTCTTGGACCTGCTGGTAGGCTCTCTGTGTC	1036
Db	859	GTTGGTGAAGACCGTGTATCTGTCTGTCTCTTCTTGGACTGCTGGTGTATGGTGGCC	918
QY	1037	TGTCGAAGCAAGCTATCTTCTTCAAGAAAGTGATGACCTCATGCAATTTGTGGCTATC	1096
Db	919	TGCCCTAGCAAAAGTGTGTCTTCAAGAAATGTGATGAACTTAATGACTTCTGTGGCATC	978
QY	1097	CTTCCCTACTTTGGGCACTGGGGCACCGAGCTGGCCGGGCGAGGAGGGTGGGCCAGAG	1156
Db	979	CTGCTTACTTTCGGGGCTGGGGCACGGAGATTAGCCGGGACGGGGGTGGGCCAGCGC	1038

OY	1157	GCATATGACAGGGCATTCCTGAGAGATCATCCGATWGTCGTCTCCGATCTTCCAG	121.6
Db	1039	GCTATGTCCCTGGGCATCTTAAGGGTATCCGATTTGGTGTCTCTCCGATCTTCCAG	109.98
OY	1217	CTGTCCCGGCATCTAAAGGGCTGCAATCTTGGGCGAGAGCCCTTCGGGCTCCATGCGT	127.67
Db	1099	CTTCTCAGGCATTTGTAAGGGGTCTACAGATCTTGGGTGACAGCTCGGGCTTCCATGCGT	115.88
OY	1277	GAGCTGGGACCTCCCTCATCTTTTTCCTCTTCATGTGGTGTGTGTCTCTCTTTTCCAGGCCCTC	133.6
Db	1159	GAGCTAGGTCTCCCATCTCTCTTCCTTCATTTGAGCGTGTCTCTTTTCCAGCGCAGTCTC	121.8
OY	1337	TACTTTGGCGAAGTTGACCGGGGTGGATCCCATTTGACTAGCATCCCTGAGTCCCTTGG	139.66
Db	1219	TACTTTGCTGAAGTGGACCGGGGTGGACCCCATTTTACCAGCATCCCGGATGCTCTTTTGG	127.87
OY	1397	TGGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCCGTCACCTGTGGT	145.6
Db	1279	TGGGAGGTGGTACCATGAGCACAGGTTGGGTATGGGAGCATGGCACCCGTCACCGTGGT	135.88
OY	1457	GGCAAGATAGTGGGCTCTCTGTGTGCCATTTGGCGGCTGCTGACTATTTTCCCTGCCAATG	151.6
Db	1339	GGCAAGATCGGGGCTCTCTGTGTGCCATTTGGCAGGTGTCTCACATCTCTCTGTGCTGTG	139.8
OY	1517	CCCGCATTTGTCTCAGATTTTTCAGTCTACTTTTATCACCGGAGACAGAGGGCGAAGAGCT	157.67
Db	1399	CTGTCTATTTGTCTTAACCTTACCTACTTTTACCACCGGAGACAGAGGGCGAAGAGCTA	145.8
OY	1577	GGGATGTTTCACCATGTGGACATGCAAGCCTTGTGGCCCACTGGAGGGCGAAGGCCAATGGG	163.6
Db	1459	GGGATGTATACAGCCATGTGGACACAGACCCCTCGGTACCTGTGAGGGCGAAGGCTAATGGG	151.8
OY	1637	GGGCTGGTGACGGGGAGTAACTGAGCTACCACTTCACCTGTGGGACACCCCGCAGGGAA	169.6
Db	1519	GGGCTGGTGAGCTCTGTGGGGGCTTGAATCTCTCCACACACTCTGGGCCCTTGCAAGGAAA	157.8
OY	1697	CACCTGGTCAACCGAAGTGTAA	171.7
Db	1579	CACATGGTGAAGTGTAA	159.9

RESULT 2  
US-08-527-152-1  
Sequence 1, Application US/08527152  
Patent No. 5827655  
GENERAL INFORMATION:  
APPLICANT: Chandu, Kananthara G.  
APPLICANT: Cahalan, Michael D.  
APPLICANT: Grissmer, Stephan  
APPLICANT: Goldin, Alan L.  
APPLICANT: Dethlefs, Brent A.  
APPLICANT: Gutman, George A.  
APPLICANT: Wasmuth, John J.  
TITLE OF INVENTION: Assay, Methods and Products Based On r  
TITLE OF INVENTION: K+ Channel Expression  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Flehr, Hobbach, Test, Albritton & Herbert,  
ADDRESSER: Attn: W.H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/527,152  
FILING DATE: UNKNOWN  
CLASSIFICATION: 435



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; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3

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Query Match	12.3%	Score 215.6	DB 4	Length 2064
Best Local Similarity	52.8%	Pred. No. 1.2e-33		
Matches 622	Conservative 0	Mismatches 499	Indels 57	Gaps 5

QY	380	GAGGAGGCTGATGCTCAACATGGCGGGGCTGCGCTTGTGAACCGGGGCGACGCTGGGAC	439
Db	190	GAGCTGATTTGCTCTCAACGTGAAGTGGGCGGAGGTTTCAACCTGGAGGACCAAGCTGGAG	249
QY	440	CGCTTCCCGAGACACTGTGCTAGGGGAGCCAGCGCGCGCGCGCTTTCACACACAGCG	499
Db	250	CGCTAACCGGACACCGTGGTGGGCGACAGGAGAAAGATTTCTTCTCAACGAGGACAC	308
QY	500	CGCCGCGAGTATTTCTTGCACCGGGACCGGCCAGCTTGACAGCGGCTCTTACTATAC	559
Db	309	--CAAGAGAGTACTTCTTCGACCGGGACCCCGAGGTTTCCGGTGGGTGCTCAACTTCTAC	366
QY	560	CAGTCCGGTGGCGGGCTGGCGGGCGGGCGACATGCTCCGCTGCAGCGTCTTCCGTGAAG	619
Db	367	C---GCACGGGGAGAGCTGCACTACCCGGCTACAGAGTGCATCTTGTCTACAGACAGAG	423
QY	620	GTGGACCTTACAGGGGCTGGGGCGGGCGGCGCTTGACAGGCTCGCGAGAGCAGAGGGCTGC	679
Db	424	CTGGCTTTACGGGCACTCTCCGGGAGATCATGCGGAGCATGCTGCTACGAGAGATACAAG	483
QY	680	CGGTCGGCGCCCGAGCGCCCCCTGCCCCCGCGGCTTGCCCCGACAGTGTGGCTGCTT	739
Db	484	GACCGCAAGGAGGAGAAACGCCGAGC-----GGCTCATG	516
QY	740	TTCCAGTTTCCCGAGACTCTTCAGGCGGGCGGGCTGCTGCGGTATGTCCTGGTCGAGC	799
Db	517	GAGCACACAGCTCGGAGAACCAACAGAGATGCATCCCTCGCTCAGCTTCCGCCAGAC	576
QY	800	ATCTCTGCTTCACATCGTGTCTTCTGCTCGAGACGCTGCCTGACTTCCGAGACAGCGC	859
Db	577	ATGTGGGGGCGCTTCGAGAACCCCAACAGCAGCAGCTGGCCCTGGTCTTACTACGAG	636
QY	860	GACGGCACGGGGCTTGCTGCTGCAGCCGCAAGCGGGCGCGGTGTCCCGCTCCGCTGAAT	919
Db	637	ACTGGCTTCTTCACGCTGTGCTGGGTATCACCAAGGTGTGAGAGCGGTGCCGCGGCGC	696
QY	920	GGCTCAGCAAAATGCTGTGAATAATCACCGCGCGCTCCCTCAATGACCGCTTCTCGAG	979
Db	697	ACGGTCCCCGGGACAGAGAGCTGCCGTGGGGAGCGCTACTCGGTGGCTTCTTCTGCG	756
QY	980	GTGGAGACGCTGTGTATTTGTTGGTTCTCTCTTGAAGCTGCTGTAGCCCTCCCTGTGTGT	1039
Db	757	CTGGACACGGGCGTGCATGATCTTACCGCTGAGATCTCTGGGGCTCTTCCGGGCT	816
QY	1040	CCAGCAAGGCTATCTTCTTCAAGAACGTATGAAACCTATGATTTTGTGGCTATCTCTT	1099
Db	817	CCGAGCGGTACCGCTTCAATCCGACAGCTATGAGATCATGAGCTGGTGGCCATCATG	876
QY	1100	CCCTACTTTGTGGACATGGGCGACCGAGATGAGCCGCGACAGAGGGGTGGCGCAGAGGCG	1159
Db	877	CCCTACTACATCGGTGTGGTCAI-----GACCAACACAGAGAC	915
QY	1160	ATGTCACTGGCCATCTGAGAGTCAATCCGATTTGGTGGCTGTCTTCCGATCTTCAAGCTG	1219
Db	916	GTGTCGGGGCGCTTTCGAC---CGTCCGGGGTCTTCCGGTCTTAGAGTTTCAAGTTT	972
QY	1220	TCCCGGAGCTCAAAAGGGCTTGCAATCTTGGGCGAAGCGTTCCGGGCTTCATGGCTGAG	1279
Db	973	TCCCGCACATCCACAGGGCGTCCGATGCTGGGCTACACACTGAAGAGCTGCTCCGAA	1032
QY	1280	CTGGGGCTCCCTCAACTTTTTCCTTCATCGAGTGTGGTGTCTCTTTTCCAGGCGCGCTAC	1339
Db	1093	CTGGGGCTTTCTTCTCTTCTCCCTACCACTAGGCCATCATATCTTGGCACCTGTATGTTT	1092

Qy	1340	TTTCCGCACTTACCCGGGAGCTCCCAATTCACATAGACTCCCGAGCCCTTCGGGG	1399
Db	1093	TATCCCGAAGGGCTCTCCGCGACAGATTCCACAGATCCCTGCTGTTTGGTAC	1152
Qy	1400	CGCGTAGTCACCATGACTTACAGTTGGCTATGAGACATCGCACCCGCTACTGTGGTGGC	1459
Db	1153	ACCATTTCTACACATGACACACACTGGGATACGGAGACATGGTGCCTTAAGACGATTCCAGGG	1212
Qy	1460	AAGATTAGTGGGCTCTCTGTGTGCCATTGGGGGCGTCTACTATTTCCTGCGCACTGCC	1519
Db	1213	AAGATCTTCGGCTCACTCTCTCTCTTGAGTGGGCTCTGTGATTCCTGCGCACTGCC	1272
Qy	1520	GTCATGTGTCACATTTCCACTACTCTTTTACACCGGGA	1557
Db	1273	GTGATGTGTTCCAACTTTAGCCGAGATTACACCAAGAA	1310

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1 RESULT 4
2 US-09-142-791A-3
3 Sequence 3, Application US/09142791A
4 Patent No. 6368823
5 GENERAL INFORMATION:
6 APPLICANT: Antoine Michel Alain Brill
7 APPLICANT: Thierry Paul Gerard Camels
8 APPLICANT: Jean-Francois Simon Pierre Faas
9 APPLICANT: Jean-Luc Javre
10 APPLICANT: Sabine Rouanet
11 TITLE OF INVENTION: NOVEL COMPOUNDS
12 FILE REFERENCE: GH-30012
13 CURRENT APPLICATION NUMBER: US/09/142.791A
14 PRIORITY FILING DATE: 1999-02-02
15 PRIOR APPLICATION NUMBER: PCT/EP98/01901
16 PRIOR FILING DATE: 1998-03-23
17 PRIOR APPLICATION NUMBER: UK 9706377.0
18 PRIOR FILING DATE: 1997-03-27
19 PRIOR APPLICATION NUMBER: EP 97402971.2
20 PRIOR FILING DATE: 1997-12-09
21 PRIOR APPLICATION NUMBER: EP 97403007.4
22 PRIOR FILING DATE: 1997-12-11
23 NUMBER OF SEQ ID NOS: 14
24 SOFTWARE: FastSeq for Windows Version 3.0
25 SEQ ID NO 3
26 LENGTH: 1072
27 TYPE: DNA
28 ORGANISM: HOMO SAPIENS
29 US-09-142-791A-3

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Query Match	12.3%;	Score 215.6;	DB 4;	Length 2072;
Best Local Similarity	52.8%;	Pred. No. 1.2e-33;		
Matches 622;	Conservative	0;	Mismatches 499;	Indels 57; Gaps 5;

OY	380	GAGGGGCTGGTGTCAACGTGTGGGGGTGGGCTTCAGAGACGGGGGGCGCCACGTGGG	439
OY	118	GAGCTGATTGTCTTCACGTAGTGGGGGGGTTCCAGACCTTGGAGACCACGCTGGAG	177
OY	440	CGCTTCCCGGACACTCTGTCTGAGGGGACCCAGCGCGCCGCGGCTTCTACGACGACGG	499
Db	178	CGCTACCCGGACACCTCTGTGGGAGCAGCAGGAGGAGTCTTCTTCAACGAGGACAC-	236
OY	500	CGCGCGGATATTTCTTCGACCGGACCGGCGCCAGCTTTCGACGGCCGTCTCTACTATC	559
Db	237	--CAAGGATACTTCTTCGACCGGGACCCGAGGTGTTCGGCTGGCTCAACTTCTAC	294
OY	560	CAGTCCGCTGGGCGGCTGGCGGCGCGGACGACGTGCCCTCGACGTCTTCTTGGAAAG	619
Db	295	C---GCACGGGGGAAGCTGCATCACTCCGCGCTACACAGTGCATCTCTGCTCTCAGACGAG	351
OY	620	GTMGCGCTTCAGCGGAGCTGGGGCGGCGGCGCCCTTCGACGCTCGCGGACGAGAGGCTGC	679
Db	352	CTGGCTCTTCAGCGGCATCTCCGGAGATCATTCGGGAGACTGTCTTCAGAGAGTACAG	411
OY	680	CCGGTGGCCCGAGCGCCCCCTTCCGCCGCGCTTCCGCCCGACGCTGTGGCTT	739

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Db 412 GACCCGCAAGAGGAGAGACCCGAGC-----GGCTCATG 444
QY 740 TTGAGTTTCCGAGAGCTCTGAGGCGGCGGCTGCTGCCCTAGTCTCCGCTGCTG 799
Db 445 GAGGACAGACGATCGGAGAACCAACGAGATCCATGCTCCGCTGCTGAGCTCCGACACC 504
QY 800 ATCTGCTGCTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
Db 505 ATGTGGCGGGGCTTGAGAGAACCCGACACGAGACGCTGGCCCTGGCTCTTCTACTACG 564
QY 860 GACGCGACGGGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
Db 565 ACTGGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 624
QY 920 GGCTCCAGCAATGCTGGAATCCACCCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Db 625 ACGGTCCCGGGGAGCAAGAGCTGCGTGGGAGCGCTACTCGGTGGCTCTCTCTCTG 684
QY 980 GTGAGAGACGCTGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1039
Db 685 CTGGACACGGCGTGGCTCATGATCTTACCGGTGAGTACTCTCTGGGCTCTTCTGGGCT 744
QY 1040 CCAAGCAAGGCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1099
Db 745 CCCAGCGCTACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 804
QY 1100 CCTACTTTGTGCACTGGGCGACCGAGCTGGCCGCGGACGAGGGGTGGGCGCCAGGCC 1159
Db 805 CCTACTATACGTGCTGTGTCAT-----GACCAACAACGAGGAC 843
QY 1160 ATGTCACTGGCATCTGTGAGAGATCCATGTTGCTGTCTGTCTGTCTGTCTGTCTGT 1219
Db 844 GTGTCCGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 1220 TCCCGGCACTCAAGGGGCTGTCAATCTTGGGCGAGACGCTTGGGCTCTCATGCTGTG 1279
Db 901 TCCCGCACTCCAGGGGCTGTGGGATCTGGGCTACACACTGMAAGAGTGTGCTCGAA 960
QY 1280 GTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1339
Db 961 CTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1340 TTTGCGAAGTTGACCGGGGTGACTCCATTTCTACTAGCATCCCTAGTCTCTGTGG 1399
Db 1021 TATGCGAAGAGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1400 GCGGTAAGTACCATGCTACTAGTGGCTATGAGACATGGACCCGCTCACTGTGGGTGC 1459
Db 1081 ACCATTGTCAACATGACCACTGAGATGAGGAGATGAGGATGAGGATGAGGATGAGG 1140
QY 1460 AAGATAGTGGGCTCTGTGGCATTTGGGGGCTGCTGACTATTTCCCTGCCAGTGGCC 1519
Db 1141 AAGATCTTGGGCTCATCTGCTCTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1520 GTCATTTCTCCAAATTTACGCTACTTTTATCAACCGGGA 1557
Db 1201 GTGATTGTTTCAACTTTAGCCGGAATTTACCAACAGAA 1238

RESULT 5
US-09-142-791A-1
; Sequence 1, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Bril
; APPLICANT: Thierry Paul Gerard Calmeils
; APPLICANT: Jean-Francois Simon Pierre Falvire
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
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; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-1

Query Match 12.3%; Score 215.6; DB 4; Length 2104;
Best Local Similarity 52.8%; Pred. No. 1.2e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;

QY 380 GACGCGCTGTGCTCAACGTCGCGGCTGCTGTGAGACGCGGCGGACGCTGGGC 439
Db 118 GAGCTATTGTCTCTCAACGATGAGTGGGCGGAGGTTCTACAGCTGAGACCAACGCTGGAG 177
QY 440 CGCTTCCGAGACCTCTGCTGAGGAGGAGCCAGCGCGCGCGCGCTTCAACGAGACCG 499
Db 178 CGCTTCCGAGACCTCTGCTGAGGAGGAGCCAGCGCGCGCGCGCTTCAACGAGACCG 236
QY 500 CGCGCGAGTATTTCTTCTGACCGGACCGGCGCGGCTGTGAGCGCGCTGTCTACTAC 559
Db 237 --CAAGAGTACTTCTTCTGACCGGAGCCGAGAGTCTCGCTGGCTGTCTCAACTCTAC 294
QY 560 CACTCGGTGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 619
Db 295 C--GCAGGGGAGGCTGACTACCGCGCTAGAGTGCATCTGTGCTTACGAGCGAG 351
QY 620 GTGGCTTCTAGGGGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 679
Db 352 CTGGGCTTCTAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 411
QY 680 CGGCTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 739
Db 412 GACCGCAAGAGGAGAAAGCGCGAGC-----GGCTCATG 444
QY 740 TTGAGTTTCCGAGAGCTCTCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
Db 445 GACGACAAAGACTCGGAGAAACAACAGAGATCCATGCTCTGCTGCTGCTGCTGCTGCT 504
QY 800 ATCTGCTGCTCCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
Db 505 ATGTGGCGGGCTTCTGAGAACCCGACACGAGACGCTGGCCCTGGCTCTTCTACTACG 564
QY 860 GACGCGACGGGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
Db 565 ACTGGCTTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 920 GGCTCCAGCAATGCTGGAATCCACCCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Db 625 ACGGTCCCGGGGAGCAAGAGCTGCGTGGGAGCGCTACTCGGTGGCTCTCTCTCTG 684
QY 980 GTGAGAGACGCTGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1039
Db 685 CTGGACACGGCGTGGCTCATGATCTTACCGGTGAGTACTCTCTGGGCTCTTCTGGGCT 744
QY 1040 CCAAGCAAGGCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1099
Db 745 CCCAGCGCTACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 804
QY 1100 CCTACTTTGTGCACTGGGCGACCGAGCTGGCCGCGGACGAGGGGTGGGCGCCAGGCC 1159
Db 805 CCTACTATACGTGCTGTGTCAT-----GACCAACAACGAGGAC 843
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QY 1160 ATGTCACTGGCCATCTGAGAGTCATCCGATGTGTCGCTCTTCCGATCTTCAAGCTG 1219
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Db 844 GTGTCCGCCCTCTCTGCA---CGCTCCGGGCTTCCGCTCTTCAAGATTT 900
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QY 1220 TCCCGGACACCAAGGCGCGCAAACTTGGGCGAGCGCTTGGGCGCTCCATCGGAG 1279
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 901 TCCCGGACACCGCGCGCGCTGCGGATCTGGCTACACACTGAAGAGCTGCTCCGAA 960
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1280 CTGGGCTCTCTCACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1339
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 961 CTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1340 TTTGCCGAAGTTGACCGGGGAGCTCCATTTCACTAGCATCCCTAGTCTCTGTGG 1399
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1021 TATGCCAGAGAGGCGCTCTCTGCGGAGCAAGTTCAGAGCATCCCTGCTGTTGGTAC 1080
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QY 1400 GCGGTACTCAACATGATACAGTTGGCTATGAGACATGGACACCGTACAGTGGGAGC 1459
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Db 1081 ACCATTCTCACATGACACACAGTGGGATACGAGACATGGCTTAAGACGATTGCAAGG 1140
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QY 1460 AAGATAGTGGGCTCTCTGTGTCATTCGCGGCGTCTGCTACTATTTCTCCAGTCCC 1519
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Db 1141 AAGATCTTCGCTCCATCTGCTCTGTGAGTGGGCTCTGCTGCTATTTGCTGCTGCT 1200
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QY 1520 GTCAATTCTCCAACTTTCAGCTACTTTTATCACCAGGA 1557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1201 GTGATTTCTTCAACTTTAGCCGGATTACACACAGAA 1238
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## RESULT 6

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US-09-178-109-1
; Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Chang Ling, Hwai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-09-178-109-1
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Query Match 12.3%; Score 215.6; DB 4: Length 2121;
Best Local Similarity 52.8%; Pred. No. 1.2e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;
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QY 380 GAGCGCTGTGCTCAAGTGGCCGGGCTCGCTTCGAGACGGGCGCGACGCTGAGC 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 GAGCTGATGTCCTCAACGTAAGTGGGCGAGGTTCACAGACCTGAGAGACACGCTGAG 249
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 440 CGCTTCCCGACACTGTGCTAGGAGACCAAGCGCGCGCGCTTCTACAGACGCG 499
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CGCTACCGGACACCCGTGGGAGCAGCAGAGAGTCTTCTTCAAGAGAGACAC- 308
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 500 CGCGGAGATTTCTTCGACCGGCGCGGCGGCTTCGACGGCGGCTCTACTAC 559
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 --CAAGAGTACTTCTTCGACCGGCGCGGAGGTTCGCTGCGCTCAACTTCTAC 366
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 560 CAGTCCGCTGGGCGGCTGCGGCGCGCGCGCTGCGCTGCACTCTTCTCTGAGAG 619
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 C---GCAGGGGAAGCTGCACTACCGCGCTACAGATGCACTCTGCTACGAGAGAG 423
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 620 GTGGCTTCTACAGGCTGGGCGCGGCGGCTGCGACCTGCGCGAGAGAGGCTGC 679
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Db 424 CTGGCTTTTACAGCATCTCCGAGATCATCGGGGACCTGTCTACGAGACTACAAG 483
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QY 680 CCGGTGCCGCCGAGCGCCCTGCCCCGCGGCTTTCGCGCGCGAGCTGTGGCTCTT 739
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GACCGCAAGAGGAGAAAGCGCGAGC-----GGCTCATG 516
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 740 TTTGAGTTTCCCGAGACTCTCAGGCGCGGCTGCTGCGCTAGTCTCCGTCTGTC 799
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Db 517 GACGACAAAGCACTGGGAAACAAACAGAGATCTCCGCTGCTACACTTTCGCAACAC 576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 800 ATCTGCTCTCCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
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Db 577 ATGTGGCGGCGCTTCTGAAACCCACACAGACAGCTGGGCTGCTCTTCTTACTACGT 636
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QY 860 GACGCAAGGCGGCTCTGCTGTCAGCGCGACCGCGCGGCTGTTCCCGCTCGCTGAAT 919
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Db 637 ACTGGCTCTTCTCATCTGCTCTGCTATCCAAAGCTGGTGGAGAGGAGCGGCTGGG 696
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QY 980 GTGGAGACGCTGTATTTGTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1039
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Db 757 CTGGACACCGCGCTGCTCATGATTTTACCGGTGAGTACTCTCTGCGGCTCTTCCG 816
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QY 1100 CCTTACTTTTGTGCTGCTGCGGACCGGCTGCGCGGAGCGAGGAGGCTGCGAGCGC 1159
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Db 877 CCTTACTTACATCGCTGCTGCTAT-----GACCAACAAAGAGAGAC 915
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QY 1160 ATGTCACTGGCGCATCTGAGAGTCAATGATGCTGCTCTCTCTCTCTCTCTCTCT 1219
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Db 973 TCCCGGACACCGCGCGCTGCGGATCTCGGCTACACAGTGAAGAGCTGTGCTCCGAA 1032
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QY 1280 CTGGGCTCTCTCATCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1339
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Db 1033 CTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092
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QY 1340 TTTGCGGAAGTGAAGCGGGGAGCTCCCATTTCTCACTGACATCCCTGATGCTGTG 1399
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Db 1093 TATGCCAGAGAGGCTCTCTGCGGAGCAAGTTCAAGACATCTCTGCTGTTTGTATC 1152
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QY 1400 GCGGTACTCAACATGATACAGTTGGCTATGAGACATGGACACCGCTCACTGTGGTGGC 1459
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Db 1153 ACCATTCTCACATGACACACAGTGGGATACGAGACATGGGCTTAAGAGATTTGACAGG 1212
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QY 1460 AAGATAGTGGGCTCTCTGTGTCATTCGCGGCGCTGCTGACTATTTCTCCAGTCCC 1519
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Db 1213 AAGATCTTCCGCTCCATCTGCTCTGAGTGGGCTCTCTGCTGATTTGCTGCGAGTCC 1272
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QY 1520 GTCAATTCTCCAACTTTCAGCTACTTTTATCACCAGGA 1557
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## RESULT 7

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US-09-336-643A-9
; Sequence 9, Application US/0933643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
```

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; TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+Hnov12
US-09-336-643A-9

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Query Match      12.2%; Score 213.2; DB 4; Length 3424;
Best Local Similarity 52.3%; Pred. No. 3.8e-33;
Matches 616; Conservative 1; Mismatches 519; Indels 42; Gaps 5;

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QY 380 GAGCGGCTGCTCAACGTGGCGGGCTGCGCTTGCAGAGACGGGGCGGCGAGCTGGGGC 439
DB 374 GAGGTTCTGTGTGACAGTGAACGGGACGGCGCTTTGAGAAATACGCTGGAC 433
QY 440 CGCTTCCCGGACACTGTCTAGGGGACCCAGCGCGCGCGCGCTTTCACAGCAGCG 499
DB 434 CGCTACCCGACACCTTGTCTGGGACACTCGGAGAAAG--GAATTTCTTACGATGCTGAC 490
QY 500 CGCCCGAATATTTCTTCACCGGACCGGCCAGCTTGAGCGCCCTCTACTACTAC 559
DB 491 TCAGCGGATCTTCTTCATGCGCCCTGACATGTTCGCCATGTCTGAACCTTCTAC 550
QY 560 CAGTCCGCTGGCGGCTGGCGGCGCGGCGGCGGCTGCGCTGACGCTTCTCGAAGAG 619
DB 551 CGAAC--GGGGCGGTGATGATGCCAGCGGAGAGTGCATCAGGCTTTCAGCAGAGAG 607
QY 620 GTGGCTTCTACGGGCTGGCGGCGGCGGCTGCGACGCGCTGCGGAGAGCAGAGGCTGC 679
DB 608 CTGGCTTCTACGGCGCTGCTCCGAGCTAGTCGCTGACGCTGCTTGAAGATATCG 667
QY 680 CGGCTCCCGCGGAGCGGCGGCGGCGGCGGCTTGGCCCGCCAGCTGTGGCTGCTT 739
DB 668 GACCGAAGAGAGATGCGAGCGGCTGCGACAGAGATGAGAGGACAGAGCAG----- 721
QY 740 TTGAGATTCCCGAGAGCTCTCAGGCGGCGGCGGCTGCGCGTACTCCGCTGCTGTC 799
DB 722 -GCCGGGAGCGGCCAGCCCTGCGACGAGCACTCTCGCGGACGCGCTCTGGGGGC 780
QY 800 ATCTGCTTCATCGCTCTCTTTCGCTTCGACGAGCGCTCTGATCTCCGCGACGAGCCG 859
DB 781 CTTCAGAAATCCACACAGC-----AGCACGCGAGCCCTGTTTCTACATATGAGCGGG 835
QY 860 GACGGCAGCGGGCTGCTCTGACGCGGAGCGCGCGGCTGTTCGCCCTCCGCTGAAT 919
DB 836 TTCTTATGCGCGTCTGCTATCGCAATGTGTGAGAACCATCCATCCCGCGGCTCT 895
QY 920 GGCCTCAGCAAAATGCTGGAATCCACCGCGCTGCTCTCAATGACCGCTTCTCGTG 979
DB 896 GCACGCGAGTCTCAAGSAGAGACCCCTTGGCGAAGCTTCCACAGGCTTTTCTGCG 955
QY 980 GTGAGAGCGCTGTATTTGTTGTTCTCTTTCAGAGCTCTGTACGCTCTCTGTCTGT 1039
DB 956 ATGACACAGCTGTGTACTCATATTCACAGGTAATACCTCTCTGTGGGCTGTGTGCGGC 1015
QY 1040 CCAACGAGGCTATCTTCTTCAAGAACGTGATGAACTATGATTTTGTGGCTATCTT 1099
DB 1016 CCCAGCGCTTGTCTCTGTGGAGGTGATGAGCTCATGACGCTGTGGGCAATCTCG 1075

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QY 1100 CCTACTTTGTGCACTGGGACCGAGCTGGCCCGAGCGAGGGGTCAGAGGCC 1159
DB 1076 CCTACTACTTTGGGCTTTT-----GGTGGCCAAAGAACGAC 1111
QY 1160 ATGTCACTGGCCATCTGTAGAGATCATCCGATTTGTGCTCTTTCGCACTTCAAGCTG 1219
DB 1112 GATGTCTGTGGCGCTTTGTACACCTGCGGTGTGTCCGGGTGTTTGCATCTTCAAGTTTC 1171
QY 1220 TCCCGGCACTCAAGGGCGCTGCAAAATCTTGGGCGAGACGTTTGGGCTTCATGCTGAG 1279
DB 1172 TCCAGGCACTCAAGGGCGCTTGGAGATCTGTGCTACACACTCAAGAGCTGTGCTGTAG 1231
QY 1280 CTGGGCTCTCTCATCTTTTCTTTCATGAGTGTGTGCTCTTTCACGCGGCTGTAC 1339
DB 1232 CTGGGCTTCTCTCTTTTCTTTCATACCATGCGCATATCTTCTTTCGCACTGTGCTTT 1291
QY 1340 TTTCGCAAGTTGACCGGGTGAATCCCATTTGCTACATAGCAATCCCTGATGCTGTGG 1399
DB 1292 TATGTGAGAGGGGCAAAACAGACAACTTACAAAGCATCCCTGGGCTTCTGTAT 1351
QY 1400 GCGGTAGTACCATGACTACATGATGATGAGATGSCACCCGCTGCTGTGGTGC 1459
DB 1352 ACCATTGTCAACATGACACAGCGCTTGGCTAGGACATGTGCTCCAGCACTATGCTGGC 1411
QY 1460 AAGATAGTGGCTCTCTGTGTGCTCATTTGGCGGCTGTGACTATTTCCCTGAGTGGCC 1519
DB 1412 AAGATTTTGGGCTGCTATCTGCTACTACATGAGGCTCTTGTGCTATTCCTGCTGTGCA 1471
QY 1520 GTGATTGTCTCAATTTACGCTACTTTTATACCGGGA 1557
DB 1472 GTGATTGTGCTCAATTTAGCCGATCTACACAGAA 1509

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RESULT 8
US-09-142-791A-5
; Sequence 5, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-5

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Query Match      12.2%; Score 212.4; DB 4; Length 2104;
Best Local Similarity 52.6%; Pred. No. 5.1e-33;
Matches 620; Conservative 0; Mismatches 501; Indels 57; Gaps 5;

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QY 380 GAGCGGCTGTGTCAACGCGCGGGCTGCGCTTGCAGAGCGGGCGGCGAGCTGGGGC 439
DB 118 GACTATATTGTCTCAACGAGTGGCGGAGGTGCTCAAGCCTGAGGACACAGCTGGAG 177
QY 440 CGCTTCCCGGACACTGTCTAGGGGACCAAGCGCGCGGCGGCTTTCACAGCAGCGG 499

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Db 178 CGCTACCGGACACCTGCTGGGACGACGAGAGTTCTTCAACAGGAGAC- 236
QY 500 CGCGGAGATTTCTTTCAGACGGGACCGGACCGGACGCTTCAGCGCGCTCTACTACT 559
Db 237 --CAAGSAGTACTTCTTTCAGACGGGACCGGAGTGTTCGGCTGCGTCTCAACTTAC 294
QY 560 CAGTCCGCTGGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 619
Db 295 C---GACGCGGGAAGCTGCTACTACGCGCGCTACGAGTGCATCTCTGCTACGACGAG 351
QY 620 GTGGCTTCTACGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 679
Db 352 CTGGCGCTTCTACGCGGCTGCTGCGGAGATATCGGGGAGCTGCTACGAGAGTTACAG 411
QY 680 CCGGTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 739
Db 412 GACCGGAGAGGAGAGAGCGCGGAC-----GGCTCATG 444
QY 740 TTGAGATTTCCGAGAGCTCTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 799
Db 445 GAGGACACAGCATCGGAGAGACAGAGAGTCCATGCGCTCGCTACGCTTCGCGACAGC 504
QY 800 ATCTGCTCTCATCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
Db 505 ATGTGGCGGCGCTTTCGAGAACCCCGACACGAGCAGCGTGGCTGCTTCTACTAGTG 564
QY 860 GAGGAGACGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919
Db 565 ACTGGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 920 GAGTCCAGACCAATGCTGAGAAATCCACCGCGCTGCTTCAATGACCGCTTCTGCTG 979
Db 625 AGGTCGCCGCGGAGCAAGAGAGTCCGCTGCGGAGGAGTCTGCTGCTGCTGCTGCTGCT 684
QY 980 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
Db 685 CTGAGACGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
QY 1040 CCAAGCAAGGCTATCTTCTTCAAGAACGATGATGACCTGATGATGATGATGATGAT 1099
Db 745 CCGAGCGGCTACCGGCTTCACTCCGAGGCTATGAGCATCTCAGCTGCTGCTGCTGCT 804
QY 1100 CCGTACTTGTGCGACTGGGACCGAGCTGGCGGCGGAGGCGGCGGCGGCGGCGGCG 1159
Db 805 CCTACTACATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
QY 1160 ATGTCACTGGCCATCTCGAGAGTATCCGATGCTGCTGCTGCTGCTGCTGCTGCTG 1219
Db 844 GTGTCCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 1220 TCCGCGACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGCTCATGCGGAG 1279
Db 901 TCCCGGCACTCCAGAGGCGCTGCGGATCTGCGGCTACACATGAAAGAGCTGCTGCCGA 960
QY 1280 CTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1339
Db 961 CTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1340 TTTCGCGAAGTTCAGCGGCTGAGCTCCCATTTCACTAGCATCCCTGAGTCTGCTG 1399
Db 1021 TATGCGGAGAGAGGCTTCTTCTGCGGAGCAGCATCCCTGCTGCTTGTGTAC 1080
QY 1400 GCGGTATTCACATGATAGTTCAGTTCGCTATGAGACATGAGACCGGCTGCTGCTG 1459
Db 1081 ACATTTCTCAGCATGACACACTGAGATACGAGACATGCTGCTTAAGACATTTGACAG 1140
QY 1460 AAGATAGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519
Db 1141 AAGATCTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1520 GTGATGTCTCAATTTCACTACTTTTATCACCAGGA 1557

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Db 1201 GTGATGTCTTCAACTTTAGCCGGATTTACCACCAGAA 1238
RESULT 9
US-08-288-405A-19
; Sequence 19, Application US/08288405A
; Patent No. 555909
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandu, Grischa
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 555909el Voltage-Gated Potassium Channel
; NUMBER OF SEQUENCES: 21
; TITLE OF INVENTION: Gene
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbertl.
; ADDRESSEE: Attn: Walter H. Dregel
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregel, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEO ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; US-08-288-405A-19
Query Match 12.1%; Score 212; DB 1; Length 271;
Best Local Similarity 93.5%; Pred. No. 4.4e-33;
Matches 232; Conservative 0; Mismatches 9; Indels 7; Gaps 1;
QY 1503 TTTCCTGCGCAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562
Db 1 TTTCCTGCGCAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 1563 AGGCGGAAGAGGCTGGGATTTTCAGCCATGTCAGCATGACGCGCTTGGGCGGCTGAGG 1622
Db 61 AGGCGGAAGAGGCTGGGATTTTCAGCCATGTCAGCATGACGCGCTTGGGCGGCTGAGG 120
QY 1623 G-----CAAGCGATGCGGCGGCTGGTGGAGCGGAGGTACTGAGCTACGACTCA 1675
Db 121 GNNCANNCNANNCATATGGGCGGCTGTGGAGCGGAGGTACTGAGCTACGACTCA 180
QY 1676 CTCTGGGACCCCCCAGGAGACACCTGCTACCGAGATGTGAGACAGATTTAGGTGCTC 1735
Db 181 CTCTGGGACCCCCCAGGAGAAACACTGTGTCACGAAAGTGTGAGGAGACATTTAGGTGCTC 240
QY 1736 AGGACCTC 1743

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Db 241 AGAATTC 248

RESULT 10

US-07-955-916-5

Sequence 5, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHLEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-955-916-5

Query Match 10.7%; Score 187.4; DB 1; Length 696;

Best Local Similarity 61.8%; Pred. No. 3.1e-28;

Matches 368; Conservative 0; Mismatches 191; Indels 36; Gaps 3;

Db 981 TGGAGAGCGTGTGATTTGTTGCTTCTCTTGGAGCTGTGAGCTGTCAGCTCTCCGTGCTGTC 1040

14 TCGAGGGCGCTGTGCTGTGCTGTGCTGACCTTCACCTTCACCTGCGGCTGATCTTCTGCC 73

1041 CAAAGAGCGTATCTTCTTCACAGAGTGATGAACCTCATGATTTTGTGGCTATCTTC 1100

74 CCAAGAGGTAGAGTTCATCAAGAACTCGTCAACATCATTTGTGGCATCTGCG 133

1101 CCACTTTTGGGACAGCGGACCGAGCTGGGCGGAGCGAGGAGGGGCGGACAGGCCA 1160

134 CTTTCTACTGAGGTGGG-----CGTAGCGGCGCTGTCTCCAAAGGACGCCAAGGAGC 187

1161 TGTCACTGGCCATCTGAGAGTCATCGATGCTGTGCTGCTCTCCGATCTTCAAGCTGT 1220

188 TG---CTGGGCTCTCGGGGCTGTGCGGTGTGCTGGCATCTTGGCATCTTTAAAGTGA 244

1221 CCGGCACTCAAGGCGCTGCAAACTTTGGGCGAGAGCGTTGGGCGCTCCATCGGTGAGC 1280

245 CCGGCACTTTGGGCGCTGCGGGTCTGTGGGCGACAGGCTCCGAGCGACAGCAAGAGT 304

Db 1281 TGGGCGCTCTCATCTTTTCTCTTCATCGGTGTGCTCTTTTCCAGCGCGCTACT 1340

305 TCTGTGCTCATCATCTTCTCTGCTGTGCGCTGTGATCTTCGACCATGATCTACT 364

1341 TTGCCGA-----AGTTACCGGGGTGACTCCCATTTCA 1373

365 ACCCGAGAGATAGGGGCGACAGCCCATGATGCCAGCGGCTGAGCACACGACTTAA 424

1374 CTAGCATCCCTGAGTCTTGTGTGGGCGGTAGTCAACCATGATTAAGTTGGATTGAG 1433

425 AGAATATCCCATCGCTTGTGTGGGCGGTGTACCATGAGACCGCTGGCTATGAG 484

1434 ACATGACCGCCCTCACTGTGTGGTGGCAAGATAGTGGCTCTGTGTGCTATGCGGGC 1493

485 ACATGTACCGGACGAGTGTGTGCGGATGCTGTGGGGGCTGTGTGCGCTGGCGGGC 544

1494 TGTGACTATTTCTCTGCGAGTGGCGGCTCATTTGTCCAAATTCAGTACTTTTA 1548

545 TCTCATCATCGCATGCGCGCTGCGCTCATCTGTAACATTTGGGATGTATTA 599

RESULT 11

US-07-955-916-6

Sequence 6, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHLEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1805 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-955-916-6

Query Match 9.9%; Score 173.8; DB 1; Length 1805;

Best Local Similarity 60.9%; Pred. No. 1.6e-25;

Matches 355; Conservative 0; Mismatches 192; Indels 36; Gaps 3;

Db 981 TGGAGAGCGTGTGATTTGTTGCTTCTCTTGGAGCTGTGAGCTGTCAGCTCTCCGTGCTGTC 1040

Db 879 TCGAGGGGCTGCGGTGCTGATTACCTTCAGTTTCCTCAATGCGTGTGCTTCCTGCG 938  
 Qy 1041 CAGCAGAGCGATCTTTCTTCAAGACGTATGAACCTCATCGATTTTGTGGCTATCCTTC 1100  
 Db 939 CCACAAAGGTGAATTCATCATAAGAACTCCCTCAATATCATTTGATGACTTGTGGCCATTTCC 998  
 Qy 1101 CCTACTTTGTGCACTGGGACCGGAGCTGGCCCGGACGGAGGAGGGGTGGGCCAGAGGCCA 1166  
 Db 999 CTTTCTTACCTTGAGAGTGG--CCTAAGCGGCTGTCTCTAAAGCCGCCAAGAGCTT-- 1054  
 Qy 1161 TGTCACTGGCCATCCTGAGATGATCATCCGATTTGGTGTCTTCCGATCTTCAAGCTGT 1220  
 Db 1055 -----CTGGGCTTCTCGGGGTGTGGTCTGGTGTGGGATCTCGGCGCATCTTCAAGCTGA 1109  
 Qy 1221 CCGGCGACTCAAGAGGCGCTCGCAAACTTTGGGGCAGACGCTTGGGGCTTCATGCGTAGC 1280  
 Db 1110 CCGGCGACTTGTGGGCTGAGGGTCTCGGGCCACAGCGTCGTCGACACCAAGAGT 1169  
 Qy 1281 TGGGCTTCCTCATCTTTTTCCTCTCATATCGGTGTGCTCTCTTTTCCAGCGGCTCTACT 1344  
 Db 1170 TCTGCTGCTTATCATCTTCTCTCTGCGCTGGAGTGTCTATCTTTGGCACATGATCTTACT 1222  
 Qy 1341 TTGCGCA-----AGTTGACGGGGGACCTCCATTTC 1372  
 Db 1230 ACGCGAGAGAGATGAGGGGCGACAGCCCATATGCCACCGCGCAGACACACACTTTA 1289  
 Qy 1374 CTAGCATCTCCTGAGTCTCTTGTGTGGGGGTAGTACACATGACTACATGTTGGCTATGAG 1433  
 Db 1290 AAAACATCCCCATCGGCTTGTGTGGGCTGTGTGCACCATGACGACATGGGCTATGAG 1349  
 Qy 1434 ACATGGCACCGGCTGACGTGTGGGTGGGCAAGTATGAGGCTCTGTGTGCTCATTTGGGGCG 1499  
 Db 1330 ACATGTTATCCCGACAGCTGTGTGGAGATGCTGTGGGACCTGTGTGCTGTGGCTGTG 1409  
 Qy 1494 TGTGACTATTTCCCTCCAGTGGCCGCTATTTCTTCAATTT 1536  
 Db 1410 TGTGACCATTTGCCATCGCGTGTGCTATCATCTGAACATTT 1452  
 RESULT 12  
 US-08-464-340A-1  
 : Sequence 1, Application US/08464340A  
 : Patent No. 5710019  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: LI, ET AL.  
 : TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: CARELLA, BYRNE, BRAIN, GILFILLAN,  
 : ADDRESS: CECCHI, STEWART & OLSTEIN  
 : STREET: 6 BECKER FARM ROAD  
 : CITY: ROSELAND  
 : STATE: NEW JERSEY  
 : COUNTRY: USA  
 : ZIP: 07068  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5 INCH DISKETTE  
 : COMPUTER: IBM PS/2  
 : OPERATING SYSTEM: MS-DOS  
 : SOFTWARE: WORD PERFECT 5.1  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/464,340A  
 : FILING DATE: June 5, 1995  
 : CLASSIFICATION: 435  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US94/08449  
 : FILING DATE: 28 JUL 1994  
 :  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: FERRARO, GREGORY D.  
 : REGISTRATION NUMBER: 36,134  
 : REFERENCE/DOCKET NUMBER: 325800-415  
 :  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 201-994-1700

```

? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 1
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 2127 BASE PAIRS
?
? TYPE: NUCLEIC ACID
?
? STRANDEDNESS: SINGLE
?
? TOPOLOGY: LINEAR
?
? MOLECULE TYPE: CDNA
?
DS-08-464-340A-1

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Query Match	Score	DB 1	Length
9.28;	161;	DB 1;	2127;

Matches	629;	Conservative	0;	Mismatches	630;	Indels	30;	Gaps	6;
---------	------	--------------	----	------------	------	--------	-----	------	----

QY	323	CGCCGGGGGCTGCGGCGCCGATGAGCGCGGGGTGCTCCGCGCCCGCGGCGGCTGCGAG	382
Db	438	CGCCAGGGGCTGTGAGCCCGGAGACCGCGCGCTGGATATCATCACTAAGCGGCGATC	497
QY	383	CGGCTGTGCTCAACGTGCGCGGGGCTGCGCTTTCGAGACCGGGGCGCGACGCTGGGCGC	442
Db	498	AAGTACTGCTGCGCCCTGGACACACGTGGAGAGATTCCTGCTACGCGGCTGGGCGCAGCTC	557
QY	443	TTCCCGGACACTGCTGAGAGGGAGCCCAAGCGCGCGCGGCGGCTTTCAGACAGCAGCGGGC	502
Db	558	AAGCGCTGCACCAACTTCGACGCAATCTTCACGTGTGGATGACTACGACGTCACTGCG	617
QY	503	CGCGAGTATTTCCTTCGACCGGGACCGGACCGAGCTTCGAGACCGCGTCTACTACTACAG	562
Db	618	AACGAGTTCTTTCGACCCACCGCGGGGCGCTTGGCAGTATCTTGACTCTTCTCTGCGC	677
QY	563	TTCCGGTGGGGGCTGCGCGCGCGCGGCGGACAGTGCCTGAGAGTCTTCTCTGGAAGAAGTG	622
Db	678	CGGGGCAAGCTGCGGCTGCTGCGCGCGGAGATGATGCGCGCTGTC--CTTCCAGGAGAGCTG	734
QY	623	GCTCTTACACGGGCTGGGCGCGCGCGGCTTGAGCACGCTTCGCGAGAGACGAGGGCTGCGCG	682
Db	735	CTGTACTGGGGCATTCGGGAGGACACACGTGAGAGGGTGTGCAAGGCGCGTCACTCGAG	794
QY	683	GTCGCGCCGACGCGCCCTGCGCCGCGCGGCTTGCGCCGACGCTGTGCTGCTTTTC	742
Db	795	AAGATTGAGAGATTCGCGGAGATGTGAGACGGAGAGAGACGACGCGCTGCAGAC	854
QY	743	GAGTTTCCGAGAGCTC--TCAGGCGCGCGCGGCTGCGCGTATGCTTCCGCTGTGCTC	799
Db	855	GAGGGCGCGCACACAGAGGGCCGCGCGGAGAGGGCGCGGCGCTGGGCGCTGCATGCGG	914
QY	800	ATCTCTGCTCCATCGTGTCTTCTGCTCGAGACGCTGCTGACTTCCGCGACGACGCG	859
Db	915	CGACTGCGGCATGATGGAGAGCGCGCACTCGGGGCTGCTGCGCAAGGATGTTCCGCTGC	974
QY	860	GACGGCACGGGGCTGTGCTGTGACGCGGACGCGCGCGGCTTTCGCGCTCGGTGAT	919
Db	975	C---TGTCGGTGTCTTTCGACCGTACCGCGCGCTCACTCTCGTAGACACTTGGCC	1031
QY	920	GGCTCACGCAAAATGCTGTGAAATCCACCCCGCGCTCCCTTAAAGACCCGTTCTCGTG	979
Db	1032	AGCGTGAAGGAGGAGAGAGGACGAGGCGCACTGTCCCAATGTGCCACAAGCTTTATC	1091
QY	980	GTCGAGACGCTGTGTATTTGTGTGCTCTCTTGAAGCTGTGTAGCGCTCTGTGTCT	1038
Db	1092	GTCGAGTGTGCTGTGCGCGGCTGCTTCTCCCTGAGATTCCTCTCGGCTCAATTCAGCG	1151
QY	1040	CCAAAGCAAGGCTATCTTCTTCAAGACGATGAGACCTATGATTTGTGGCTATCTT	1099
Db	1152	CCACGACAGTTGCGCTTCTCGCGAGACCGGCTGACGCTGATGACCTGGTGCCATCTTG	1211
QY	1100	CCCTACT-----TTGTGGCACTGGGACACGAGACTGGCCGCGAGGAGGGGTG	1147
Db	1212	CCCTACTACATCAACGCTGCTGGTGGAGACGGCGCGCGCGGACGCGCTGCGAAGCCGGGCG	1271
QY	1148	GCGCAG-----CAGGCACTGTACTGGCCATCTGAGAGTATCCGATTGTGTGCTGC	1201
Db	1272	GCGCAACGCTACTGGACAAGGTGGGGGCTGTGTGCTGCGCTGCTCGGGCGCTGCGATC	1331



Db 1452 TTGGCGCCCTGCTGCTACGATCAGAGACAGATGGCCACAGCCCCGAGTTCCACAGC 1511  
QY 1379 ATCCCTGAGCTCTTCTTGGGGCGGTAGTACCATCTAGTCTAGTGGCTATGAGACATG 1438  
Db 1512 ATCCCTGCTGCTGCTAGTGGCTGCTGCTATCACCATGACGAGGCTGATGAGACATG 1571  
QY 1439 GCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1498  
Db 1572 GTCCCGAGGAGACACCCCGGCGCAGGTAGTGGCCCTGAGACATCTGAGCGGATCCTG 1631  
QY 1499 ACATTTTCCCTGCGAGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1558  
Db 1632 CTCATGCTCTCCAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1691  
QY 1559 ACAGAGGCGAGAGGCTGGATGTTTCAG 1587  
Db 1692 AACAGAGCAGAGAGGATGATGTTTCG 1720

RESULT 14  
US-08-464-340A-3  
; Sequence 3, Application US/08464340A  
; Patent No. 5710019  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,340A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449  
; FILING DATE: 28 JUL 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEO ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA  
; US-08-464-340A-3

Query Match 8.7% Score 152.8; DB 1; Length 2483;  
Best Local Similarity 53.0%; Pred No. 2e-21;  
Matches 350; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 980 GTGAGACGCTGTGATTTGTTGCTCTGAGCTGCTGACCTGCTGCTGCTGCTGCTGCTG 1039  
Db 1357 GTGAGAGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416  
QY 1040 CCAAGCAAGGCTATCTTTCAAGAAAGTGAACCTCATGATTTTGTGCTATCTTT 1099

Db 1417 CCCAACAAGCTGCACTTCTGCGCTGTCTCTTATGAAATGTTGAGACGTGCGCATCTC 1476  
QY 1100 CCCACTTTTGGGACAGTGGGACACGAGCTGGCCCGGAGAGGGGGGCGGACAGAGCC 1159  
Db 1477 CCCCTTACGTGAGACCTGACGCTGACGCTGAGCTGGGTCCCGCATGATGAGAGTACCAAC 1536  
QY 1160 ATGTCACTGGCCATCTGAGAGTCAATCCGATTTGGTGGCTGCTTCCGATCTTCAAGCTG 1219  
Db 1537 GTGAGAGAGGCGGTGCAAG---GGCTGCGGATCATATGCGCATTCGGCGCATCTTCAACCTG 1593  
QY 1220 TCCCGGACCTCAAGAGGCGCTGCAAAATCTTGGCCAGACGCTTGGGGCTTCATGCGTAG 1279  
Db 1594 GCCCGCATCTCTCGGCGCTGAGAGACCTCATGATGCTTCAAGCGCACCTTCAAGGAA 1653  
QY 1280 CTGGGCTCTGCAATCTTTTCTCTTCTGATGAGGTGGTGTCTCTTTCCAGCGCGCTGAC 1339  
Db 1654 CTGGGCTGCTGCTCATGATGATGAGTGGATGCTTCTGCTTCTGCTGCTGCTGCTGCTGCT 1713  
QY 1340 TTGCGCAAGTTCACGCGGTGAGTCCCATTTTCATGATGATGATGATGATGATGATGATG 1399  
Db 1714 ACCATGAGAGAGAGGACATTCAGAGACCTGTTTAAAGACATCCCGCATCTTCTGCTG 1773  
QY 1400 GCGGTAGTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1459  
Db 1774 GCCATGATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1833  
QY 1460 AAGTATGTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1519  
Db 1834 AAGCTCAAGCGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1893  
QY 1520 GTGATGCTTCAATTTGACCTTTTATCACCGGAGACAGAGGCGAAGAGGCTGAG 1579  
Db 1894 CCCATGATCAACAATTTGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1953  
QY 1580 ATGTTACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1639  
Db 1954 AAGCAGAGCTGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2013

RESULT 15  
PCT-US94-08449A-3  
; Sequence 3, Application PC/TUS9408449A  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Potassium Channel protein 1 and 2  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449A  
; FILING DATE: SUBMITTED HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2483 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA  
; PCT-US94-08449A-3

Query Match 8.7%; Score 152.8; DB 5; Length 2483;  
Best Local Similarity 53.0%; Pred. No. 2e-21;  
Matches 350; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 980 GTGGAGACGCTGTATTTGGTTGCTTCTTGTAGCTGCTGTAGCCCTCGTCTGT 1039  
Db 1357 GTGGAGACGCGGTGATTTGGCTGTACCTGGAGTACCTGCGCTTCTGTCTCA 1416  
QY 1040 CCAAGCAAGGCTATCTTCTTCAAGACGTGATGACCTCATGATTTTGGCTATCTT 1099  
Db 1417 CCAACAAAGCTGACTTCCGGCTGCTCTTCATGACATGTGACGTGCTGGCATCTC 1476  
QY 1100 CCGTACTTTGTGGCACTGGGCAACGAGCTGGCCGAGGAGGGGTGGGCCAGAGCC 1159  
Db 1477 CCGTCTAGGTGAGCCTCAGCTCAGCAGCTGGGTGGCCGATGATGAGCTGACCAAC 1536  
QY 1160 ATGTCACTGGCCATCCTGAGAGCATCCGATTTGGTGTCTTCCGATCTTCAAGCTG 1219  
Db 1537 GTGCACAGACCGGTGAG--GCGTGGGATCATCGCATCGCGCATCTTCAAGCTG 1593  
QY 1220 TCCCGGACCTCAAGGGCTGCAATCTTGGGCAAGACGCTTGGGCTTCATGCTGAG 1279  
Db 1594 GCCCGCATCTCCGCGGCTCGAGACCTCACCATGCTTCAAGGCAAGCTTCAAGAA 1653  
QY 1280 CTGGGCTCTCTCATCTTTTCTCTTCATCGGTGTGGTCTCTTTTCCAGGCGCTTAC 1339  
Db 1654 CTGGGCTCTCTCTCATCTTACCTGGGAGTGGGTATCTGCTTCTGCTGGGCTAC 1713  
QY 1340 TTGGCGAAGTTGACGGGTTGACCTCCATTCACATGATCCCTGATGCTCTGTGG 1399  
Db 1714 ACCATGGACAGACCATCCAGAGACCTGTTAAGAACATCCCAAGTCTTGTGG 1773  
QY 1400 GCGGTAGTACCATGACTAGTTGGCTATGAGACATGAGACCCGCTCACTGGGTGGC 1459  
Db 1774 GCCATCATCACCATGACACACGCTGGCTAAGGGACATCTACCCCAAGACAGCTGAGC 1833  
QY 1460 AAGATAGTGGGCTCTGTGTGTCATTTGCGGGCTGCTGACTATTTTCCCTGCGAGTCCC 1519  
Db 1834 AAGCTCAAGCGGCTCATGACTTCTGTGTGTCATTTGCTGCGCCCTGCGCATCCAC 1893  
QY 1520 GTCATTTGCTCAATTTCAAGTCTTTTATCAACGGGAGACAGAGGGCCGAAGAGCTGG 1579  
Db 1894 CCGATCATCAACACTTTTGTCAAGTACTACAAACAGAGGCGTCTGTGAGACCGCGGCC 1953  
QY 1580 ATGTTAGCCATGTGACATGAGCCTTGTGCGCCACTGAGGGCAAGGCCAATGGGGG 1639  
Db 1954 AAGCAGAGCTGAGCTGATGGAACCTCACTCAGACAGCGGGGCGAAGGCAAGACGGG 2013

Search completed: February 20, 2003, 06:35:04  
Job time : 102.811 secs









## ORIGIN

Query Match 23.5%; Score 410.8; DB 14; Length 1058;  
Best Local Similarity 68.9%; Pred. No. 3.5e-70;  
Matches 601; Conservative 0; Mismatches 252; Indels 19; Gaps 2;

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OY 457 GCTAGGAGACCGACGCGCGCGCTCTTACGACGACGCGCGCGAGTATTTCTT 516
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 19 GCTGGGCGACCCCAACGCGGCGCATGAGTACTTCGACCGCGCTCCGACAGGACTTCTT 78
OY 517 CGACGCGACCGCGCGCGCTTGCAGCGCGCTCTTACTACTACAGTCCGGTGGCGGCT 576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 CGACGCGACCGCGCGCGCTTGCAGCGCGCATCTCTACTACTATCAGTCCGGGCGCGCAT 138
OY 577 GGGGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 636
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 CGCGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 198
OY 637 GGGGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 696
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 GGGGCGAGGAGCGCGCATGAGTATTCGCGAGGAGGAGGCGCTTCTGCGGAGGAGGAGCG 258
OY 697 CCCCCGCGCGCGCGCGCTTGCAGCGCGCTGCGCTGCGCTTTCGAGTTTCCGAGAG 756
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 GCGCTTGGCGCGCGCGCGCTTGCAGCGCGCATGAGTATTCGCTGCTGAGTACCGGAGAG 318
OY 757 CTCTGAGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 816
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 319 CTCCGCGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 378
OY 817 CGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 379 CATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
OY 877 TCGTGCAGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 GTGCGAGGAGTATTCGAGGAG-----CCGGGAGACGCGAGCTGCGG 480
OY 937 TGGAAATTCACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 GTCCGCGCGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 997 TTTGTTGTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 CATCTGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 1057 CTTCAGGAGCGTATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1116
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 CTGCGGAAACATCATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 660
OY 1117 GGGGACGCGAGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 GGGTACCGAGCTGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
OY 1177 GAGAGTCATCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 GGGGTCATCCGCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
OY 1237 CCGGCAATCTTGGCGGAGCGCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 GCTGAGATCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
OY 1296 TTTTCTCTTCAATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327
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DB 841 TCTTCCCTTTAATGAGGAGGAGTCTTTTTC 872
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RESULT 3  
LOCUS AO939702 443 bp DNA linear GSS 23-AUG-2000  
DEFINITION NR5-028R Human NotI clones Homo sapiens genomic, DNA sequence.  
ACCESSION AO939702  
VERSION AO939702.1 GI:7216080

KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 443)

AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovsky,V.V., Xie  
L., Muravenko,O.V., Kozirev,S., Petrenko,L., Skobeleva,N., Li,J.,  
Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlstedt,C.  
NotI clones in the analysis of the human genome

JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)

MEDLINE Contact: Podowski RM

COMMENT Center for Genomics Research

17177 Stockholm, Sweden

Tel: +46-8-728-6372

Fax: +46-8-337983

Email: Raf.podowski@cgr.ki.se

Class: NotI site.

Location/Qualifiers

1..443

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Human NotI clones"

/note="Organ: Lung; DNA was isolated from A549 cells after

sodium arsenite exposure for 4 weeks. This fragment was

differentially methylated relative to untreated controls

and was identified using methylation sensitive Ap-Pcr and

sequenced."

BASE COUNT 43 a 167 c 152 g 80 t 1 others

ORIGIN

Query Match 22.9%; Score 399.4; DB 17; Length 443;  
Best Local Similarity 99.1%; Pred. No. 5.2e-68;  
Matches 422; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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OY 477 GCGGCGCTTCTGAGACGACGCGCGCGAGTATTTCTTGCAGCGGACCGCGCGCT 536
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DB 1 GCGGCGCTTCTGAGACGACGCGCGCGAGTATTTCTTGCAGCGGACCGCGCGCT 60
OY 537 TCGACGCGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TCGACGCGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 120
OY 597 CGCTGACGCTTCTGAGAGAGTGGCTTCTTACGAGGCTGGGCGCGCGCGCTTGGCAC 656
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CGCTGACGCTTCTGAGAGAGTGGCTTCTTACGAGGCTGGGCGCGCGCGCTTGGCAC 180
OY 657 GCGTGGCGGAGGAGGAGGCTGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCT 716
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 GCGTGGCGGAGGAGGAGGCTGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCT 240
OY 717 TCGCGCGCGAGCTGTGGCTCTTTTTCGAGTTTCCGAGAGCTTCAAGGCGCGCGGTGC 776
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 TCGCGCGCGAGCTGTGGCTCTTTTTCGAGTTTCCGAGAGCTTCAAGGCGCGCGGTGC 300
OY 777 TCGCGGAGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 TCGCGGAGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
OY 837 TGCCTGACTTCCGCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 895
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 TGCCTGACTTCCGCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 419
OY 896 CCGGTG 901
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 420 CCGGTG 425
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RESULT 4  
LOCUS CNS02RD3/ 900 bp DNA linear GSS 14-MAY-2000  
DEFINITION CNS02RD3/

DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 15H12 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL210432.1 GI:7869251
VERSION	AL210432
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
AUTHORS	1 (bases 1 to 900) Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 900) Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
TITLE	Unpublished
JOURNAL	3 (bases 1 to 900)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
FEATURES	location/Qualifiers
source	1..900 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="159H12" /clone_1lb="G" /note="Genoscope sequence ID : C0AG159D06LP1-end : 77"
BASE COUNT	206 a 242 c 283 g 166 t 3 others
ORIGIN	
Query Match	21.1%; Score 368.2; DB 17; Length 900;
Best Local Similarity	68.4%; Pred. No. 6.9e-62;
Matches 589; Conservative 1; Mismatches 224; Indels 47; Gaps 4;	
QY	712 CGCCTTCGCCGCCGACGCTGTGCTCTTTGAGATTTCCCGAGACTCTCAGCGCGG 771
Db	899 CGATTTTCAAGCGGAGATCTGGCTCTCTCTGAGTACCGGAGACTCTCAGCGCGAG 840
QY	772 CGTGTCCGCGGAGTCTCCGTCGTGGTATCTCGTCCATCGTCTTCTGCTCGA 831
Db	839 GGGCATTCGGGTGCTCTCCGCTCTGTATCTCATCTCATGTGATCTTGTGCTGGA 780
QY	832 GACGCTGCCTGACTTCCGCGAGACCGGACGGGCGGCTGCTGTCAGCCGACG 891
Db	779 GACGCTGCGGGAGTTCAAGGAGAGAGA-----GTAAGTGGACCGCGGG 733
QY	892 CGGCGCGGTGTTCCCGCTCCGCTGTAATGGCTCCAGCCAAATGCTGGAATTCACCCG 951
Db	732 GCAATCTCCAGCGGACCGACCGACGATTTTAC----- 702
QY	952 CCTGCGCTTCAATGACCGCTTCTTGCTGGTGGAGACGCTGTATTTGTTGGTCTCTT 1011
Db	701 ---GCCTTCAACGACCCCTTTTATGTGTGGAGAGGCTGTGCATCATCTGGTCTCTT 645
QY	1012 TGAGCTGCTGAGACCTCTCGTGGTGTGTCACAAAGCTATCTCTTCAAGACGTAT 1071
Db	644 TGAGATTATAGTGTGCTCTTTCGCCAGCCGCCAGCAAAAGCGCTTCTTTAAACATCAT 585
QY	1072 GAACCTCATCATTTTGTGGCTATCTTCCCTACTTGTGTGGCATGGGACCGAGCTGGC 1131

Df	584	GAACTCCATAGACATCGTGTCCATTGTCCTTATTTCATCACTCTGGCAGGACTTGCC	525
Oy	1132	CCGGAGGAGGAGGGGAGGCCACAGACCATGTCACATGGCACATCCCTGAGAGTATCCGATT	1191
Df	524	CCAGCACCAGGAGCAAGGGGACAGAACGCATGAS - TTGCGCATCTCGAATAATATCCGGCT	466
Oy	1192	GGTGGCTGTCTTCGCGATCTTTCACAGCTGTCCCGGCACTCCAAAGGGCGCTGAATCTTGGG	1251
Df	465	GGTCCGCGGTGTCCGATCTTTCATCTCCAGACATCCCAAAGGGGCTGCAGATCTTGGG	406
Oy	1252	CCAGACGCTTGGGGGCTCCATGCTGAGCTGGGCGCTCCCATCTTTTCTCTTCATCGG	1311
Df	405	CCATACCCCTGCGCGGACATGAGGAGACTGGCCCTCTCATTTTCTTGTGTAATCG	346
Oy	1312	TGTGTCCTCTTTTCCAGCGCGCTTACTTTGCGAATTCACCGGCTGAGACTCCCATTT	1371
Df	345	CGTCACTCTCTTCTTCACAGCGGCTTACTTGGCGAGGCGGAGCCGACCTCCCATTT	286
Oy	1372	CACTAGCATCCCCTGAGTCTTGTGTGGGCGGTAGTCACCATGACTACAGTTGGCTATGG	1431
Df	285	CACGACATCCCGGAGCGGTGTGTGGGCTGTGTAACCATGACGAGCGTGGCTACGG	226
Oy	1432	AGACATGGCAGCCCGTCACTGTGGGAGAAATAGTGGGCTCTCTGTGTGCCATTTGGCGG	1491
Df	225	CGATATGGAACCTATACAGGTGTGGGAGAAGTCTGTGGCTCCCTGTGCGCATTCGGCGG	166
Oy	1492	CGTGTGATATTTTCTTCCAGTGTCCCGGTCAATTTGTCTTCCAAATTTACAGTCTTTATCA	1551
Df	165	CGTGTAAAGATCGGCGCTGCC - GTCCGCGTCACTGTGTCCAATTTAATTACTTTTACA	107
Oy	1552	CCGGAGAGACAGAGGGCGAAGA	1572
Df	106	CCGGAGAGCGATTAACGAAGA	86
RESULT 5			
LOCUS	CNS03DK/C		
DEFINITION	CNS03DKC	839 bp DNA	linear GSS 15-MAY-2000
	Tetradon nigroviridis genome survey sequence T7 end of clone		
	017A20 of library G from Tetradon nigroviridis, genomic survey		
	sequence.		
ACCESSION	AL339205		
VERSION	AL339205.1	GI:7898340	
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetradon nigroviridis.		
ORGANISM	Tetradon nigroviridis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Aclimopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorphi; Acanthopterygii; Perciformes; Tetraodontifomes;		
	Tetraodontidae; Tetraodon.		
REFERENCE	1 (bases 1 to 839)		
AUTHORS	Roeest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,		
	Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F.,		
	Saurin,W. and Weissbach,J.		
TITLE	Human gene number estimate provided by genome wide analysis using		
JOURNAL	Tetradon nigroviridis DNA sequence		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 839)		
	Roeest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C.,		
	Bouneau,L., Billaud,A., Quetler,F., Saurin,W., Bernot,A. and		
	Weissbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the		
JOURNAL	freshwater pufferfish Tetradon nigroviridis		
REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 839)		
	Genoscope.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (12-APR-2000)		
AUTHORS	This sequence is a single read and was generated as part of a large		
COMMENT	scale clone-end sequencing project of the Tetradon nigroviridis		
	genome. For more information, please take a look at		
	<a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .		





cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: L1CM1826 row: d column: 21  
High quality sequence stop: 830

BASE COUNT	179 a	264 c	233 g	200 t
ORIGIN				

Qy	1163	TCGGGCGCATCCGAGAGGTATCGATTGGGTGGCTCTCCGATC--TTCAGAGCTC	1221
Db	623	TCCTGGGCATCTTCAGGCTATCCGCTTGGTAAGGTTTTAGATCTTCAAGCTCTC	682
Qy	1222	CCGGCAGCTCAAAAGGCGCTGCAAAATCTTGGGCGAGACGCTTCGGGCTTCATCGCTGAG--	1279
Db	683	CCGGCAGCTCAAAAGGCGCTTCAGAAATCTGGGCGAGAACTCAAGCTAGTAATGAGAGAG	742
Qy	1280	CTGGGCGCTCTCATCTTTTTCTCTTCA--TCGGTGTGGTCTCTTTTCCAGGCGCT-	1335
Db	743	CTAGGCGCGCTCATCTTTTTCTCTTCAATCGGGGCGATCCTGTTTTAGTGCATGTG	802
Qy	1336	CTACTTTTCCGGAAGTTGACCGGGTGGACTCCCATTTCACT--AGCATCCCTAGTCCCTTT	1394
Db	803	GTACTTTTCCGAGGGCGGAAGAACGTCGATCTCGGACTATCTCAGTTATCCCGATTTTTCT	862
Qy	1395	GGTGGGCGGTAGT	1407
Db	863	GGTGGGCGGTGT	875

RESULT	9
AZ339279/c	
LOCUS	AZ339279
DEFINITION	636 bp DNA linear
ACCESSION	U0070M07R Mouse 10kb plasmid uUGC1m library Mus musculus genomic
VERSION	AZ339279 Clone uUGC1m0070M07 R, DNA sequence.
KEYWORDS	AZ339279.1 GI:10413383
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus

## FEATURES

### source

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114/bp/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT  
ORIGIN

Query Match 18.5%; Score 323.8; DB 17; Length 636;  
Best Local Similarity 72.0%; Pred. No. 3e-53;  
Matches 450; Conservative 0; Mismatches 172; Indels 3; Gaps 2;

QY 977 GTGGTGAAGACGCTGTATTTGTTGTTGCTTCCCTTGAAGCTGCTGACGCTCTCTGTC 1036  
DB 636 GTGGTGAAGACGCTGTATTTGTTGTTGCTTCCCTTGAAGCTGCTGACGCTCTCTGTC 577  
QY 1037 TGTCCAAAGAGGCTATCTTCTTCAAGACGTGATGAACCTCATGATTTTGGCTATC 1096  
DB 576 TGTCCAAAGAGGCTATCTTCTTCAAGACGTGATGAACCTCATGATTTTGGCTATC 517  
QY 1097 CTTCCTTCTTGTGACCTGGGACCGACGCTGGCCGGGAGGGTGGCCACAG 1156  
DB 516 ATTCTTATTTTATCACTGTGGGACCTGAGCTGCTGACGACAAAGTAATGGGACAG 457  
QY 1157 GCCATGTCATGGGACCTGACAGATGATGATGCTGCTGCTTCCGCTTTCAAG 1216  
DB 456 GCCATGTCATGGGACCTGACAGATGATGATGCTGCTGCTTCCGCTTTCAAG 397  
QY 1217 CTGTCGCGGACCTCAAGAGGCTGCAATCTTGGGACGACGCTTCCGCTCCATGCT 1276  
DB 396 CTGTCGCGGACCTCAAGAGGCTGCAATCTTGGGACGACGCTTCCGCTCCATGCT 337  
QY 1277 GAGCTGGGCTCTCTCATCTTTTCCCTTCATGCTGCTGCTTCCGCTCCATGCT 1336  
DB 336 GAGCTGGGCTCTCTCATCTTTTCCCTTCATGCTGCTGCTTCCGCTCCATGCT 277  
QY 1337 TACTTTCCCAAGTGAACGGGGTGAAGCTCCCATTTCACTAGATCCCTGCTTCTGG 1386  
DB 276 TACTTTCCCAAGTGAACGGGGTGAAGCTCCCATTTCACTAGATCCCTGCTTCTGG 217  
QY 1397 TGGGCGGTAGTCAACATGATGCTGCTATGAGACATGACCGGCTGCTGCTGCT 1456  
DB 216 TGGGCGGTAGTCAACATGATGCTGCTATGAGACATGACCGGCTGCTGCTGCT 157  
QY 1457 GGCAGATAGTGGGCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515  
DB 156 GGCAGATAGTGGGCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 97  
QY 1516 GCGGCTATGCTGCTCA -ATTTCAGTACTTTTATACCGGAGACAGAGGCGAAGAG 1573  
DB 96 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 37  
QY 1574 GCTGGATGTTCAAGCCTGTGACA 1598  
DB 36 CTAGCCAGTACATGACGCTGGGCA 12

RESULT 10  
LOCUS BM963332 745 bp mRNA linear EST 18-MAR-2002  
DEFINITION UT-M-EO0-bm-1-05-0-UT-1 N1H-BMAP\_E00 Mus musculus cDNA clone  
IMAGE:5697484 5', mRNA sequence.  
ACCESSION BM963332  
VERSION BM963332.1 GI:19546752  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES  
source

Location/Qualifiers

1. 745  
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/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:5697484"

/tissue\_type="whole brain"

/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/note="Organ: brain; Vector: pYX-Asc; Site: 1; Ecov: I; site: 2; Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 18 agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then sequenced directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT 139 a 216 c 202 g 188 t

Query Match 18.5%; Score 322.4; DB 14; Length 745;  
Best Local Similarity 71.5%; Pred. No. 5.7e-53;  
Matches 453; Conservative 0; Mismatches 151; Indels 30; Gaps 1;

QY 990 TGTGTATTTGTTGCTTCTTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049  
DB 1 TGTGTATTTGTTGCTTCTTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
QY 1050 CTATCTTCTTCAAGAGTATGAACTCATGCTTTTGGCTATCTTCCCTACTTTG 1109  
DB 61 CGGGCTCTTCTTCAAGAGTATGAACTCATGCTTTTGGCTATCTTCCCTACTTTA 120  
QY 1110 TGGCAGTGGGACGAGCTGAGCTGGGACGAGGAGGCTG----- 1147  
DB 121 TCACTTGGGACGAGCTGAGCTGGGACGAGGAGGCTG----- 180  
QY 1148 -----GGCCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199  
DB 181 GTCAAGATGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 1200 TCTTCCGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259  
DB 241 TGTTCGCAATCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 1260 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319  
DB 301 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY	1330	TCCTTTCCAGGCGCGCTACTACTTTGGCGAAGTTGACCGGGTGGACATCCCATTTCCATAGCA	1379
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QY	1380	TCCTCTGAGTCCTTCTGTGTGGGCGGTAGTGCACCATGACTACAGTTGGCTATGAGACATGG	1439
Db	421	TCCAGAGTCCCTTCTGTGTGGGCGTGTGGTTAACATATACACCGTAGTATATGGGACATGT	480
QY	1440	CACCGGTACTGTGGGTGGCAAGATAGTGGGCTCTGTGTCCTCAATGGCGGGCGAGTGA	1499
Db	481	ACCCATATACGGGTAGGGGGCAAGATGTGTGGGCTACTGTGCCCAATTGCTGGGGTCTCA	540
QY	1500	CTAATTCCCTCCGACATGCCCCGTCAATTGTCTCCAAATTTCAGCTACTTTTATACCGGGAGA	1559
Db	541	CCATTGCAATTACCGGTACCGGTCAATTTGTCTCCAAATTTCAACTACTTTCACCCAGAGAGA	600
QY	1560	CAGAGGGCGAAGAGGCGTGGGATGTGCACCCATGT	1593
Db	601	CGGAGCAGGAGAGGAGCCAGTATACCCACGT	634

RESULT	11
BIF64377	
LOCUS	772 bp mRNA linear EST-25-SEP-2001
DEFINITION	G03046295.F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186518 5' , mRNA sequence.
ACCESSION	BIF64377
VERSION	BIF64377.1 GI:15755955
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE 1 (bases 1 to 772)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: L14M1465 row: n column: 23  
High quality sequence stop: 772.

**FEATURES**  
**source**

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186518"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). *MSCC Library."
BASE COUNT
150 a 240 c 236 g 146 t
ORIGIN

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Query Match	17.8%;	Score 311.4;	DB 13;	Length 772;
Best Local Similarity	76.68;	Pred. No. 8e-51;		
Matches 416; Conservative	0;	Mismatches 106;	Indels 21;	Gaps 2;

OY	1055	TTCTTCAAGAACGATGATACACCTTATGCATTTTGGCTATCTCTCCCTACTTTTGGCA	1114
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OY	1115	CTGGGACACCGAGTGGCCCGCAGCGAGGGGTG-----GGCCAGC	1154
Db	79	CTGGGACACCGAACTGGCAGAGAGCAGCGAGGGGGGAGAGAGCGGCCAAGATGGGCGAGC	138
OY	1155	AGGCATGTCACTGGCCATCTCGAGAGTCAATCCATTTGGTGGCTGTCTTCCGATCTTCA	1214
Db	139	AGGGCATGTCCCTGGCATCTCCGAGTCAATCCGCTGTCCGGTGTTCGCGATCTTCA	198
OY	1215	AGCTGTCCCGGACCAAGAGGGGCTCGAAATCTTGGGCGAGCGGCTTGGCGTCCATATGC	1274
Db	199	AGCTTCTCCCGCACCTCCAAAGGGGCTGCAGATCTCTGGGCAAGACCTTGGCAGGCTTCATGA	258
OY	1275	GTGAGCTGGGGCTCCCTATCTTTTTCNCTTCATCCGATGTGGTCCCTTTTCCAGCGCG	1334
Db	259	GGGAGCTGGGGGTGCTCATCTTCTCTTCATCGGGGTCATCCTCTTCCAGTGGCG	318
OY	1335	TCTACTTTGGCGAAGTTACCGGGGTGGACTGCCATTTACTAGCATCTCCTAGTCTTCT	1394
Db	319	TCTACTTTGGCAGAGGCTACAAACGAGAA--CCCATTTCTTAGCAATCCCTACGCGTCTCT	377
OY	1395	GGTGGCGGTAGTACCATGACTACAGTTGGTATGAGAGCATGGCACCAGCATCTGG	1454
Db	378	GGTGGCGAGTGTACCATGACCATGTGGGGTACGGGGACATGAGGCCATCACTGTGG	437
OY	1455	GTGGAGAGATAGTGGGCTCTCTGTGTGCCATTTGCGGGGCTGTCGACTATTTTCCCTGCAG	1514
Db	438	GGGGCGAAGATGCTGGGGCTGCTGTGTGGCATATGGCGGGGGTCTCTACCATTTGCCCTGGCTG	497
OY	1515	TGCGCGTCAATGTCTCCAAATTTACAGTACTTTTATCACCGGAGACAGAGGGCGAAGAGG	1574
Db	498	TGCGCGTCAATGTCTCCAAATTTACAGTACTTTTATCACCGGAGAGGAAAGGATCAGCAGGAGC	557
OY	1575	CTG	1577
Db	558	CGG	560

RESULT	12
LOCUS	BM128683
DEFINITION	575 bp linear mRNA EST 12-MAR-2002
ACCESSION	U147408.1
VERSION	1
KEYWORDS	Human
SOURCE	Human
ORGANISM	Homo sapiens

REFERENCE	AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 575)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, L., Seearce, M., Bresnelli, J., Graowm, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wile, T., Martin, D., Blistahn, A., Schmitt, A., Theising, B., Rilter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., Mccann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.	Endocrine Pancreas Consortium
Unpublished (2000)	
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue	

Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmeitone@hcmp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center for information on





QY	1207	CATCTCAAGCTGTCGCCGACCTCAAAAGGCGCTGCAAACTTTGGGCGACGACCTTCGGAG	1266
Db	121	CATCTCAAGCTGTCGCCGACCTCCAAAGGCGCTGCAAGTCTCGGGCAAAAGCTTAAAGC	180
QY	1267	CTCCATGCGAGCTGGGCGCTCCATATCTTTTTCCTCTCATCGGTTGAGTCCTTTTC	1326
Db	181	GTCCATCGGGAGCGCTGGGATTTGCTATCTCTCTTTATTTGGGCGATCCCTTTCTC	240
QY	1327	CAGGCGCGTCTACTTTTGGCCGAAGTTGACCGGGTGAGTCCCATTTTCACTAGCATCTCTGA	1386
Db	241	CAGGCGCGTCTACTTTTGGCCGAGAGACGACCCCACTTTCAGGTTTTCACAGCATCCCGGA	300
QY	1387	GTCTCTTGAGTGGGGGGTAGTACCATATGTAAGTTGGATGGAGATAGGACCCCGT	1446
Db	301	TGCTCTTGAGTGGGGAGGTGTATCCATATCAACAATGGGATAGGCGGATATGACCCCACT	360
QY	1447	CACCTGTGGGTGGCAAGATAGTGGGCTCTCTGTGTCCTATTCGGGGCGTGTACTATTTC	1506
Db	361	GACCATAGGGGGCAAGATGTGGGATCTCTGTGCCATCGCGGTGTCTTGACCATGGC	420
QY	1507	CTTGCCAGTGGCCGCTCATTTGTCTCCAAATTTAGCTACTTTTATTCACGGGAGACAGAGG	1566
Db	421	ATTGCGCAATTTCCCGATGTTGTTCCAACTTCAATTACTTCAACACCGGAGACAGAGG	480
QY	1567	CGAAGAGCGCTGGATGTTTCAAGCATGTTGG	1595
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RESULT 14	LOCUS	DEFINITION
BO807519	BO807519	628 bp mRNA linear EST 31-JUL-2002
	NISC_Rk05c10.y2	NCI-CCAP_Brn72 Macaca mulatta CDNA clone
	IMAGE:5330682.5	mRNA sequence.

ACCESSION	B0807519
VERSION	B0807519.1
KEYWORDS	GI:22031728
SOURCE	EST.
ORGANISM	rhesus monkey. Macaca mulatta

REFERENCE	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Ceropithecidae; Cercopithecinae; Macaca.
TITLE	1 (bases 1 to 628)
JOURNAL	NCI-CCGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

FEATURES  
source  
Email: cgapds-remail.nih.gov  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
info@image.llnl.gov  
Plate: LLAM11839 row: E column: 19  
Seq primer: M13RPL reverse primer (ABI).  
Location/Qualifiers  
1. .628

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/_db_host="DHL0B (phage-resistant)"
/_note="Organ: brain; Vector: pCMV-SPORT6, ccdb; Site:1:
Not; Site:2: EcoRV; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 2.2 kb. Constructed by
Invitrogen. Note: this is a NCL_CGAP Library."
BASE COUNT. 105 a 212 c 181 g 130 t
ORIGIN

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query Match	17.3%;	Score 302;	DB 14;	Length 628;
Best Local Similarity	68.5%;	Pred. No. 5.3e-49;		
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QY	525	ACGGCCCGCAGCTTGCAGCCCGTGCCTACTACTACAGTCCGGTGGGCGGCTCGCGGCGC	584
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QY	585	CGGGCCAGTCCCGCTGCAGCGTTCCTGGAAGAGTGGCCCTTCAAGGGGCGGGCGGG	644
Db	63	CGGTCAACGTGCCCATCAATCATCTTCTCCGAGGAATCCGCTTTCACAGCTGGGGGAGG	122
QY	645	CGGGCTTCGGCAACGCTTCGGCGAGAGAGAGGGGTGCCCGGGTGCGCCCGACGCCCTTC	704
Db	123	AGGGCCATGGAAGAATTCCGGCGAGAGAGAGGGCTTCTGGGGAGAGAGAGCGGCCCTTGC	182
QY	705	CCCCCGCGCCTTCGCCCGGCCAGCTGTGGCTCTTTTGCAGTTTCCCGAGAGCTCTCAG	764
Db	183	CCCCCGCGAGCTTCAGAGGCCAGAGTGGCTCTTTCGAGTACCCCGGAGACTCCGGGC	242
QY	765	CGCGCGCGGTGTCGCGCTAGTCTCGTGGCTGGTATCCTCTCTCCATCGTCTCTTCT	824
Db	243	CAGCCCGGGGCGATCGCATCGTGTCCGTCTGTCTATCTCATCTTCATCTGTCTATCTTCT	302
QY	825	GCGTTCGAGACGTGCTCTGACTTTCGCGAGACCGCGAGCGGCAACGGGGCTTGTCTGCAG	884
Db	303	GCGTCGAGACGCTGCGGGAATTCGCCGACGAGAAAGACTACCCCGCGCTCGCCAGG	362
QY	885	CGGCGCGCGCGGCTGTTCCTCCGCTCGCTAATGGCTCCAGCCAAATGGCCGGAATTC	944
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QY	945	CACCCCGCCTGCCCTTTCATATGACCCGTTCTCTGTGGTGAAGACGCTGTATTTTGTGGT	1004
Db	418	-----CTTCTCGGATCCCTTCTTCTGTGGTGAAGACGCTGTATCATCATCTGTCT	464
QY	1005	TCTCCTTTGAGCTGTGGTATCGCTCCGCTGTGTGTCACGAAGAAGGTATCTTCTTCAAGA	1064
Db	465	TCTCCTTTGAGCTGTGTGGTGGCTTCTTCTGCTTGTCTTACGAAGCAACCTCTCTCGCGA	524
QY	1065	ACGTGATGAACCTCATGATTTTGTGGCTATCCTTCCCTACTTTTGTGGCACTGGGCACCG	1124
Db	525	ACATCATGAACCTCATGATTTGTGGCATTTGGCCATCATCCCTATTTTATCATCTGGGATACG	584
QY	1125	AGCTGGCCCGGAGGAGGAGGGTGGGCCAGACAGCCATGTCACTG 1168	
Db	585	AGCTGGCCGAACGACAGGCGCAAGCAAGCAAGCCATGTCTGTG 628	

[illegible]

Thu Feb 20 15:28:12 2003

us-09-804-014a-7.rst

Page 12

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Job time : 2924.68 secs
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FEATURES	SOURCE
AUTHORS	Roest-Crolius,H., Jallion,O., Dasilva,C., Fitzmes,C., Fisher,C., Bonneau,L., Billault,A., Quetler,F., Sarrin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater puiferfish Tetraodon nigroviridis
JOURNAL	unpublished
REFERENCE	(bases 1 to 1060)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/tetraodon">http://www.genoscope.cns.fr/tetraodon</a> .
BASE COUNT	238 a 239 c 231 g 309 t 43 others
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Matches 437; Conservative 0; Mismatches 198; Indels 4; Gaps 2;	/db_xref="taxon:99883"
	/clone="020L19"
	/clone_1lb="A"
	/note="Genoscope sequence ID : C0A0A20CF10C1-end : T7"
997 TGGAAATCCACCCGCCGCCCTTCATATGACCCCTTCTTCGGTGGAGAGCGCTGTAT	17.0%; Score 296.6; DB 17; Length 1060;
8 TGCACACCATCTCCNNAAGCCATCTCCNATCCCTTTCATCTCGAGACCGTTGAT	68.4%; Pred. No. 6.4e-48;
997 TTTGTTGTTCTCTTTGAGCTGCTGTGACGCGCTCCTGCTGTGTCACAGCAAGGTATCTT	0; Mismatches 198; Indels 4; Gaps 2;
68 TGCTTGGTTCTTTTGTAGCTGTGTGTCAGATTTTGGGCTGTCTCTACAGAAAGATT	
1057 CTTCAAGACGTGATGAACCTTCATCGATTTTGTGGCTATCCTTCCCTACTTTTGGCACT	
128 CTTCCACACCTTCATGAACAATTTGATATGATATGATATTCATCCCTTATTTTGTAAACGT	
1117 GGGACCCGAGCGCGCGCGACGCGAGGGGTGGGC--CAGACGGCATGTACATGGCCAT	
188 GGTTCACAGAAATCTTCACAAACCGGAGGAGAGCTCAGAGACAGAAATGTCTTGGCCAT	
1174 CCTGAGAGTCATCCGATTTGTGTCGTCCTCCGATCTTCAAGCTGTCCCGCACTCAAA	
248 TCTGCGCATCTTCGCTGGTTAGAGTATTCGATCTTTTCAAACTCTCAGCAATTCGAA	
1234 GGGCCTGCAAAATCTTGGGCGCAGACGCTTGGGCTTCATCGGTGAGCTGGGCTCTCTAT	
308 GGGTGTGAGATCTCCGAGACAGACCCTGAAGAAAGCATGTGGTGA-NTTGGTTGGCTCAT	
1294 CTTTTCCTCTTCATCGGTGTGTCGTCCTTTTCCAGCCGCGCTCTCTTGTGCGAAGTTGA	
367 TTTTTCCTCTTCATCGGGGCTCATCTCTTCTCCAGTCTATCTACTTGTCCGAGGTGCA	
1354 CCGGCTGAGCTCCATTTCTACTAGCATCCCTGAGTCTTCTGTGGTGGGCGGTAGTCACCAT	
427 CGAGCCAAACACGCGAGTTGTTAGATACCCGATGCGCTTGTGGTGGCGCTGTTACCAT	
1414 GACTACAGTTGGGATGAGACATGGACACCGCTCATCTTGGGTGGCAAGATAGTGGCTC	
487 GACTACTGTGGGATATGGGAGCATGTGTCCATCATCCTTGGGAGGCAAAATGTGGGGCAC	
1474 TCTGTGTGCCATTTGGGCGCTGTGACTATTTTCCCTGCGCATGGCCGATTTGTCCAA	
547 GCTGTGGCCCATTCGTGGAGTGTACCATATGTCTGTGCTCTCCCGCATTTGTTCGAA	
1534 TTTCAGCTACTTTTATACCGCGGAGACAGAGGCGGAGAA 1572	
607 CTTTAACACTTCTACACAGAGAGACAGAGAGCTGAGGA 645	







QY	1574	GGCCACTGGAGGGGCAAGGCATGGGGGGCTGTGTACGCGGGAGGTACTAGCTAACAC	1633
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QY	1634	CTCCACTCTGGGCGACCCCGCCAGGAACACTGTGTACCGCAAGTGTGA	1680
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LOCUS			
DEFINITION	Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete cds.	1447 bp	linear PRI 19-JUN-2001
ACCESSION	AF315818		
VERSION	AF315818.1	GI:14485554	
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ORGANISM	Homo sapiens.		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1447)		
TITLE	Bardien-Kruger, S., Wulff, H., Arleff, Z., Brink, P., Chandy, K.G. and Corfield, V.		
JOURNAL	KCNAT, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)		
REFERENCE	2 (bases 1 to 1447)		
AUTHORS	Bardien-Kruger, S., Wulff, H., Arleff, Z., Brink, P., Chandy, K.G. and Corfield, V.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape town 7535, South Africa		
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Best Local Similarity	99.4%;	Pred. No. 3.1e-19;	
Matches 1405; Conservative	0;	Mismatches 3;	Indels 5; Gaps 2;
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QY	328	CCGTGCGGCTGCTGTCGAGCGGCTGTGCTCAACGTGCGCGGCTGCGCTTCGAGACGGG	387
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QY	388	GCGGCGACGCTGCGCGCTTCCCGACACTGTGCTAGGGGACCCAGCGCGCGCGCGCGC	447

Db	119	GGCGGAGCGCTGGGCCGCTTCCGGAGCACTGCTGCTAGGGGAGACCCAGCGGGCGCGCGCG	178
QY	448	TTCTACGAGCAGCGCGCGCGCAGTATTTTCTTGACCGGCACCGGCCCACTTTCAGCGCC	507
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QY	508	GTGCTCTACTACTACCAAGTCGGGTGGGGGGGTGCGGGGGCGCGGCGCAGTGGCGCTGCGAC	567
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QY	988	CGCCTTCCTGGCTGTGTCGAAGCAAGGCTATCTTCTTCAGAAGCTGATGAACCTCATCAT	1047
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RESULT 5  
LOCUS 126643 1599 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 9 from patent US 5559009.  
ACCESSION 126643  
VERSION 126643.1 GI:1606513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1599)  
Chandy, K.G., Kailman, K., Chandy, G. and Gutman, G.A.  
Voltage-gated potassium channel gene, Kv1.7, vectors and host cells  
comprising the same, and recombinant methods of making potassium  
channel proteins  
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;  
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Location/Qualifiers  
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Query Match 63.6%; Score 1069; DB 6; Length 1599;  
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LOCUS AF032099  
DEFINITION Mus musculus voltage-gated potassium channel Kv1.7 (Kvnc7) mRNA,  
complete cds.  
ACCESSION AF032099  
VERSION AF032099.1 GI:3004906  
KEYWORDS  
SOURCE Mus musculus.



ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 1599)  
 TITLE  
 Kalkan, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G.,  
 Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M.,  
 Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.  
 Genomic organization, chromosomal localization, tissue  
 distribution, and biophysical characterization of a novel mammalian  
 Shaker-related voltage-gated potassium channel, Kv1.7  
 J. Biol. Chem. 273 (10), 5851-5857 (1998)  
 JOURNAL  
 MEDLINE  
 PUBMED  
 9488722  
 2 (bases 1 to 1599)  
 REFERENCE  
 Kalkan, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G.,  
 Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M.,  
 Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.  
 Direct Submission  
 Submitted (30-OCT-1997) Physiology and Biophysics, University of  
 California at Irvine, Irvine, CA 92697, USA  
 AUTHORS  
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DEFINITION Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.			
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VERSION AC008687.5 GI:15887249			
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AUTHORS 1 (bases 1 to 157633)			
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.			
JOURNAL Direct Submission			
AUTHORS Unpublished			
TITLE 2 (bases 1 to 157633)			
JOURNAL DOE Joint Genome Institute.			
AUTHORS Direct Submission			
TITLE Direct Submission			
AUTHORS Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell			
JOURNAL Drive, Walnut Creek, CA 94598, USA			
REFERENCE 4 (bases 1 to 157633)			
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.			
AUTHORS Direct Submission			
TITLE Direct Submission			
AUTHORS Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell			
JOURNAL Drive, Walnut Creek, CA 94598, USA			
COMMENT On Oct 3, 2001 this sequence version replaced gi:10312243.			
Direct Sequence Produced by DOE Joint Genome Institute			
www.jgi.doe.gov			
Finishing Completed at Stanford Human Genome Center			
www.shgc.stanford.edu			
Quality: Phrap Quality >=40 99.9% of Sequence;			
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Matches 819; Conservative 0; Mismatches 8; Indels 0; Gaps 0;			
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Dd	82137	CTTCCCTGAGTTCCTCCCGCTCGGTGAATGGCTCCAGCCAAATGCTGGAAATCCACCCC	82138
OY	914	GCTTCGCCCTTCATATACCCGTTCTTCGATGATGAGAACGCTGTATTTGTTGTTCTCTCT	973
Dd	82137	GCTTCGCCCTTCATATACCCGTTCTTCGATGATGAGAACGCTGTATTTGTTGTTCTCTCT	82078
OY	974	TTCAGCTCTGCTGATACCCCTCTGTCGTGTGCCAAGAAGGCTATCTTTCTTCAAGAACGTGA	1033

Db	82077	TTGAGCTCTGGTACGCTCCGGTCTGTGCCAAGCAAGGCTATCTTTCAAGAACGTGA	82018
Qy	1034	TGAACCTCATGCATTTTGTGGCTATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGG	1093
Db	82017	TGAACCTCATGCATTTTGTGGCTATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGG	81958
Qy	1094	CCCCGACACGAGGGGTGGGGCCAGCGAGGCGATGTCACCTGGGCCATCCTGAGAGTCATCCGAT	1153
Db	81957	CCCCGACACGAGGGGTGGGGCCAGCGAGGCGATGTCACCTGGGCCATCCTGAGAGTCATCCGAT	81898
Qy	1154	TGTCGTCTGTCTTCCGCATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCMAATCTTGG	1213
Db	81897	TGTCGTCTGTCTTCCGCATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCMAATCTTGG	81838
Qy	1214	GCCAGAGCTTGGGGCTCCATGCGTGAAGCTGGGGCTCCTCATCTTTTTCCTCTTCATCG	1273
Db	81837	GCCAGAGCTTGGGGCTCCATGCGTGAAGCTGGGGCTCCTCCTCATCTTTTTCCTCTTCATCG	81778
Qy	1274	GTCGTGCTCTCTTTCACAGCCCGCTCTACTTTGCCGAGTTGACCGGGGTGAGCTCCCAT	1333
Db	81777	GTCGTGCTCTCTTTCACAGCCCGCTCTACTTTGCCGAGTTGACCGGGGTGAGCTCCCAT	81718
Qy	1334	TCACAGCATCCCTGAGTCCTTCTGTGGGGCGGTATGCACATGACATGACATGCTGCTATG	1393
Db	81717	TCACAGCATCCCTGAGTCCTTCTGTGGGGCGGTATGCACATGACATGACATGCTGCTATG	81658
Qy	1394	GAGACATGGCACCCGTCACACTGTGGGTGGCAAGATAGTGGGCTCTGTGTGGCCATTTGCGG	1453
Db	81657	GAGACATGGCACCCGTCACACTGTGGGTGGCAAGATAGTGGGCTCTGTGTGGCCATTTGCGG	81598
Qy	1454	GGGTCTACACTATTTTCCCTGGCAGAGTCCCGTCATTTGCTCCAAATTCAGCTATTTTATC	1513
Db	81597	GGGTCTACACTATTTTCCCTGGCAGAGTCCCGTCATTTGCTCCAAATTCAGCTATTTTATC	81558
Qy	1514	ACCGGAGACAGAGGGGCGCAAGAGCTGTGGAGTTTCAGCCATGTGGACATGACAGCTTGTG	1573
Db	81537	ACCGGAGACAGAGGGGCGCAAGAGCTGTGGAGTTTCAGCCATGTGGACATGACAGCTTGTG	81478
Qy	1574	GCCCACTGAGGGGCAAGGCCAATGGGGGGCTGTGGACGGGGAGGTACCTGAGCTACAC	1633
Db	81477	GCCCACTGAGGGGCAAGGCCAATGGGGGGCTGTGGACGGGGAGGTACCTGAGCTACAC	81418
Qy	1634	CTCCACTCTGGGCAACCCCCAGAGGAACACTGTGTACCCGAAGTGTGA	1680
Db	81417	CTCCACTCTGGGCAACCCCCAGAGGAACACTGTGTACCCGAAGTGTGA	81371
RESULT 8			
LOCUS	OCU38240	1551 bp	DNA
DEFINITION	Oryctolagus cuniculus glibenclamide-sensitive voltage-gated potassium channel (Kv1.3-glib) gene, complete cds.		
ACCESSION	U38240		
KEYWORDS	U38240.1 GI:3264840		
SOURCE	Oryctolagus cuniculus.		
ORGANISM	Oryctolagus cuniculus		
REFERENCE	1 (bases 1 to 1551)		
AUTHORS	Yao, X., Chang, A.Y., Boulpaep, E.L., Segal, A.S. and Desir, G.V.		
TITLE	Molecular cloning of a glibenclamide-sensitive, voltage-gated potassium channel expressed in rabbit kidney		
JOURNAL	J. Clin. Invest. 97 (11), 2525-2533 (1996)		
MEDLINE	96249424		
PUBMED	8647945		
REFERENCE	2 (bases 1 to 1551)		
AUTHORS	Desir, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-OCT-1995) Gary Desir, Medicine, Yale, 2074 LMP 333 Cedar Street, New Haven, CT 06510, USA		
COMMENT	On Jun 29, 1998 this sequence version replaced gi:1033191.		





<b>Db</b>	2438	TCTTGACCATGCATTCGCGATTCCCGGATTTGGTTCACAATTACTTAATTCTTCAGCACCC	2497
<b>Oy</b>	1517	GGGAGCAGAGGGCGAGAGCGCTGGGATGTTCACGCATGTGG	1558
<b>Db</b>	2498	GGGAGACAGAAAGGGGAMAGAGCAATCCAGTACATGACAGTGG	2539
<b>RESULT 10</b>			
<b>AL365361/c</b>			
<b>LOCUS</b>			
<b>DEFINITION</b>	Human DNA sequence from clone RP11-284N8 on chromosome 1, complete sequence.		
<b>ACCESSION</b>	AL365361		
<b>VERSION</b>	AL365361.1		
<b>KEYWORDS</b>	HTG.		
<b>SOURCE</b>	human.		
<b>ORGANISM</b>	Homo sapiens		
<b>REFERENCE</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
<b>AUTHORS</b>	1 (bases 1 to 155343)		
<b>TITLE</b>	Mashreghi-Mohamadi,M.		
<b>JOURNAL</b>	Direct Submission		
<b>COMMENT</b>	Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk On or before May 15, 2001 this sequence version replaced g1:7283305, g1:12718091. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems; such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/RGP/chr1 RP11-284N8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6 <b>IMPORTANT:</b> This sequence is not the entire insert of clone RP11-284N8 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-284N8 is at 1 in this sequence. The true left end of clone RP1-244G5 is at 155244 in this sequence. The true right end of clone RP11-470J19 is at 76605 in this sequence.		
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<b>SOURCE</b>	Location/Qualifiers		
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	/clone_1lb="RPCI-11.1"		
	119305..119344		
<b>misc_feature</b>	/note="Sequence from overlapping clone AL513469. Assembly confirmed by restriction digest."		
	126615..127120		
<b>misc_feature</b>	/note="Sequence from overlapping clone AL513469. Assembly confirmed by restriction digest."		

BASE COUNT	43992 a	32617 c	34987 g	43747 t	
Query Match	38.3%; Score 643.2; DB 9; Length 155343;				
Best Local Similarity	66.3%; Pred. No. 3.3e-79;				
Matches 983; Conservative	0; Mismatches 473; Indels 26; Gaps 3				
OY	83	GCGGGCGGGGGGGGGGGGGGCGAGGCGAGGGCGGGCGTCCGGCAGAGAGGGGGCGGGG	142		
Db 121634	GCCCGCACCGGGCCACCTCTTACAGCCCGCAGCGAGCGAGCGGGTCCACACGCTG	121575			
OY	143	GCCCTGTGCGCCCTCCGCCCGCGGGGGGTACAGTGGCCCCCTCCCTGGCCCTTACGGCG	202		
Db 121574	GTTAGACACAGCGCTACGCGGAGGCCCGCGAGGCCCGGAGCTGCGCCGACATGACGTG	121515			
OY	203	CTGGCGGCTATTATTTTAAAGCGCGAGACCGGACCGGACCGGAGACCGGGCTGGGGCGGGTGG	262		
Db 121514	GTCGCCGGGGGA--CCACCTGCTGAGACCGGAGGTGGCCGATGATGGAGGGGCCCCGCTC	121457			
OY	263	GGGGCCACACGTGGGTTCGGGGGTCCCGGGGGCTGGCGGGGCCATGGAGGCGGGTCCCG	322		
Db 121456	AAGGCGGCTGTGGCGGGCGGCTCGAGCCGTACAGCGCGCTGCCGCCCTTACTACTCCG	121397			
OY	323	CCGC-----CCCGTGGCGGCTGCTGGAGCGGCTGGTGTCTCAACGTGGGCCGGCTCGCT	376		
Db 121396	CGCGGGGAGAGAGAGACTTCTCGGGGAGCGCGTGTCTATCAACATCTCCGGCTTCGCT	121337			
OY	377	TGAGACCGGGGGCGGCGACGCTGGGGCGGCTTCCCGGACACTGCTGTAGGGGACGACGC	436		
Db 121336	TGAGACGCGAGCTGAAAGACCTTTGGCAATTCGCCGAGACGGTGTGGGGGACCCCAAG	121277			
OY	437	GCCGGCGCGCTTCTTACAGCAGCAGCGCGCGCGAGTATTCTTTCAGCCGACCGGCCCA	496		
Db 121276	GCGCATGAGTACTTCGACCCGCTCCGCAAGAGTACTTTCGACCCCAACCGGCCCA	121217			
OY	497	GCTTGACGCGCGCTGCTACTACTACACTCCGCTGGGGGGGGGGCGGGCGCGGCGGACAG	556		
Db 121216	GCTTGAGCGCCATCCTTACTACTATCACTCCGGGGGCGCATCCGCGGGGTAAAG	121157			
OY	557	TGCCCTCGACCTTCTTCCGGAAGAGTGGCTTTCACGGGGTGGGGCGGCGGCCCTG	616		
Db 121156	TGCCCATGACATTTTCTTCCGAGAGATTCGGTCTTACACAGTGGGGCGAGAGGCATGG	121097			
OY	617	CACGCCCTGCGGAGAGCAGAGGGCTGCGCGGTGCGCCCGACAGCGCGCCCTTCCCGCCG	676		
Db 121096	AGAACTTCCGCGAGGACGAGGGCTTCTTCCGGAGAGAGAGGGCGCTTTCGCCCGCGCG	121037			
OY	677	CCTTGCGCGGACGCTGCTGCGGAGAGTTCCTTTCAGAGAGTCTCAAGCGCGCGCGG	736		
Db 121036	ACTTCCAGGGCCAGAGGTGTGCTCTTTCGAGTACCCCGAGAGACTCCGGCGGGCGCGG	120977			
OY	737	TGCTTCGCGCTAGCTTCCGCTGCTGATCTCTGTCATCTGTCATCTGCTTCTTCCGCTGAGA	796		
Db 120976	GCATGGCCATCGTGTTCGCTGCTGATCTCTTCTCATCTTGTGATCTTCTGCTGGAGA	120917			
OY	797	CGCTGCTGACTTCCGCGAGCAGACCGCGAGCGGAGCGGCGTGTGCTGAGCGCGACCGG	856		
Db 120916	CGCTCGCGGAGTTCGCGCGAGGAAAGACTTACCCCGCTTCGACGTGCGAGACTCATTTG	120857			
OY	857	GCCCGGTGTCCCGCTCCGCTGTAATGGCTCCAGCCAAATGCTTGGAAATCCACCCCGCG	916		
Db 120856	AAGCAGCC-----GGCAACAGCAGTGGGGGTCGCCGCGAGGAGCT	120815			
OY	917	TGCCCTTCATAGCCCGTCTTCGAGTGGAGACGCTGTGTATTTTCTGGTTTCTCCTTGG	976		
Db 120814	CGAGCTTCTCCGATCCCTTCTTCGTGTGTGAGAGAGCTGTGTCATCTGTGTTCTCTTGG	120755			
OY	977	AGCTGCTGGTACGCTCTGCTGTCTGTCCAAAGCAAGGCTATCTTCTTCAAGAAAGCTATGA	1036		
Db 120754	AACCTGCTGGTGGGTTCCTTCGCTGTGCTTACGAAGCCACCTTCTTCGGCAACATCATGA	120695			
OY	1037	ACCTCATGATTTTGGCTATCTTCCCTACTTTGTGGCACTGGGACCGAGCTGGCC	1096		







Query Match	Score	DB	Length
37.9%	637.4	DB 9	3004
70.4%	Pred. No. 4.2e-78		

  

Query Match	Score	DB	Length
37.9%	637.4	DB 9	3004
70.4%	Pred. No. 4.2e-78		

	Matches	876:	Conservative	0:	Mismatches	351:	Indels	18:	Gaps
QY	314	CGGTGCGCCGCGCCCGCTGCGGCTGCTGCGACGCGGCTGGTCTCAACGTCGCCGGGCTGC	373						
Db	208	CGCGCGCGGGGCGAGGAGGAGCTGCGGGGAGCGCGGTGCTATCAACATCTCGCGGCTTC	267						
QY	374	GGTTCGAGACGGGGGGGCGGCGACGCTGGGGCGGCTCCCGGACACTCGTGCATAGGGGACCCG	433						
Db	268	GGTTCGAGACGGAGCTGAAGACCTTTTGGCAAGTTCCCGAGACGCTGCTGGGCGAACCCA	327						
QY	434	CGCGCGCGCGCGCTTCTCAAGACGACGCGCGCGCGAGTATTTCTTCGACGCGCACCGCG	493						
Db	328	ACGGGGCGCATGAGAGTACTTCGACCGCGCTCCGCAACGAGTATCTTCGACCGCAACCGCG	387						
QY	494	CCAGCTTCGACGCCCGGCTCTACTACTACACTCGGTGGGGGGGCGTGGCGCGCGCGCGCG	553						
Db	388	CCAGCTTCGACGCCCATCTCTACTACTATCACTCCGGGGGCGCATCCGCGCGCGGTCA	447						
QY	554	ACGTGCGCGCTCGACGCTCTCTGGAAGAGAGTGGGCTTCTACGAGGCGTGGGCGCGCGCG	613						
Db	448	ACGTGCGCCATCGACATTTTCTCCGAGGAGATCCGGTTCACAGAGTGGGCGAGAGGCCA	507						
QY	614	TGGCACGCTCGCGCGAGAGCGAGGGCTGCCCGGTGCGCCCGACGCGCCCTTGCCCGCC	673						
Db	508	TGGAGAAAGTTCGCGCGAGGACGAGGGCTTCTCGGGAGGAGGAGCGCGCTTGCCCGCC	567						
QY	674	GGCGCTTCGCGCGCGCAGGCTGGGCGCTTTTGAGATTTCCGAGAGGCTTCAGGCGCGCG	733						
Db	568	GGGACTTTCAGGCGCCAGGAGTGGGTGCTCTTTGAGATACCCCGAGAGCTCCGGGCGCGCC	627						
QY	734	GGGTGCTGCGCGCTAGTCTCGTCCGTTGTCATCTCGTCTCATCTGTCGTTCTGCTCG	793						
Db	628	GGGGCATCCCATCTGATCGTCCGTGTCGTCATCTCTCATCTGTCATCTTCTGCTCG	687						
QY	794	AACAGCTGCTGCTACTTCGCGCGACGACCGCGAGCGCAACGGGGCGTGTGCTGACGCGCG	853						
Db	688	AACAGCTGCTCGAGATTCGCGCGACGAGAGAGACTACCCCGCTCGACGTCGACGAGATCAT	747						
QY	854	CCGGCGCGGTGTTCCCGCGCTCCGCTGAAATGGCTCCAGCCCAATATGCTGAAATTCACCC	913						
Db	748	TGGAAGCAG-----CGGCAACGACGTCGGGGTCCCGCGCAGGAG	789						
QY	914	GGCTGCGCTTCATATACCCGCTTCTTGTCGTGTCGACAGCGTGTGATTTTGTGGTCTCT	973						
Db	790	CCCTCAGCTTCTCCCATATCCCTTCTTGTCGTGTCGACAGCGTGTGTCATCATCTGTCTCT	849						
QY	974	TTGAGCTGCTGTAGCGCTCGCTGTCGTGTCGCAAGCAAGGCTATCTTCTTCAGAAACGTGA	1033						
Db	850	TGCACTGCTGGTGGGTTCTTCGCTGTGTCGTCAGCAAAACCACTTCTTCGCAAAACATCA	909						
QY	1034	TGAACCTCATGATTTTGTGCTATCTCTTCTCTCTACTTTGTGCACTGGGACCGGACGTGG	1093						
Db	910	TGAACCTCATGACATTTGTGGCATCATCTCTTATTTATCATCTGTGGGTACCGAGCTGG	969						
QY	1094	CCCGGCGAGGAGGGGGGGGCGCGACGCGGCACTGCACTGGGCGCATTCGAGAGATCATCCGAT	1153						
Db	970	CCGAAAGCAGAGGGCAATGAGACAGCGGCCATCTCTGTGGCATCTCTGAGGGGTCATCCGCC	1029						
QY	1154	TGGTGTGTGTCTTCGCGATCTTCAAGCTGTCCCGGCACTCAAAAGGCGCTGCAAAATCTTGG	1213						
Db	1030	TGGTAAAGGTTCTTCGCGATCTTCAAGCTTTCGCGCATCTCAAAAGGCGGTGCGATCTCG	1089						
QY	1214	GCCAGACGCTTGGGGCTCTCATGCTGAGCTGGGCTCTCATCTTTTCTCTCTCATCG	1273						
Db	1090	GCCAAACGCTGAAGGCGTCCATGCGGAGACTGGGATGTGCTCATCTTCTTCCCTTTATGG	1149						
QY	1274	GGTGGTGTCTTTTTCACGCGCGCTACTACTTTCGGAATTCGCGGGGAGATCCCATTT	1333						
Db	1150	GGGTATCTCTTTTCTTCACGCGCGGTCTACTTTTCCGAGGCAACGACCCACTTAAAGTT	1209						
QY	1334	TCACTAGCATCCCTAGTCTTCTGTGTGGCGGTATGTCACCATGATCATGTTGGCTATG	1393						
Db	1210	TATAGAGCATCCCGGATGCTCTCTGTGTGGCGGTGTATACCATGTCAACACAGGGGTTACG	1269						



OY	1394	GAGATATTGGACCCCTGACTGTGGGTGGCAGAATGTGGGCCTGTGTGGCAATTTGGG	1453
Dd	1270	GCGAATATGCACCACCACTGACCATATGGGGCACAATTGTGGATCTTCTGTGGCAATGCCG	1329
OY	1454	GGTGTCGTAATAATTTCCCTGCCAGTAGCCCGATCTGTCTCCAAATTCAGTACTTTATTC	1513
Dd	1330	GTGTGTGACCATTCGATTTGCGAGTTCCCGATGATTGTTTCCAAATTCATTAATCTTCAC	1389
OY	1514	ACCGGAGACAGAGAGGGCGCAAGAGCTGGGAGATTGATGCCCATTTGG	1558
Dd	1390	ACCGGAGACAGAGAGGGAAGAGCAATCCAGTACATGCACAGTTGG	1434
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RESULT 14			
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HUMPCD	DEFINITION	Human potassium channel protein (HPCN3) gene, complete cds.	
HUMPCD	VERSION	M55515	
HUMPCD	KEYWORDS	M55515.1 GI:189672	
HUMPCD	SOURCE	potassium channel protein.	
HUMPCD	ORGANISM	Human DNA.	
HUMPCD	REFERENCE	Homo sapiens	
HUMPCD	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
HUMPCD	REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
HUMPCD	REFERENCE	Phillipson,L.H., Lamendola,J., Bell,G.I. and Steiner,D.F.	
HUMPCD	REFERENCE	Genomic sequence of a human potassium channel related to RCK3	
HUMPCD	REFERENCE	Unpublished (1990)	
HUMPCD	REFERENCE	2 (bases 1 to 1820)	
HUMPCD	REFERENCE	Phillipson,L.H., Hice,R.E., Schaefer,K., Lamendola,J., Bell,G.I.,	
HUMPCD	REFERENCE	Neilsen,D.J. and Steiner,D.F.	
HUMPCD	REFERENCE	Sequence and functional expression in Xenopus oocytes of a human	
HUMPCD	REFERENCE	insulinoma and islet potassium channel	
HUMPCD	REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 88 (1), 53-57 (1991)	
HUMPCD	REFERENCE	91095456	
HUMPCD	REFERENCE	1986382	
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Best Local Similarity	70.3% ; Pred. No. 7.6e-78 ;		
Matches	875 ; Conservative 0 ; Mismatches 352 ; Indels 18 ; Gaps 1 ;		
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Dd	250	CGGCGCGCGGCGGAGAGAGACTGTCTGGGAGCGGCTGTATCAACATCTCCGGGCTGC	309
OY	374	GCTTGAGAGACGGGGCGGCACGCTGGGCGCTTCCCGGACACCTGCTGATGGGACCCAG	433
Dd	374	GCTTGAGAGACGGGGCGGCACGCTGGGCGCTTCCCGGACACCTGCTGATGGGACCCAG	433

[illegible]

QY 1514 ACCGGAGACAGAGCGGAGAGCTGGATGTTCAACCTATGG 1558  
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RESULT 15  
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LOCUS Canis familiaris delayed rectifier K+ channel mRNA, partial cds.  
DEFINITION U08596  
ACCESSION U08596  
VERSION U08596.1 GI:475721  
KEYWORDS  
SOURCE  
ORGANISM  
Canis familiaris.  
Canis familiaris.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 1780)  
Overturf, K.E., Russell, S.N., Carl, A., Vogalis, F., Hart, P.J.,  
Hume, J.R., Sanders, K.M. and Horowitz, B.  
Cloning and characterization of a Kv1.5 delayed rectifier K+  
channel from vascular and visceral smooth muscles  
Am. J. Physiol. 267 (5 Pt 1), C1231-C1238 (1994)  
JOURNAL MEDLINE 95068303  
PUBMED 7977686  
REFERENCE 2 (bases 1 to 1780)  
Overturf, K.E.  
AUTHORS  
TITLE  
Direct Submission  
Submitted (08-APR-1994) Overturf K. E., University of Nevada at  
Reno, Department of Physiology, North Virginia St., Reno, NV 89557,  
USA

FEATURES  
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CDS  
BASE COUNT 293 a 608 c 577 g 302 t  
ORIGIN

Query Match 37.1%; Score 624; DB 4; Length 1780;  
Best Local Similarity 64.9%; Pred. No. 3.1e-76;  
Matches 988; Conservative 0; Mismatches 500; Indels 34; Gaps 3;

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QY 402 CCGCTTCGCGACACCTGTGTAGGAGCCAGCGCGCGCGCGCTTCTGAGACGCG 451  
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QY 522 CCACTCGGCTGGCGCGCTGGCGCGCGCGCGCGCGCGCTGCGCTGAGCTTCTTGAAGA 581  
Db 495 CCACTCGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCTGCGCTGAGCTTCTTGAAGA 554  
QY 582 GGTGCGCTTCTAGGCGCTGGCGCGCGCGCGCGCGCGCGCGCTGCGCGAGAGAGGCG 631  
Db 555 GATCGCTTCTTACAGCTGGGGGACGAGCGCTTGGAGCTTCTTCCGAGAGAGAGGCTT 614  
QY 642 CCGCGTCCCGCTGCT 701  
Db 615 CATCAAGAGAGAGAGAGAGCGCGCTGCCCGCAACGAGTTCCAGACGAGAGTGGCTT 674  
QY 702 TTTCGAGTTTCCGAGAGCTCTCAGCGCGCGCGCGCTGCGCTGCTGCTGCTGCT 761  
Db 675 CTTCGAGTACCCGAAAGCTCCGCGTCCGCAAGGCGCATGCTGCTGCTTCTTCT 734  
QY 762 CATCTCGTCTCATGCTGCTGCTTCTGCGCGAGAGCGCTGCTGCTGCGAGAGAGCG 821  
Db 735 CATCTCATCTCATCATCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794  
QY 822 CGAGCGACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875  
Db 795 CGAGCTGCTGCGCGCATCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 854  
QY 876 GCTGAATGCTCCAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935  
Db 855 GCAGCG 914  
QY 936 CTTCGCTGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995  
Db 915 CTTCATCTGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974  
QY 996 GGTCTGTCAGCAAGGCTATCTTCTTCAAGAGCGTGAACCTCATGATTTTGGC 1055  
Db 975 CGCGTCCCGCAGCAAGCGAGGCTTCTGCGAACAATCATGATATGACTGCTGGC 1034  
QY 1056 TATCTCTCCCTACTTGTGAGCTGCGACCGAGCTGCGCGCGCGCGCGCGCGCG 1102  
Db 1035 CATCTTCCCTTACTTATCATCTTGGGACCGAGCTGCGCGCGCGCGCGCGCGCG 1094  
QY 1103 -----GAGGCGTGGCGCAGCGCGCATGTCAGTGGCGCATCTGAGAGTATCGGANT 1154  
Db 1095 AGGGGCTGCGCAATGAGCGAGCGCATGTCCTGCGCGCATCTCATGAGTATCGGCT 1154  
QY 1155 GGTGCTGCTTCCGATCTTCAAGCTGTCGCGCACTCAAAAGGCGCTCAAAATTTGG 1214  
Db 1155 GGTGCGGCTGCTTCCGATCTTCAAGCTTCCGCGCACTCAAAAGGCGCTCAAAATTTGG 1214  
QY 1215 CCAAGAGCTTGGCGCTTCAAGCTGAGCTGGGCTCTCATCTTTTCTTCTTCAATCG 1274  
Db 1215 CAAGAGCTTGAAGGCTTCAATGAGGAGCTGGGCTCTCATCTTTCTTCTTCAATCG 1274  
QY 1275 TGTGCTCTCTTTTCCAGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1334  
Db 1275 TGTGCTCTCTTTTCCAGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1334







XX 20-SEP-2001.  
PD  
XX  
XX 12-MAR-2001; 2001WO-US07735.  
PF  
XX 10-MAR-2000; 2000US-0188277.  
PR 10-MAR-2000; 2000US-0188316.  
PR 14-MAR-2000; 2000US-0189139.  
PR 14-MAR-2000; 2000US-0189140.  
PR 17-MAR-2000; 2000US-0190231.  
PR 17-MAR-2000; 2000US-0190401.  
XX  
PA (CURA-) CURAGEN CORP.  
PI Padigaru M, Vernet CM, Fernandes E, Shinkets RA, Spaderna SK;  
PI Majumder K, Li L;  
XX  
XX WPI: 2001-570869/64.  
DR P-PSDB; AAU08660.  
XX  
XX Novel polypeptides and nucleic acids homologous to members of collagen,  
PT potassium channel, tufellin family of proteins for diagnosing, treating  
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders  
PT  
XX  
XX  
PS Claim 9; Page 15-16; 128bp; English.  
XX  
XX The invention relates to isolated NOVX (NOVX1-11) polypeptides and  
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides  
CC and anti-NOVX antibodies are useful for treating or preventing a  
CC pathology associated with NOVX polypeptide in humans and for treating a  
CC syndrome associated with human disease e.g. disorders characterised by  
CC altered cell motility, proliferation and migration e.g. cancer,  
CC angiogenesis and wound healing (NOVX-3), neurological disorders, e.g.  
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's  
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,  
CC asthma, hypertension and seizure (NOV4), enamel defects, such as  
CC amelogenesis imperfecta and disorders involving enamel defects,  
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic  
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem  
CC encephalitis occurring during testicular cancer, diabetes, reproductive  
CC health, metabolic and autoimmune disorders, gastrointestinal disorders,  
CC immune disorders and autoimmune diseases, respiratory disorders, bone  
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell  
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and  
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders  
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that  
CC binds to it and a cell expressing NOVX polypeptide is useful for  
CC identifying a therapeutic agent for use in treatment of a NOVX related  
CC pathology. The antibodies and a polypeptide having 95% sequence identity  
CC to NOVX polypeptide are useful for treating a pathological state in a  
CC mammal. The present sequence encodes NOV4, a possible voltage gated  
CC potassium channel.  
XX  
XX  
SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;  
Query Match 100.0%; Score 1680; DB 22; Length 1747;  
Best Local Similarity 100.0%; Pred. No. 2, 4e-301;  
Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 218 CTTCTCGGCGCCCTAGCCGCTGCGGGCTATTTCAGCGGACACGGACACCGGA 277  
Qy 241 CACCGGCGTGGGGCGGGGTGCGGGCCACAGTGGTTCGGGGTCCGGGGCTGGCG 300  
Db 278 CACCGGCGTGGGGCGGGGTGCGGGCCACAGTGGTTCGGGGTCCGGGGCTGGCG 337  
Qy 301 CGCCATGAGCGCGGTGCGGGCCCGCGCGGTGCGGTGCGAGCGGTGCTCAAC 360  
Db 338 CGCCATGAGCGCGGTGCGGGCCCGCGCGGTGCGGTGCGAGCGGTGCTCAAC 397  
Qy 361 GTGGCGGCGGTGCGGTGCGAGCGGGCGCGGTGCGGGTCCGGGACGACTG 420  
Db 398 GTGGCGGCGGTGCGGTGCGAGCGGGCGCGGTGCGGGTCCGGGACGACTG 457  
Qy 421 CTAGGGGACCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 480  
Db 458 CTAGGGGACCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 517  
Qy 481 GACCGGACCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 540  
Db 518 GACCGGACCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 577  
Qy 541 CGCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 600  
Db 578 CGCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 637  
Qy 601 GCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 660  
Db 638 GCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGCGGATTTCTTC 697  
Qy 661 CCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 720  
Db 698 CCGCGCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 757  
Qy 721 TCTAGCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 780  
Db 758 TCTAGCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 817  
Qy 781 GTCTTCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 840  
Db 818 GTCTTCGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 877  
Qy 841 GCTCAGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 900  
Db 878 GCTCAGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 937  
Qy 901 GGAATCAGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 960  
Db 938 GGAATCAGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 997  
Qy 961 TGTTCGTTCTTCGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTG 1020  
Db 998 TGTTCGTTCTTCGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTG 1057  
Qy 1021 TTCAAGAACGTGATGAACTGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1080  
Db 1058 TTCAAGAACGTGATGAACTGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1117  
Qy 1081 GGCACCGAGTGGCGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 1140  
Db 1118 GGCACCGAGTGGCGCGCGGTTCACAGCAGCGCGCGGATTTCTTC 1177  
Qy 1141 AGATTCATCGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200  
Db 1178 AGATTCATCGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1237  
Qy 1201 CTGCAAAATTTGGGCGAGAGCTTGGGCGTTCATGCTGAGCTGCTTCATCTTT 1260  
Db 1238 CTGCAAAATTTGGGCGAGAGCTTGGGCGTTCATGCTGAGCTGCTTCATCTTT 1297  
Qy 1261 TTCTCTTTCATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320

Db 1298 TTCCTTCATCGGTGTGCTCTTTTCCAGCCCGCTACTTTCGCAAGTTGACCGG 1357  
OY 1321 GTGACATCCCATTTCACTAGCATCCCTGAGTCTTCTGGTGGGGGAGTACCATGACT 1380  
Db 1358 GTGACATCCCATTTCACTAGCATCCCTGAGTCTTCTGGTGGGGGAGTACCATGACT 1417  
OY 1381 ACAGTTGGCTATGAGACATGAGACCCGTCACATGTGGGTGGCAAGATAGTGGCTCTCG 1440  
Db 1418 ACAGTTGGCTATGAGACATGAGACCCGTCACATGTGGGTGGCAAGATAGTGGCTCTCG 1477  
OY 1441 TGTGGCATTTGGGGGCTGTGACTATTTCCCTCCAGTCCCGCTCATTTGTCCTCAATTTTC 1500  
Db 1478 TGTGGCATTTGGGGGCTGTGACTATTTCCCTCCAGTCCCGCTCATTTGTCCTCAATTTTC 1537  
OY 1501 AGCTACTTTTATACCGGGGAGACAGAGGGGGAAGAGGCTGGATGTTTACGCATGTGGAC 1560  
Db 1538 AGCTACTTTTATACCGGGGAGACAGAGGGGGAAGAGGCTGGATGTTTACGCATGTGGAC 1597  
OY 1561 ATGACAGCTTTGTGGCCCACTGAGAGGCAAGGCCAATGGGGGCTGTGTGACGGGAGGTA 1620  
Db 1598 ATGACAGCTTTGTGGCCCACTGAGAGGCAAGGCCAATGGGGGCTGTGTGACGGGAGGTA 1657  
OY 1621 CCGAGACTACACACTCTGCGGCAACCCCGAGGGACACTGTGTACCGAAGTGTGA 1680  
Db 1658 CCGAGACTACACACTCTGCGGCAACCCCGAGGGAAACACTGTGTACCGAAGTGTGA 1717

## RESULT 2

AAD37899  
ID AAD37899 standard; cDNA: 1792 BP.

AC AAD37899;

DT 10-SEP-2002 (first entry)

XX Human ion channel protein encoding cDNA.

XX Human; novel human protein; NHP; ion channel protein; forensic biology;

KW pharmacogenomic; drug screening; mental disorder; biological disorder;

KW symptomatic manifestation; phenotypic manifestation; medical disorder;

KW gene; SS.

XX Homo sapiens.

XX OS

XX FH

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

XX FT CDS

CC The present invention relates to novel human proteins (NHPs), human ion  
CC channel proteins and polynucleotides encoding such proteins. Sequences of  
CC the invention are useful in therapeutic, diagnostic and pharmacogenomic  
CC applications. They are useful for the identification of protein coding  
CC sequences, for mapping a unique gene to a particular chromosome, as  
CC additional DNA markers for restriction fragment length polymorphism  
CC (RFLP) analysis and in forensic biology, for screening libraries,  
CC isolating clones, preparing templates for cloning and sequencing, as  
CC hybridisation probes, in microarrays or other assay formats, to screen  
CC collections of genetic material from patients who have a particular  
CC medical condition, to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay. NHPs are useful  
CC for the detection of mutant human proteins or inappropriately expressed  
CC proteins for the diagnosis of disease, for the generation of antibodies,  
CC for screening for drugs effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of the  
CC protein in the body, for identification of other cellular gene products  
CC related to the protein and as reagents in assays for screening for  
CC compounds that can be used as pharmaceutical agents in the therapeutic  
CC treatment of mental, biological or medical disorders and diseases. The  
CC present sequence is a cDNA encoding human ion channel protein.

SQ Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other:

Query Match 82.8%; Score 1390.2; DB 24; Length 1792;  
Best Local Similarity 99.1%; Pred. 7.7e-248;  
Matches 1420; Conservative 0; Mismatches 8; Indels 5; Gaps 2;

OY 248 CTGGGGGCGGGGCGGGGCGGACACAGTGGTGGGCGGGGCGGGGCGGGGCGGCATG 307

Db 36 CGGGGCGGGGCGGGGCGGGGCGGACACAGTGGTGGGCGGGGCGGGGCGGGGCGGCATG 95

OY 308 GAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 367

Db 96 GAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 153

OY 368 GGTGCGCTTCAGAGCGGGGCGGGGCGGACAGTGGGCGGGGCGGGGCGGGGCGGGGCGGC 427

Db 154 GGTGCGCTTCAGAGCGGGGCGGGGCGGACAGTGGGCGGGGCGGGGCGGGGCGGGGCGGC 213

OY 428 ACCGAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 487

Db 214 ACCGAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 273

OY 488 ACCGAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 547

Db 274 ACCGAGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGC 333

OY 548 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607

Db 334 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393

OY 608 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 667

Db 394 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453

OY 668 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727

Db 454 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 513

OY 728 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787

Db 514 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573

OY 788 GCTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 847

Db 574 GCTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633

OY 848 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907

Db 634 CGGCGCGAGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 690

OY 908 CACCGCGCTGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967

Db 691 CACCCGCGCGCCCTTCAATGACCGGTTCTCGGTGGAGACCGCTGTATTTGTTGGT 750  
 Qy 968 TCTCTTTGAGACCTGCTGTAACGCTCCGCTGCTGTCCAGCAAGAGGCTATCTTTCAAGA 1027  
 Db 751 TCTCTTTGAGACCTGCTGTAACGCTCCGCTGCTGTCCAGCAAGAGGCTATCTTTCAAGA 810  
 Qy 1028 ACGTATGAAACCTATGATTTTGTGGCTATCTCTCCCTACTTTGTGGCACTGGGCAACG 1087  
 Db 811 ACGTATGAAACCTATGATTTTGTGGCTATCTCTCCCTACTTTGTGGCACTGGGCAACG 870  
 Qy 1088 AGCTGGCCCCGACGAGAGGGTGGGCCAGCAGGCCATGTACTGTGGCCACTCTGAGAGTCA 1147  
 Db 871 AGCTGGCCCCGACGAGAGGGTGGGCCAGCAGGCCATGTACTGTGGCCACTCTGAGAGTCA 930  
 Qy 1148 TCCGATTTGTCGTCTGTCTTCCGCAATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAAA 1207  
 Db 931 TCCGATTTGTCGTCTGTCTTCCGCAATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAAA 990  
 Qy 1208 TCTTGGGCGCAGACGCTTCGGGCGTCCATGCGTGAAGTGGGCGCTCTCTATCTTTTCTCTCT 1267  
 Db 991 TCTTGGGCGCAGACGCTTCGGGCGTCCATGCGTGAAGTGGGCGCTCTCTCTATCTTTTCTCTCT 1050  
 Qy 1268 TCATCGGTGTGTGCTCTCTTTTCCAGGCGCGTCTACTTTGGCCGAAGTGTACCGGGTGGACT 1327  
 Db 1051 TCATCGGTGTGTGCTCTCTTTTCCAGGCGCGTCTACTTTGGCCGAAGTGTACCGGGTGGACT 1110  
 Qy 1328 CCCATTTTCACTAGCATCCCTGATGCTCTTCTGTGGCGGTAGTACCATGACTACAGTTG 1387  
 Db 1111 CCCATTTTCACTAGCATCCCTGATGCTCTTCTGTGGCGGTAGTACCATGACTACAGTTG 1170  
 Qy 1388 GCTATGAGACATGACACCCGCTCACTGTGGTGCCAGAGATAGTGGGCTCTCTGTGTGCCA 1447  
 Db 1171 GCTATGAGACATGACACCCGCTCACTGTGGTGCCAGAGATAGTGGGCTCTCTGTGTGCCA 1230  
 Qy 1448 TTGGGGGCGTCTGACTATTTCCCTGCGAGTCCCGCATTTGTCCTCAATTTGACGTACT 1507  
 Db 1231 TTGGGGGCGTCTGACTATTTCCCTGCGAGTCCCGCATTTGTCCTCAATTTGACGTACT 1290  
 Qy 1508 TTTATCAACCGGAGACAGAGGCGCAGAGAGGCTGGGATGTTTCAGCCATGTGACATGACAGC 1567  
 Db 1291 TTTATCAACCGGAGACAGAGGCGCAGAGAGGCTGGGATGTTTCAGCCATGTGACATGACAGC 1350  
 Qy 1568 CTTTGTGGCCCACTGAGAGGCAAGGCCAATGAGGGGCTGTGTGAGCGGAGGTACCTGAGC 1627  
 Db 1351 CTTTGTGGCCCACTGAGAGGCAAGGCCAATGAGGGGCTGTGTGAGCGGAGGTACCTGAGC 1410  
 Qy 1628 TACCAACCTCCACTGTGGGACCCCGCAGAGGGAACACCTGTGTACCGGAAAGTGTGA 1680  
 Db 1411 TACCAACCTCCACTGTGGGACCCCGCAGAGGGAACACCTGTGTACCGGAAAGTGTGA 1463  
 RESULT 3  
 AAS78540  
 ID AAS78540 standard; cDNA; 1686 BP.  
 AC AAS78540;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #14344.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PE 30-MAR-2001; 2001MO-US08631.  
 XX

PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 XX P-PSDB; ABG14353.  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID No 14344; 103bp; English.  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations in  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;  
 Query Match 79.48; Score 1333.6; DB 23; Length 1686;  
 Best Local Similarity 99.38; Pred. No. 2.2e-237;  
 Matches 1361; Conservative 0; Mismatches 4; Indels 5; Gaps 2;  
 Qy 248 CTGGGGCGCGCGTGGGGCCACAGCTGCTTCCGGGCTCGCGGGGCTGCGCGCCATG 307  
 Db 322 GGGGGCGCGGGGTGGGGCCACAGCTGCTTCCGGGCTCGCGGGGCTGCGCGCCATG 381  
 Qy 308 GAGCGCGGTGCGCGCGCGCGCGCTGCGGAGCGGCTGTGCTCAAGCTGGCGG 367  
 Db 382 GAGCGCGGTGCGCGCGCGCGCGCTGCGGAGCGGCTGTGCTCAAGCTGGCGG 439  
 Qy 368 GGTGCGCTTGAAGACGCGGGGCGGCAAGCGTGGGCGGCTTCCGGACACTGTGTAAGG 427  
 Db 440 GGTGCGCTTGAAGACGCGGGGCGGCAAGCGTGGGCGGCTTCCGGACACTGTGTAAGG 499  
 Qy 428 ACCGAGCGCGCGCGCGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 487  
 Db 500 ACCGAGCGCGCGCGCGCGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 559  
 Qy 488 ACCGAGCGCGCGCGCGCTGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 547  
 Db 560 ACCGAGCGCGCGCGCGCGCTGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 619  
 Qy 548 CGGGCGACGTGGCGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 607  
 Db 620 CGGGCGACGTGGCGCTTCAAGCAAGCGCGCGCGAGTATTTCTTCAGCGGC 679  
 Qy 608 CGGGCGGTGACGCGCTGCGAGAGAGGAGGCTCCCGGTGCGCGCGAGCGCCCTGCG 667  
 Db 680 CGGGCGGTGACGCGCTGCGAGAGAGGAGGCTCCCGGTGCGCGCGAGCGCCCTGCG 739



QY	668	CCGCGCGGCGCTTGGCCCGCAGCTGTGGCTCTTTTGAGTTTCCCGAGACTCTCAGG	727
Db	740	CCCGCGCGGCGCTTGGCCCGCAGCTGTGGCTCTTTTGAGTTTCCCGAGACTCTCAGG	799
QY	728	CCGCGCGGCGCTTGGCCCGCAGCTGTGGCTCTTTTGAGTTTCCCGAGACTCTCAGG	787
Db	800	CCGCGCGGCGCTTGGCCCGCAGCTGTGGCTCTTTTGAGTTTCCCGAGACTCTCAGG	859
QY	788	GCGTCGAGAGCGTGCCTGACTTCCGCGAGACCGCGAGCGGAGCTTGGCTGCAG	847
Db	860	GCGTCGAGAGCGTGCCTGACTTCCGCGAGACCGCGAGCGGAGCTTGGCTGCAG	919
QY	848	CCGAGCGCGGCGCGGCTTCCCGCTCCGCTGTAATGTCTCAGCCAAATGCTTGAATTC	907
Db	920	CCGAGCGCGGCGCGCGGCTTCCCGCTCCGCTGTAATGTCTCAGCCAAATGCTTGAATTC	976
QY	908	CACCGCGCGCTTCCCGCTTCAATGACCGCTTCCGCTGAGAGCGGCTGTAATTTGTCGT	967
Db	977	CACCGCGCGCTTCCCGCTTCAATGACCGCTTCCGCTGAGAGCGGCTGTAATTTGTCGT	1036
QY	968	TCCTCCCTTGAAGTCTGCTGTACGCGCTCTGCTGTGTCAGCAGCAGGCTATCTTCTTCAAGA	1027
Db	1037	TCCTCCCTTGAAGTCTGCTGTACGCGCTCTGCTGTGTCAGCAGCAGGCTATCTTCTTCAAGA	1096
QY	1028	ACGTGATGAACCTCATGATGATTTGTGTGCTATCTTCCCTACTTTGTGACACTGGGACCG	1087
Db	1097	ACGTGATGAACCTCATGATGATTTGTGTGCTATCTTCCCTACTTTGTGACACTGGGACCG	1156
QY	1088	AGCGGCGCGGCGAGCGGGGTGGGCGACAGGCGCATGTCATGTGGCCATCCGCGAGAGCA	1147
Db	1157	AGCGGCGCGGCGAGCGGGGTGGGCGACAGGCGCATGTCATGTGGCCATCCGCGAGAGCA	1216
QY	1148	TCCGATTTGTGCTGTCTTCCGATCTTGAAGCTGTCCCGGACTCAAAAGGCGCTGCAGAA	1207
Db	1217	TCCGATTTGTGCTGTCTTCCGATCTTGAAGCTGTCCCGGACTCAAAAGGCGCTGCAGAA	1276
QY	1208	TCCTTGGCGCAGACGCTTCCGGGCTCCATGCGTGAAGCTGGGCGCTCTCTATCTTTTCTCT	1267
Db	1277	TCCTTGGCGCAGACGCTTCCGGGCTCCATGCGTGAAGCTGGGCGCTCTCTATCTTTTCTCT	1336
QY	1268	TCATCGGTGTGGTCTCTTTCCAGGCGCGTCACTTTCGGAACCTGAACCGCGGAGACT	1327
Db	1337	TCATCGGTGTGGTCTCTTTCCAGGCGCGTCACTTTCGGAACCTGAACCGCGGAGACT	1396
QY	1328	CCCATTTTCATACATACATCCCTGAGTCCCTTCTGTGGGCGGTAGTCAACATGACTACAGTTG	1387
Db	1397	CCCATTTTCATACATACATCCCTGAGTCCCTTCTGTGGGCGGTAGTCAACATGACTACAGTTG	1456
QY	1388	GCTATGAGACATATGCGACCCGCTCATCTGTGGGTGGCAAGATATGGGCTCTCTGTGTGCCA	1447
Db	1457	GCTATGAGACATATGCGACCCGCTCATCTGTGGGTGGCAAGATATGGGCTCTCTGTGTGCCA	1516
QY	1448	TTTGGGGCGGTGCTGACTATTTCCCTCCGACAGTCCGCTCATTTCTTCACAAATTCACACTCT	1507
Db	1517	TTTGGGGCGGTGCTGACTATTTCCCTCCGACAGTCCGCTCATTTCTTCACAAATTCACACTCT	1576
QY	1508	TTTATTCACCGGAGAGACAGAGGCGGAGAGAGCTGTGATCTTCAACCATGTGACATGACAGC	1567
Db	1577	TTTATTCACCGGAGAGACAGAGGCGGAGAGAGCTGTGATCTTCAACCATGTGACATGACAGC	1636
QY	1568	CTTGTGCGCCACTGTGAGGCGCAGGCGCAATGTGGGGGCTGTGTGACGGGCGAG	1617
Db	1637	CTTGTGCGCCACTGTGAGGCGCAGGCGCAATGTGGGGGCTGTGTGACGGGCGAG	1686

RESULT 4	
ABL57038	
ID	ABL57038 standard; cDNA; 1341 BP.
XX	
AC	ABL57038;
XX	
DT	22-JUL-2002 (first entry)
XX	

DE	Human potassium channel 12189 partial cDNA.	
KW	Potassium channel1; ion transport; 12189; noctropic; anticonvulsant;	
KW	neuroprotective; antiparkinsonian; hypotensive; neuroleptic;	
KM	antidepressant; antimanic; tranquillizer; anorectic; anti migraine;	
KM	antiarteriosclerotic; vasotropic; vulnerary; antiarrhythmic;	
KM	cardiant; antiinflammatory; cytotactic; osteopathic; hepatotropic;	
KM	antidiabetic; immunosuppressive; antiarthritic; antirheumatic;	
KM	antiproliferative; antitumor; dermatological; antianemic;	
KM	antiasmatic; antiallergic; ophthalmological; immunomodulator;	
KM	analgesic; virucide; human; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1341
FT		/*tag= a
FT		/product= "12189"
FT		/partial
FT		/note= "The CDS does not include a start codon"
XX		
PN	WO200194390-A2.	
XX		
PD	13-DEC-2001.	
XX		
PF	06-JUN-2001; 2001WO-US18340.	
XX		
PR	06-JUN-2000; 2000US-209845P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Curtis RAJ;	
XX		
DR	WPI: 2002-401589/43.	
DR	P-PSDB; ABB76166.	
XX		
PT	New potassium channel family member polypeptide and polynucleotide,	
PT	useful for diagnosing, treating viral diseases, neurological, cardiac	
PT	cellular proliferative or differentiative, bone, immune, liver and	
PT	metabolic disorders	
XX		
PS	Claim 1; Page 135-136; 158pp; English.	
XX		
CC	The present sequence is that of a partial cDNA for human 12189	
CC	(see ABB76166), a novel potassium channel family member. 12189	
CC	contains a potassium channel tetramerisation domain, an ion	
CC	transport protein domain and a core membrane region including 6	
CC	transmembrane domains. The invention provides human potassium	
CC	channel 52906, 33408 and 12189 nucleic acids and proteins, as well	
CC	as antisense nucleic acid molecules, recombinant expression vectors,	
CC	host cells, transgenic animals, fusion proteins, antigenic peptides	
CC	and antibodies. Also claimed are: a method for detecting the	
CC	presence of a 52906, 33408 or 12189 nucleic acid; a method for	
CC	modulating the activity of a 52906, 33408 or 12189 polypeptide using	
CC	a compound that binds the polypeptide; a method for identifying a	
CC	compound which modulates the activity of the polypeptide; a method	
CC	of treating or preventing an ion flux-related disorder using an	
CC	agent that modulates the activity or expression of a 52906 or	
CC	12189 polypeptide or nucleic acid, especially a peptide,	
CC	phosphopeptide, small molecule, antibody, antisense molecule,	
CC	ribozyme, a triple helix molecule, or a 52906 or 12189 nucleic	
CC	acid. The ion flux-related disorders include: potassium channel	
CC	associated disorders, such as neurological disorders and central	
CC	nervous system disorders such as cognitive and neurodegenerative	
CC	dementia, e.g. Alzheimer's disease, Parkinson's disease, senile	
CC	dementia, Huntington's disease, Gilles de la Tourette's syndrome,	
CC	multiple sclerosis, progressive supranuclear palsy, epilepsy,	
CC	Jacob-Creutzfeldt disease, autonomic function disorders such as	
CC	hypertension and sleep disorders, neuropsychiatric disorders such	
CC	as depression, schizophrenia, mania, anxiety disorders or phobic	
CC	disorders, learning or memory disorders, amnesia or age-related	
CC	memory loss, attention deficit disorder, obsessive-compulsive	
CC	disorder, migraine or obesity; cardiac-related disorders such as	

CC arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial  
 CC inflammation, tachycardia, congestive heart failure, myocardial  
 CC infection and arrhythmia. The polypeptides and nucleic acids are  
 CC also useful as diagnostic targets and therapeutic agents for:  
 CC controlling cellular proliferative and/or differentiative disorders  
 CC e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma;  
 CC disorders associated with bone metabolism such as osteoporosis,  
 CC rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic  
 CC hypercalcaemia; immune disorders such as autoimmune disorders,  
 CC diabetes mellitus, arthritis, including rheumatoid arthritis,  
 CC osteoarthritis and psoriatic arthritis, multiple sclerosis,  
 CC myasthenia gravis, autoimmune thyroiditis, ulcerative colitis,  
 CC psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma,  
 CC allergic asclama, conjunctivitis, aplastic anaemia, Grave's disease,  
 CC chronic active hepatitis, autoimmune uveitis, scleroderma; liver  
 CC disorders including storage disorders such as Gaucher's disease,  
 CC glycogen storage disease, haemochromatosis and peroxisomal  
 CC disorders; viral diseases; pain; or metabolic disorders such as  
 CC obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.  
 CC  
 XX  
 SQ Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Query Match 78.7%; Score 1321.6; DB 24; Length 1341;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-235;  
 Matches 1337; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 337 TGGTCGAGGCGGTGTCATCAACGTGGCCGCGCTGCGCTTCGAGACGCGGCGCGACG 396  
 Db 1 TGGTCGAGGCGGTGTCATCAACGTGGCCGCGCTGCGCTTCGAGACGCGGCGCGACG 60

QY 397 CTGGGCGGCTTCCCGGACACTTGTAGGGACCCAGCGCGCGCGCGCTTTCACGAC 456  
 Db 61 CTGGGCGGCTTCCCGGACACTTGTAGGGACCCAGCGCGCGCGCGCTTTCACGAC 120

QY 457 GACGCGCGCGGAGATATTTCTTCGACCGGACCGCGCCAGCTTCGAGCGCGCTTCAC 516  
 Db 121 GACGCGCGCGGAGATATTTCTTCGACCGGACCGCGCCAGCTTCGAGCGCGCTTCAC 180

QY 517 TACTACCAATCCGATGGGCGGCTGCGGCGCGCGCGACGTCGCGCTTCGAGCTTCCTG 576  
 Db 181 TACTACCAATCCGATGGGCGGCTGCGGCGCGCGCGACGTCGCGCTTCGAGCTTCCTG 240

QY 577 GAAGAGTGGCTTCTACGCGGCTGGGCGCGCGCGCGCGCTTCGAGCGCGCTTCGAG 636  
 Db 241 GAAGAGTGGCTTCTACGCGGCTGGGCGCGCGCGCGCGCTTCGAGCGCGCTTCGAG 300

QY 637 GCGTCGCGCGGTGCG 696  
 Db 301 GCGTCGCGCGGTGCG 360

QY 697 CTGCTTTTCGAGTTTCCGAGAGCTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCG 756  
 Db 361 CTGCTTTTCGAGTTTCCGAGAGCTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

QY 757 CTGTATCT 816  
 Db 421 CTGTATCT 480

QY 817 GACGCGCGGAGCGGCGGCTGCTGTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 876  
 Db 481 GACGCGCGGAGCGGCGGCTGCTGTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 537

QY 877 CTGAATGGCTCCAGCCAAATGCTGGAATTCACCCCGCGCTTCGAATGACCGCTTC 936  
 Db 538 CTGAATGGCTCCAGCCAAATGCTGGAATTCACCCCGCGCTTCGAATGACCGCTTC 597

QY 937 TTGCTGGTGAAGAGCTGTGTATTTGTTGCTTCCTTTGAGCTGCTGTAAGCGCTCTG 996  
 Db 598 TTGCTGGTGAAGAGCTGTGTATTTGTTGCTTCCTTTGAGCTGCTGTAAGCGCTCTG 657

QY 997 GTCTGTCCAGCAAGCTATCTCTTCACAAAGCTATGAACTCATCATGATTTTGTGGCT 1056  
 Db 658 GTCTGTCCAGCAAGCTATCTCTTCACAAAGCTATGAACTCATCATGATTTTGTGGCT 717

QY 1057 ATCCCTCCCTACTTTTGGGACCTGGGACCGAGCTGGCCCGCGACGAGGGGTGGCCAG 1116  
 Db 718 ATCCCTCCCTACTTTTGGGACCTGGGACCGAGCTGGCCCGCGACGAGGGGTGGCCAG 777

QY 1117 CAGCCCATGTACCTGGCCATCTCTAGAGTATCCGATTTGGTGGCTGTCTTCCGATCTTC 1176  
 Db 778 CAGCCCATGTACCTGGCCATCTCTAGAGTATCCGATTTGGTGGCTGTCTTCCGATCTTC 837

QY 1177 AAGCTGTCGCGGACCTCAAAAGGCGCTCAAAATTTGGGCGAGAGCTTCGGGCGCTCCATG 1236  
 Db 838 AAGCTGTCGCGGACCTCAAAAGGCGCTCAAAATTTGGGCGAGAGCTTCGGGCGCTCCATG 897

QY 1237 CGTAGAGTGGGCGCTTCATCTTTTTCCTTCATTCGAGTGGTGTCTCTTTTTCAGCGCC 1296  
 Db 898 CGTAGAGTGGGCGCTTCATCTTTTTCCTTCATTCGAGTGGTGTCTCTTTTTCAGCGCC 957

QY 1297 GTCTACTTTGGCGGAATTTGACCGGGGTGGACTCCCATTTCACTACATCCCTGATCTTC 1356  
 Db 958 GTCTACTTTGGCGGAATTTGACCGGGGTGGACTCCCATTTCACTACATCCCTGATCTTC 1017

QY 1357 TGTGGGCGGTGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1416  
 Db 1018 TGTGGGCGGTGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1077

QY 1417 GGTGGCAAGATAGTGGGCTCTGTGTGTCATTTGGGCGGCGGTGTGATTTTCCCTGCCA 1476  
 Db 1078 GGTGGCAAGATAGTGGGCTCTGTGTGTCATTTGGGCGGCGGTGTGATTTTCCCTGCCA 1137

QY 1477 GTGCCGCTCATGTCTCCATTTTACGCTACTTTTATACCGGGAGACAGAGGGGAGAG 1536  
 Db 1138 GTGCCGCTCATGTCTCCATTTTACGCTACTTTTATACCGGGAGACAGAGGGGAGAG 1197

QY 1537 GCTGGATGTTTCAGCCATGTGAGCATGACGCTGTGGCCATGAGAGGCGCAAGGCCAAT 1596  
 Db 1198 GCTGGATGTTTCAGCCATGTGAGCATGACGCTGTGGCCATGAGAGGCGCAAGGCCAAT 1257

QY 1597 GGGGGCTGTGTGAGGAGGAGTACCTGAGCTACACCTCCACTCTGGGACCCCGCAG 1656  
 Db 1258 GGGGGCTGTGTGAGGAGGAGTACCTGAGCTACACCTCCACTCTGGGACCCCGCAG 1317

QY 1657 GAACACCTGTGTCACCGCAAGTGTGA 1680  
 Db 1318 AAACACCTGTGTCACCGCAAGTGTGA 1341

RESULT 5  
 AAT04953  
 ID AAT04953 standard; cDNA; 1598 BP.  
 XX  
 AC AAT04953;  
 XX  
 DT 11-APR-1996 (first entry)  
 XX  
 DE Mouse Kv1.7 voltage-gated potassium channel coding sequence.  
 XX  
 KW Mouse Kv1.7 voltage-gated potassium channel;  
 KW Insulin antagonist drug screening; insulin agonist drug screening;  
 KW non-insulin-dependent diabetes mellitus; ds.  
 OS Mus musculus.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 1..1598 /+tag= a  
 FT /note="specification states sequence is 1598.  
 FT Incomplete stop codon given"  
 XX  
 PN MO9523858-A1.  
 XX  
 PD 08-SEP-1995.  
 XX  
 PF 23-FEB-1995; 95WO-US02221.



XX Human ion channel gene, ion-166.  
 DE Human: ion channel; neurological disorder; psychiatric disorder;  
 XX Schizophrenia; attention deficit hyperactivity disorder; depression;  
 KW Proliferation disease; migraine; ischemia; neurodegenerative disease;  
 KW macular degeneration; Alzheimer's disease; congestive heart failure;  
 KW glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;  
 KW high blood pressure; restenosis; metabolic disease; neuroprotective;  
 KW obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;  
 KW alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 566..658  
 FT /tag= a  
 FT /product= "Human ion channel ion-166"  
 FT /note= "CDS does not include start and stop codon"  
 FT /partial  
 XX  
 PN MO200192303-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US16967.  
 XX  
 XX 26-MAY-2000; 2000US-207119P.  
 PR 26-MAY-2000; 2000US-207152P.  
 PR 26-MAY-2000; 2000US-207257P.  
 XX  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 XX  
 PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL, Gotow LF;  
 XX WPI: 2002-147617/19.  
 DR P-SDB: AAEL8034.  
 XX  
 PT New human ion channel polypeptides and nucleic acids, useful for  
 PT treating or diagnosing neurological, psychiatric or neurodegenerative  
 PT diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or  
 PT Parkinson's disease  
 XX  
 XX Claim 1; Page 76; 126pp; English.  
 PS  
 XX  
 XX The invention relates to ion channel polypeptides designated as ion-x  
 CC (where x is 157-175) and their corresponding nucleic acids. The ion-x  
 CC sequences and their modulators are useful for the treatment of human  
 CC diseases and conditions such as neurological or psychiatric disorders.  
 CC These compounds are useful for treating schizophrenia, attention deficit  
 CC hyperactivity disorder, depression, anxiety, stroke, migraine, ischemia  
 CC or neurodegenerative disease (e.g. macular degeneration, Alzheimer's  
 CC disease, glaucoma, or Parkinson's disease). The compounds that modulate  
 CC ion channels can be used for treating of cardiovascular diseases (e.g.  
 CC congestive heart failure, arrhythmia, high blood pressure or restenosis),  
 CC metabolic diseases and disorders (e.g. diabetes or obesity), hormonal  
 CC disorders (e.g. polycystic ovarian syndrome or alopecia) and  
 CC proliferation diseases and cancers. The ion channels are also useful as  
 CC targets for discovering ligands or drugs to treat many diverse disorders  
 CC and defects. The ion-x sequences and their modulators may also be used  
 CC in diagnostic assays for such diseases or conditions. Ion-x nucleic  
 CC acids are used in gene therapy. The present sequence is a DNA encoding  
 CC human ion channel designated as ion-166.  
 CC  
 XX  
 SQ Sequence 691 BP; 113 A; 207 C; 185 G; 186 T; 0 other;  
 Query Match 35.8%; Score 601.4; DB 24; Length 691;  
 Best Local Similarity 99.0%; Pred. No. 3..2e-102;  
 Matches 605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 854 CGGGCCGGGTGTCCTCCGCTGATGCTCCAGCAAAATGCTGGAATCCACCC 913  
 DB 81 CTTCCCTGAGTTCCTCCGCTGCTGATGCTCCAGCAAAATGCTGGAATCCACCC 140

QY 914 GCTGCCCCATATGACCCGTTCTTGTGTGTGAGACGCTGTATTTGTTGTTCTCT 973  
 DB 141 GCTGCCCCATATGACCCGTTCTTGTGTGTGTGAGACGCTGTATTTGTTGTTCTCT 200  
 QY 974 TTGAGCTGTGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033  
 DB 201 TTGAGCTGTGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260  
 QY 1034 TGAACCTATGATTTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1093  
 DB 261 TGAACCTATGATTTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320  
 QY 1094 CCCGACGAGAGGGGTGGCCAGCAGGACATGTCATGCGCCATCTGAGATCCGAT 1153  
 DB 321 CCCGACGAGAGGGGTGGCCAGCAGGACATGTCATGCGCCATCTGAGATCCGAT 380  
 QY 1154 TGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1213  
 DB 381 TGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440  
 QY 1214 GCCAGACGCTTGGGGCTCCATGAGCTGAGCTGAGGCTCTCATCTTCTTCTTCATCG 1273  
 DB 441 GCCAGACGCTTGGGGCTCCATGAGCTGAGCTGAGGCTCTCATCTTCTTCTTCATCG 500  
 QY 1274 GTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1333  
 DB 501 GTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 560  
 QY 1334 TCACTAGATCCCTGATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1393  
 DB 561 TCACTAGATCCCTGATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 620  
 QY 1394 GAGACATGGACCCGCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1453  
 DB 621 GAGACATGGACCCGCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 680  
 QY 1454 GCGTGTGACT 1464  
 DB 681 GCGTGTGACT 691  
 RESULT 7  
 ABN95856 standard; DNA; 2867 BP.  
 ID ABN95856;  
 XX  
 AC ABN95856;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Gene #2354 used to diagnose liver cancer.  
 XX  
 KW Gene: liver cancer; ds: hepatocellular carcinoma; hepatotropic;  
 KW metastatic liver tumour; cytostatic; expression profile; disease state;  
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200229103-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 02-OCT-2001; 2001WO-US30589.  
 XX  
 PR 02-OCT-2000; 2000US-237054P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
 DR WPI: 2002-426119/45.  
 PT Diagnosing and detecting the progression of liver cancer,

Pt		hepatocellular carcinoma or metastatic liver tumor in a patient.
Pt		Involves detecting the level of expression of two or more genes in a
Pt		liver tissue sample -
PS		
XX		Claim 1; SEQ ID NO 2354; 298bp; English.
CC		The invention relates to a novel method for diagnosing and detecting the
CC		progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC		tumour in a patient, and differentiating metastatic liver cancer from
CC		hepatocellular carcinoma in a patient, involving detecting the level of
CC		expression of two or more genes represented in ABN93503-ABN97455 in a
CC		tissue sample. The method of the invention has hepatotropic, and
CC		cytostatic activity. The method is useful for diagnosing and detecting
CC		the progression of liver cancer, hepatocellular carcinoma and metastatic
CC		liver carcinoma in a patient. The method is useful for identifying
CC		expression profiles which serve as useful diagnostic markers as well as
CC		markers that can be used to monitor for disease states, disease progression,
CC		drug toxicity, drug efficacy and drug metabolism.
CC	Note:	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
CC		
XX		
SQ	Sequence	2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;
	Query Match	35.5%; Score 596.2; DB 24; Length 2867;
	Best Local Similarity	68.6%; Pred. No. 3.2e-101;
	Matches 873;	Conservative 0; Mismatches 358; Indels 42; Gaps 2.
OY	310	GCGCGGTGCCCGGCCCCGGCGGTCTGCAGAGCGGTCTGTCACGTGGCGGG 369
Db	553	GACCAAGCCTCTGTGGACAGCGGCTCCCTGCACACACAGCGTCAATCAACATCTCCGAG 612
OY	370	CTGCGCTTGAGACGCGGGGCGCACGGCTGGGGCGCTTCCGGACACTCTGTAGGGAGAC 429
Db	613	CTGCGCTTTGAGAACCCACACTGGGACACCAGAGCGCATTTCCACAACACTCTGGGGGAC 672
OY	430	CCAGGCGCCCGGGCGCGCTTCTACGACACGAGCGGCGCGGATATTCTTCGACCGGAC 489
Db	673	CCCAGCAAGCGCTCCCTGACTTGAACCCCCGTGAGAAAGAGTAATCTTCTTCGACCGCAAC 732
OY	490	GCGCCACACTTTCGAGCGCGCTCTACTACTACAGTCGCGGTGGCGGCTGGCGGGCGCG 549
Db	733	CAGCCACTTTCGAGCGGTATCTCTACTACTACAGTCGCGGGGCGCGCTGGGAGGCGCG 792
OY	550	GCGCAGTGC CGCTCGACGCTTCTCTGGAAGAAGTGGCCCTTACGGGCTGGGCGCGGCG 609
Db	793	GTCACAGTCTCCCTCGAGCGTGTTCGCGGACGAGATAAGCTTCTACACGCTGGGGGACGAG 852
OY	610	GCCCTGGGACGCTCGCGGAGACGAGGCTCCCGGTCCCGCCCGAGCGCCCTCGGCC 669
Db	853	GCCATGGAGCGCTTTCGGGAGAGATAGGGCTTCAATTAAGAGAGAGAGAGGCCCTCTGTC 912
OY	670	GCGCGCGCTTTCGCGCGAGCTGGGGCTGTTTTCGAGTTTCCGAGAGCTCTACGGCC 729
Db	913	GCGAAGGATTCACAGCGCCAGGTGTGGCTTATCTTCGTGATATCCGAGAGCTCTGGGTCC 972
OY	730	GCGCGCTGTCTCCCGGTAGTCTCTCGTGTGATCATCTGTCATCATCTCTCTCTCTCTCG 789
Db	973	GCGGGGGCATGGCATGTGTCTGCGGTCTGGTATTCATCTCATCATCATCACTCTCTGCG 1032
OY	790	CTCGAGAGCGTCTCTGACTTCTCCGCGACGACCGCGAGCGGACCGGGCTCTGCTGACGCC 849
Db	1033	TTCGAGACCTCTCTCTGATATTCAGGGATGAACCTGAGCTCTCCGCCACCTCCGGCGCCC 1092
OY	850	GCAGCGGGCGCGGTATCCCGCTCCGGCGAATG-----CTCC 888
Db	1093	CACCAAGCTCCCGCGCCGCCCTCTGGGGCCAAGGAGCGGGGTCAATGGCCCGCCCTCT 1152
OY	889	AGCCAATGCTCTGAAATCCACCCGCGCTCTTCATGACCGCTTCTCTGTGGAG 948
Db	1153	GGCCCTTAGGTGGACCGCGCTCTGCGCCAGAGACCTGGCGGACCCCTTCTTCAATGTGGAG 1212
OY	949	ACGCTGTATTTGTTGTTCTCTTGAAGTGTGTGTACGCCCTCTGCTGTCTCAACG 1008

Db	1213	ACCAAGTCGTCATCTGGTTACCTTGGAGCTGCTCGTGGCTTCTTCCGCTGCCACG	1272
Qy	1009	AAGGCTATCTTCTTCAAGAACGATGAACCTCATGATTTTGTGGCTATCTTCCCTAC	1068
Db	1273	AAGGAGGGGTTCTCCCGGAACATCATGAACTCATGATGTTGGGCAATCTTCCCTAC	1332
Qy	1069	TTTGTGGCACTGGGCACTGGAGCTGGCCCGGACAGGAGGGGTGGG-----	1113
Db	1333	TTTCATCACCTTGGGGCACCGAAGCTGGCAGAGACGACGAGGGGGCGAGGAGGCGGACG	1392
Qy	1114	-----CAGCAGGGCATGTCACTGAGCCATCCTGAGAGTCATCCGATTTGGCGGTCTTC	1167
Db	1393	AATGGCGAGCAGGGCATGTCCCTGGCCATCTCCGAGTCATCGCCTGGTCCGGGTTC	1452
Qy	1168	CGCATCTTCAAGCTGTCCCGGCACTCAAAAGGGCCTGCAGAAATCTTGGGCGCACGACCTTCG	1227
Db	1453	CGCATCTTCAAGCTGTCCCGGCACTCAAAAGGGGCTGCAGATCCTGGGCAAGACCTTCAG	1512
Qy	1228	GCCTCATGCGGTGAAGCTGGGCTCCTCATCTTTTCTCTTTCATCGGTGTCTCTTT	1287
Db	1513	GCCTCATGAGGAGAGCTGGGGCTGCTCATCTTCTTCCCTTTCATCAGGGGTCACTCTTTC	1572
Qy	1288	TCACAGCGCGCTCATCTTGGCCGAAGTTGACCGGGGTGGACCTCCCATTTCACTAGATCCCT	1347
Db	1573	TCACATGCGCGTCACTTCTGCAAGAGCTGACACACGAGGAACCTTCTCTAGCATCCCT	1632
Qy	1348	GAGTCTCTTCTGTTGGGCGGTAGTACACATGACTACAGTTGGCTTATGGAGCATGGCACCC	1407
Db	1633	GAGCGCTTCTGTGGGGCAGTGGTCAACATGACACACTGTGGGCTACGGGGACATAGGCCCC	1692
Qy	1408	GTCACCTGTGGGTGGCAGAGATAGTGGGCTCTGTGTGGCCATTCGGGCGTGTGACTATT	1467
Db	1693	ATCACTGTGTGGGGGAGATGATGTTGGTGGCTGTGTGTGCATCGCGGGGTTCTTCCACTT	1752
Qy	1468	TCCCTGGCAGAGCCCGCATGTGTGCCAATTTCAGCTACTTTATCACCGGGAGACAGAG	1527
Db	1753	GCCCTGCTGTGGCCGCTGTATGCTTCAACTTCAACTTACTTCTTACACACGGGAACGGAT	1812
Qy	1528	GGCGAAGAGCGCTG 1540	
Db	1813	CACGAGGAGCCGG 1825	
RESULT 8			
ABL65917			
ID	ABL65917	standard; DNA; 2867 BP.	
AC	ABL65917;		
XX			
DT	15-MAY-2002 (first entry)		
DE	Lung cancer related gene sequence SEQ ID NO:4254.		
XX			
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KW	cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;		
gene; ds.			
OS	Homo sapiens.		
XX			
PN	WO200194629-A2.		
XX			
PD	13-DEC-2001.		
XX			
PF	30-MAY-2001; 2001WO-US10838.		
XX			
XX	05-JUN-2000; 2000US-209473P.		
PR	05-JUN-2000; 2000US-209531P.		
PR	18-SEP-2000; 2000US-233133P.		
PR	18-SEP-2000; 2000US-233617P.		
PR	20-SEP-2000; 2000US-234009P.		
PR	20-SEP-2000; 2000US-234034P.		

PR 20-SEP-2000; 2000US-234052P.  
 PR 22-SEP-2000; 2000US-234509P.  
 PR 22-SEP-2000; 2000US-234567P.  
 PR 25-SEP-2000; 2000US-234923P.  
 PR 25-SEP-2000; 2000US-234924P.  
 PR 25-SEP-2000; 2000US-235077P.  
 PR 25-SEP-2000; 2000US-235082P.  
 PR 25-SEP-2000; 2000US-235134P.  
 PR 25-SEP-2000; 2000US-235280P.  
 PR 26-SEP-2000; 2000US-235637P.  
 PR 26-SEP-2000; 2000US-235638P.  
 PR 27-SEP-2000; 2000US-235711P.  
 PR 27-SEP-2000; 2000US-235720P.  
 PR 27-SEP-2000; 2000US-235840P.  
 PR 27-SEP-2000; 2000US-235863P.  
 PR 28-SEP-2000; 2000US-236028P.  
 PR 28-SEP-2000; 2000US-236032P.  
 PR 28-SEP-2000; 2000US-236033P.  
 PR 28-SEP-2000; 2000US-236034P.  
 PR 28-SEP-2000; 2000US-236109P.  
 PR 28-SEP-2000; 2000US-236111P.  
 PR 29-SEP-2000; 2000US-236842P.  
 PR 29-SEP-2000; 2000US-236891P.  
 PR 02-OCT-2000; 2000US-237172P.  
 PR 02-OCT-2000; 2000US-237173P.  
 PR 02-OCT-2000; 2000US-237278P.  
 PR 02-OCT-2000; 2000US-237294P.  
 PR 02-OCT-2000; 2000US-237295P.  
 PR 02-OCT-2000; 2000US-237316P.  
 PR 03-OCT-2000; 2000US-237425P.  
 PR 03-OCT-2000; 2000US-237598P.  
 PR 03-OCT-2000; 2000US-237604P.  
 PR 03-OCT-2000; 2000US-237606P.  
 PR 03-OCT-2000; 2000US-237608P.  
 PR 01-NOV-2000; 2000US-244867P.  
 PR 01-NOV-2000; 2000US-245084P.  
 PR (AVAL-) AVALON PHARM.  
 PR Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 P1 Soppet DR, Weaver Z;  
 PR WPI: 2002-188264/24.  
 DR  
 XX  
 XX Screening for anti-neoplastic agent involves exposing cells to a  
 PT chemical agent to be tested for anti-neoplastic activity, and  
 PT determining a change in expression of a gene of a signature gene set -  
 PT  
 XX  
 PS Claim 1; SEQ ID 4254; 44pp; English.  
 XX  
 XX The present invention describes a method (M1) for screening for an  
 CC anti-neoplastic agent. The method involves exposing cells to a chemical  
 CC agent to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664  
 CC to ABL0110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening  
 CC an anti-neoplastic agent, and can be used for producing a product which  
 CC is the data collected with respect to the anti-neoplastic agent as a  
 CC result of M1, and the data is sufficient to convey the chemical  
 CC structure and/or properties of the agent. M1 can be used in the  
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 CC oesophagaeal, ovarian, kidney, prostate or pancreatic cancer.  
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 CC carcinoma, papillary carcinoma and Wilms' tumour.  
 XX  
 SQ Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;

QY	310	GCACGGGTCGCCCCGCCCCGCGTGGCGGGCTCTGGGAGACGGCTGGTCTCAAGTGGCCGG	369
Db	553	GACCAGGCTCTGGGACAGGGGCTCCCTGGCACACACAGGGCTCCACATCAACATCTCCGGC	612
QY	370	CTGGCGCTTCAGAGACGCGGGGCGCACGCTGGGGCCGGTTCGCCGACACTCTGCTAGGGAC	429
Db	613	CTGGCGCTTCAGAGACGCGGGGCTCCCTGGCACACACAGGGCTCCACATCAACATCTCCGGC	612
QY	430	CCAGCGCGCCGCGGGCCGGCTTCTACGACGACGGCGCCGGAGTATTCTTGGACCGGCAC	489
Db	673	CCCCCAAGGGCGCCGGTCTTCCGACCCCTGGAGAAAGCATCTTCTTGGACCGCAAC	732
QY	490	CGGGCCACGCTTCGACGGCCGGTCTCTACTACTACACATCCGGTGGCGGCTCGCGCGCGC	549
Db	733	CGGGCCACGCTTCGACGGCCGGTCTCTACTACTACACATCCGGTGGCGGCTCGCGCGCGC	792
QY	550	GCGCAGCTGGCCGCTCGACGTCCTTCGGAAGAGTGGCCCTTCCTACGGGCTGGCGCGCGC	609
Db	793	GTCACAGCTCTCCGAGCGGTTCGCGGACGAGATACGCTTCTTACCACTGGGGGACGAG	852
QY	610	GCCCTGGCACGGCTGGCGCGAGAGACAGAGGGCTGCCGGTGGCCCGGACGGCCCTGGCC	669
Db	853	GCCATGAGGCGCTTCGGCGGAGATGAGGGCTTCATTAAAGAGAGAAAGCCCTTCGTC	912
QY	670	CGCGCCCTCTCGCCCGCCGACGCTGGTGGCTTTCGATTCCTCCGAGAGCTTCAGGCC	729
Db	913	CGCAGACGATTCACGAGCGCCAGAGTGTGGCTTATCTTGAGATATCGGAGAGCTGGGGTCC	972
QY	730	GCGCGCTGCTCGCGCTAGTCTCTCGCTGGTGTATCTCTGTCATCTGTCGTCTTCTGCG	789
Db	973	GCGGGGGCCATTCGCGATCTGCTGGTGGTGTATCTTCATCTCATATCACTTCTGCG	1032
QY	790	CTCAGACGCGTCCGCTGACTTCCGCGACGACCGGAGCGGAGCGGAGGCTTGTGCTGACGC	849
Db	1033	TTGGAGACCTGCTGCTAGTTCAGAGATGACGATGACGTACTGCTCGGCACCTTCGCGCGCC	1092
QY	850	GCACGCGCGCCGGTTCCTCCCGCTCCGCTGAAATG-----CTCC	888
Db	1093	CACACAGCTCTCCGCGCCCGCCCTCGGGGACACAGGAGCGGGGTATGGCCCGCGCTCT	1152
QY	889	AGCCAAATGCGCTGGAAATCCACCCCGGCGCCCTTCATATGACCGCTTCGTGGTGGAG	948
Db	1153	GGCCCTACGGTGGGACCGGCTCTGCGCCAGGACCCCTGTGGCGACCCCTTCTTATGCTGAG	1212
QY	949	ACGCTGTGATTTTGTGGTCTCTCTTGGACGTGCTGTAAGCGCTCTGCTGTGCAAGC	1008
Db	1213	ACACAGTGGCGTACATCGGTTCACCTTCGAGCTGCTGCTGCTTCGTGGCTGGCCCGCAGC	1272
QY	1009	AAGGCTATCTTCTTCAAGAACGATGAGAACCTATCGATATTTGTGGCTATCTTCCCTAC	1068
Db	1273	AAGGCAAGGTTCTCCGGAACATCAATGAACTATCGATGATGTGTGGCATCTTCCCTAC	1332
QY	1069	TTTGTGGCACTGGGACACGAGCTGGCCCGGACGAGGAGGGTGGG-----	1113
Db	1333	TTTATCAACCTGGGACACCGAATCTGGGAGACGACGACGAGGGGGGAGAGAGGGGGCAG	1392
QY	1114	-----CAGAGGCCATGTACTCTGGCCATCTGAGAGTATCCGATTTGGTGGCTGTTC	1167
Db	1393	AATGGGACAGAGGCAATGTCTCCGGGCATCTCCGCGATCTCCGCTGGTCCGGGTGTT	1452
QY	1168	GCGATCTTCAAGGTCGCCGGGACCTCAAAAGGGGCTGGCAATTTTGGGCGAGACGCTTGG	1227
Db	1453	GCGATCTTCAAGCTCTCCGCGCACTCCAAAGGGGCTGCAAGATCTTGGCGAAGACTTGGAG	1512
QY	1228	GCTCATAGCGTAGCTGGGCTCCTCATCTTTTTCCTTTCATCGGATGGGTGCTCTTT	1287
Db	1513	GCTCATAGAGGAGCGTGGGGGTGCTCATCTTCTTCCTTCATCTGGGGTTCATCCTTTC	1572
QY	1288	TCGACGCGCGCTACTTGTGCCAAGTTGACCGGGTGGATCTCCGATTTCAATCAATGATCCT	1347
Db	1573	TCGACGCGCGCTACTTGTGAGAGGCTGCTCAACACAGGGAACCATTTCTTGAACATCCT	1632

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QY 1348 GAGTCTTCCTGGTGGGCGGTAGTCAACCAATGATACAGTGGCTATGAGAACATGCGACCC 1407
Db 1633 GACGCTTCCTGGTGGGCGGTAGTCAACCAATGATACAGTGGCTATGAGAACATGAGGCC 1692
QY 1408 GTCACTGTGGGTGTGAGATAGTGGGCTCTCTGTGTGTCATTTGCGGGCGTGTGACTATT 1467
Db 1693 ATCACTGTGGGGGGCAATGATGCTGGGCTGCTGTGTGCATGTGCGGGGTCTCTACACATT 1752
QY 1468 TCCCTGCCAGTGGCGGCTGATTTGTTCACATTTTACGCTACTTTTATTCACGGGAGACAG 1527
Db 1753 GCCCTGCTGTGGCGGCTGATGCTTCACCACTTCAACTACTTCTACACCGGGAACGGAT 1812
QY 1528 GCGGAGAGGCGTG 1540
Db 1813 CACGAGAGCGCG 1825

RESULT 9
AAH21452
ID AAH21452 standard; DNA; 1836 BP.
XX
AC AAH21452;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human Kv1.5 DNA.
XX
KW Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
KM activator; ds.
OS Homo sapiens.
XX
MO M0200151519-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP00055.
XX
PR 11-JAN-2000; 2000DE-1000651.
XX
PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI Leberer E, Leeuw T, Ritscher A;
XX
DR WPI: 2001-442137/47.
XX
PT Identifying inhibitors and activators of eukaryotic potassium channels,
PT for use as pharmaceuticals, comprises using yeast cells that express
PT heterologous, but no endogenous, potassium channels -
XX
PS Disclosure: Page 45-46; 78pp; German.
XX
CC This sequence represents a novel method for identifying inhibitors or
CC activators (A) of a eukaryotic potassium channel (KC) by applying a test
CC compound to a mutant Saccharomyces cerevisiae cell in which: (i) the
CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a
CC eukaryotic KC is expressed heterologously, where the effect of the
CC compound on the eukaryotic KC is then determined. The method is used to
CC identify inhibitors or activators (A) of a eukaryotic potassium channel.
CC (A) are potentially useful as pharmaceuticals. The method is easily
CC automated for parallel processing of many samples, using either different
CC concentrations of test compounds and/or different levels of heterologous
CC gene expression. It allows identification of compounds that inhibit human
CC KC selectively. This sequence represents the human Kv1.5 encoding DNA
CC described in the method of the invention.
XX
SQ Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other:

Query Match 35.0%; Score 588.2; DB 22; Length 1836;
Best Local Similarity 68.7%; Pred. No. 9,3e-100;
Matches 875; Conservative 0; Mismatches 353; Indels 45; Gaps 3

310 GCCCGGCGTGGCGGCGGCGGCTGCTGCTGAGACGGGCTGGTCTCAACGTGCGCGG 369

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[illegible]



Db 1399 GAGCCCTTGTGGGAGGAGTGATCATGACACAGTGGGCTACGGGAGCATGAGGCC 1458  
 Qy 1408 GTCACTGTGGTGCAAGATAGTGGCTCTGTGTGCATTTGGGGCTGCTGACTATT 1467  
 Db 1459 ATCACTTTTGGGGGCAAGATGCTGGGCTCGTGTGTGCATCGGGGCTCTCACTTT 1518  
 Qy 1468 TCCCTGCCAGTGGCCGTGATGTTCTGCATTTACGTTTATTCACCGGAGACAGAG 1527  
 Db 1519 GCCCTGCTGTGGCCGCTCATGCTCTCCAACTTCACTTACACCGGAGAAAGCAT 1578  
 Qy 1528 GCGAGAGAGGCTG 1540  
 Db 1579 CACGAGAGCGCG 1591

## RESULT 10

AB199654 ID AB199654 standard; cDNA; 3147 BP.

AC AB199654;

DT 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:683.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX Mus musculus.

PN W0200188188-A2.

PD 22-NOV-2001.

PE 18-MAY-2001; 2001MO-JP04192.

PR 18-MAY-2000; 2000UP-0145977.

XX (UNNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PA Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

DR P-PSDB; ABB57250.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring

PT expression levels of particular genes defined in the specification or

PT by determining the expression profile of a gene group comprising these

PT genes -

XX Claim 2; Page 1705-1709; 2690pp; English.

XX The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular

CC genes (I) in a test sample or determining the expression profile of a

CC gene group in the sample comprising genes selected from (I). The method

CC is useful for examining the ischaemic condition (e.g. compressive

CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring

CC expression levels of particular genes (AB199202 to AB199912, encoding

CC the protein sequences in ABB57020 to ABB57374) or by determining the

CC expression profile of a gene group comprising these genes. The

CC expression levels or expression profiles produced by these genes are

CC used as an indicator when screening for ischaemic condition-improving

CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914

CC represent PCR primers for a mouse ischaemic condition related sequence,

CC which are used in the exemplification of the present invention.

XX Sequence 3147 BP; 704 A; 859 C; 887 G; 697 T; 0 other;

XX Query Match 32.5%; Score 546; DB 24; Length 3147;

XX Best Local Similarity 66.7%; Pred. No. 6e-92;

XX Matches 833; Conservative 0; Mismatches 370; Indels 45; Gaps 2;

Qy 315 GGTGCGCGCGCCCGCCGCTGCTGAGACGGCTGCTGCTCAAGTGGCGGGCTGCG 374  
 Db 1537 GCGGACACAGACAGACACCAAGATGCTGGAGCGGGTATTAACAATCTCCGGGCTGCG 1596  
 Qy 375 CTGGAGACGGGGGCGGACAGCTGGGCGGCTTCCCGGACACTGCTGTAAGGAGCCAGC 434  
 Db 1597 CTTCGAAACCGAGGCTCAAGACTGTGGACAAGTTCGCCAACCGCTGTGGCAACCGAA 1656  
 Qy 435 GCGCGCGCGCGCTTCAACGACGAGCGCGCGGAGATATTTCTGACGCGGACCGGC 494  
 Db 1657 GAACGCAATGGCTACTTGTAGACCCCTGAGAACGAGACTCTTTTACCGCAACCGCGC 1716  
 Qy 495 CAGCTTGACGCGGCTGCTACTACTACCACTCCGCTGGGCGGCTGCGGGCGCGCGCA 554  
 Db 1717 CAGCTTGATGCTCATCTTCTTACTACTACCACTCCGCGGCGCGCTGCGGCGCTCA 1776  
 Qy 555 CGTGCCTGAGCTGCTTCTCGGAAGAGTGGCGCTTCCAGCGGCTGGGCGGGGCGGCT 614  
 Db 1777 CGTGCCTGAGCAATGTTCTCCGAGAGATTTAAATTTTACAGTTGGGCGAGAGCCAT 1836  
 Qy 615 GGCACGCGTGGCGAGAGACGAGGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCG 674  
 Db 1837 GGAGAAATTCGCGGAAGATGAGGGCTTCATCAAGAAAGAGAGCGCGCGCGCGCGAGAA 1896  
 Qy 675 CGCCTTGGCGCGCAGCTGTGGCTGCTTTTCCGAGAGCTCTAGGCGCGCG 734  
 Db 1897 GGAATACAGGCGAGGCTGTGGCTGCTTTTGAATATCCGAGAGCTCAGAGCTGCGCG 1956  
 Qy 735 CGTGTGCGGCTACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794  
 Db 1957 GGTATTGCTCATTTGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2016  
 Qy 795 GAGCTGCTGACTTCCGCGACGACCGCGACGCGGCGGCTTCTGCTGAGCGCGAGC 854  
 Db 2017 GACTTCCCTGAGCTGAAAGAGACGACGAACTTACCGG----- 2055  
 Qy 855 CGGCGCGGTTTCCCGCTCCGCTGAATGCTCCAGCCAAATGCTTGAATCCACCGCG 914  
 Db 2056 -----CACCATCCACCGCATGACACACACACATCATCTATCTTC 2097  
 Qy 915 CCTGCCCTCAATGACCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974  
 Db 2098 CAACATCTTCAACAACCCCTTCTCATTTGGAACCTTGTATTCATCTGCTCTCTTT 2157  
 Qy 975 TGAGCTGCTGTAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034  
 Db 2158 TGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217  
 Qy 1035 GAACCTCATGATTTTGTGCTATCTTCCCTACTTGTGTGCTGCTGCTGCTGCTGCTGCT 1094  
 Db 2218 GAACCTCATGACATTTGTGCTATCTTCCCTACTTGTGTGCTGCTGCTGCTGCTGCTGCT 2277  
 Qy 1095 CCGGACGAGG-----GGTGGGCGCAGACGGGCGCATGCTGCGCATTCGAGAGTCAT 1148  
 Db 2278 TGACGACGAGGAAATAGAAAGGCGAGCGGCGCATTCCTGCGCATTCGAGAGTCAT 2337  
 Qy 1149 CCGATTTGCTGCTGCTTCCGATCTTCAAGCTTCCCGGACACTCAAGAGGCGCTGCAAT 1208  
 Db 2338 CCGTGTGTAAGGCTGTTCAGAACTTCAAACTTCCCGGACACTCAAGAGGCGCTGCAAT 2397  
 Qy 1209 CTGGGCGCAGAGCTTGGGCGCTTCATGCGTGAAGCTGGGCGCTCTCATCTTTTCTCTT 1268  
 Db 2398 CTTGGGCGCAGAGCTTCAAACTAGTAGAGGAGTGTAGGCTGCTCATCTTTTCTCTT 2457  
 Qy 1269 CATGGGTGTGCTCTTTTCCAGCGGCGCTACTTTCCGGAAGTTACCGGCTGAGCTC 1328  
 Db 2458 CATGGGTGTGCTCTTTTCTAGCGAGTGTATTTTGGCGAGGCGGAGAAAGCTGAGTC 2517  
 Qy 1329 CATTTACTAGCATTCCTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
 Db 2518 GCACTTTCAGATATCCCGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577  
 Qy 1389 CTATGAGACATGACCGCTCACTGTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCTCAT 1448



DB 2578 ATACGGTGCACATTTACCTGTGACATTTGAGAGCAAGATGCGCTCCCTGTGTGCAT 2637  
1449 TCGGGCGCTGCTACTATTTCCCTGCGAGTGCCTGCATATGTCATTCATTTACACTT 1508  
DB 2638 CGGTGCTGTGCTACATTTGCTCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2697  
QY 1509 TTATCAACCGGAGACAGAGGCGGAGAGGCTGGATGTCAGCATGT 1556  
DB 2698 CTACCCACCGAAGCTGAGGGGAGAGGAGCGCTCAGTTCCTCAGT 2745  
RESULT 11  
AB019704  
ID AB019704 standard; DNA; 994 BP.  
XX  
AC AB019704;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP10074.  
XX  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
PR 05-SEP-2000; 2000DE-1044543.  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guettig D;  
XX  
DR WPI: 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue  
CC types and for investigating cell differentiation. The method allows the  
CC methylation status of many C residues to be determined simultaneously.  
CC AB013410-AB013412 represent genomic DNA sequences used to illustrate the  
CC method for determining the degree of cytosine methylation described in  
CC the disclosure of the invention.  
XX  
SO Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;

Query Match 28.9%; Score 485; DB 24; Length 994;  
Best Local Similarity 74.2%; Pred. No. 1e-80;  
Matches 676; Conservative 0; Mismatches 185; Indels 50; Gaps 3;  
QY 2 TGGAGAGACCGACAGATCCCGGCGGAGAGGACGAGAGAAAGGAGACCCGGG 61  
DB 71 TGGAGAGACCTAGATAGGATTTGCGGAGTAGAGAGAGAGAGAGAGAGATTTGGGA 130  
QY 62 CGGAAAGCGGACAGACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 121  
DB 131 CGGAAAGCGGATAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 190  
QY 122 CCGGCGAGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 181  
DB 191 TTTGCGAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 250  
QY 182 CTCCCTCGCGCCCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
DB 251 TTTTTCGCGCTTTTATGCTTTTGTGCGGCTTATTTTATGCGCGGATATCGGA 310  
QY 241 CACCGGCTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258  
DB 311 TATCGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 370  
QY 259 -----GTGCGGCGCACAGCTGCGGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 313  
DB 371 CGGCGCTGGGCTTATACGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 430  
QY 314 CGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 373  
DB 431 CGGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 488  
QY 374 GCTTGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 433  
DB 489 GTTTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 548  
QY 434 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 493  
DB 549 CGCGTGGCGGCTGCTTTTACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 608  
QY 494 CAGCTTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 553  
DB 609 TTAGTTTCGACGCTGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 668  
QY 554 ACCTGCGGCTGACGCTTCTCGAGAGGCTGCTTCTTACGCGGCGGCGGCGGCGGCGG 613  
DB 669 ACCTGCTGCTTTCGACGCTTTTTCGAGAGGCTGCTTTTACGCGGCGGCGGCGGCTT 728  
QY 614 TGGCAGCGCTGCGGCGGAGAGAGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673  
DB 729 TGTACGCTTGGCGGCGGAGAGAGGCTTTCGCTGCTTTCGAGCGGCTTTTTCGCTG 788  
QY 674 GCGCTTTCGCGGCGGCGGAGGCTGCTTTCGAGCTTTCGAGAGCTTCGAGCGGCGG 733  
DB 789 GCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG 848  
QY 734 GCGTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT 793  
DB 849 GCGTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT 908  
QY 794 AGACGCTGCTTTCGCTTTCGCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 853  
DB 909 AGACGCTTTCGCTTTCGCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 968  
QY 854 CCGGCGGCGGCGG 864  
DB 969 TCGGTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG 979  
RESULT 12  
AB019705/c  
ID AB019705 standard; DNA; 994 BP.  
XX







Query Match 21.9%: Score 367.4; DB 24; Length 7642;  
Best Local Similarity 57.8%: Pred No 6e-59;  
Matches 684; Conservative 0; Mismatches 481; Indels 18; Gaps 1;

QY 344 AGCGGCTGGTGTCAACGAGGCGGGGCTGCTTCGAGACGGGGCGCCAGCTGGGCGC 403  
DB 2401 AACGGCTATTCATCAACATCTCCGAACTACGCTTCGAAACGGAACTAAACACCTTTAC 2442  
QY 404 GCTTCCCGACACTCTGCTAGGGGACCCAGCGCGCGCGCTTCTACGACGACCGC 463  
DB 2341 AATTCGCCCAACGCTACTAAACGACCCCAACGACGATAAATCTTCGACCCCTCC 2282  
QY 464 GCGGAGATTTCTTCGACCGGACCGGCGCTTCACGCGCGCTTCTACTATACC 523  
DB 2281 GCAACGAATCTTCTTCGACCGGACCGACCGACCTTCGACGCGCTTCTACTATAC 2222  
QY 524 AGTCGGTGGGCGGCTGCGGGCGCGCGGCTGCGGCTGCGGCTTCTGGAAGAG 583  
DB 2221 AATCCGAAACCGCATCCGCGACCGATCAGTACCATTTCTCCGAAAAA 2162  
QY 584 TGGCCTTTCACGGGCTGGGGCGGGCGCGCTGCGACGCTGCGGAGAGAGGCTGCC 643  
DB 2161 TCCGCTTTCACCACTAAACGAAAAACCATAAATAATTCGCGAAACGAAACCTTCC 2102  
QY 644 CGTGGCGCGCGGCGCGCGCGCGCGCGCTTCGCGCGCGCGCGCTTCTT 703  
DB 2101 TACGAAAAAAGAACGACCTTACCGCGCGCGCTTCACGCGCAATATATACTCT 2042  
QY 704 TCGAGTTTCCGAGAGCTCTCAGGCGCGCGGCTGCTGCGCTGCTGCTGCTCA 763  
DB 2041 TCGAATACCCGAAACCTCCGAAACGAAACGAAACATGCGATCGTACTATCA 1982  
QY 764 TCGTCTTCCCATCGCTGCTTCTGCTGAGACGCTGCTGCTTCCGAGACGCGG 823  
DB 1981 TCGTCTTCCCATCTATCATCTTCTACTAAAAAGCTACCGAAATTCGCGAGAAAAA 1922  
QY 824 ACGGCAAGGGGCTTGTGCTGACGCGCGCGCGGCTGCTGCGCGCTGCGCTGATG 883  
DB 1921 ACTACCGCGCGCTGAGCTGCGCAAACTCATTCGAAACACCGCAACACGCTGCAAT 1862  
QY 884 GCTCAGCCAATGCTGGAATTCACCCGCGCTGCGCTTCATGACCGCTTCTGCTG 943  
DB 1861 CCGGCGCAAAAA-----CCTCAACTTCTCGGATCCCTTCTGCTAA 1820  
QY 944 TGGAGAGGCTGTATTTGTGTTCTCTTGTAGCTGCTGAGCTGCTGCTGCTGCTG 1003  
DB 1819 TAAAAAGCTATACATCATTAATTCCTGCACTACTAATACGATTCCTTGGCTATC 1760  
QY 1004 CAAGCAAGGCTATCTCTTCAAGAACGTATGAACTCATGATTTTGTGGCTATCTTC 1063  
DB 1759 CTAAACAAAACGACTTCTGCGCAACATATAACTTAATCGACATTTATACCATATTC 1700  
QY 1064 CCTACTTTGTGCACTGGGACGAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGCA 1123  
DB 1699 CTATATTTATCACTTAATACGAACTAACGACGACAAACAAATTAACAAACCA 1640  
QY 1124 TGTCACTGGCCATCTCGAAGATCATCGATGCTGCTTCCGATCTTCAAGCTGT 1183  
DB 1639 TATCTCTAACCATCTTAAATAATCTCGGCTAATAAAATCTTCGCACTCTCAAACTAT 1580  
QY 1184 CCGGCACTCAAAAGGCGCTGCAAAATCTTGGGCGAGAGGCTTGGGCGCTCCATGCGAGC 1243  
DB 1579 CCGGCGCACTCCAAAAAAGTACAAATCTCTGACAAACGCTAAAAAGCTCATGAAAAAC 1520  
QY 1244 TGGGCGCTCTCATCTTTCTCTTCATCGGTGTGCTCTTTCAGCGCGCTACTT 1303  
DB 1519 TAAATTTACTCATCTTCTCTCTTATTAATAATCACTTTCTCCAAAGCGATCACT 1460  
QY 1304 TTGCGCAAGTTGACGGGAGGAGCTCCCATTTCTAGCACTCCCTGAGTCTTGTGGG 1363  
DB 1459 TTACGAAACAAACGACCCCATCTTCAAAATTTCAACAAACATCCGAAATACCTCTAATAA 1400

QY 1364 CGGTACTACCATGACTACTAGTTGGCTATAGAGACATGCGACCCGCTCACTGTGGTGGCA 1423  
DB 1399 CATATATTAACCATTAACACATATAATTAACAGATATACCCCAATTAACATTAACAAACA 1340  
QY 1424 AGATAGTGGGCTCTCTGTGTGCGCATTTGCGGGCGGTGACTATTTCCCTGCGAGTCCCG 1483  
DB 1339 AATTAATAAATCTCTATATACCATGCGGATATCTTAACCATGCGATTAACCAATTCGCG 1280  
QY 1484 TCATTTCTCCATTTTCAGCTACTTTTATACCGGAGACAGA 1526  
DB 1279 TAATTAATTCCAACTTCAATTTACTTCTACACCGAAAAACAAA 1237

Search completed: February 20, 2003, 06:32:37  
Job time : 439.041 secs





Query Match 63.6%; Score 1069; DB 1; Length 1599;  
Best Local Similarity 81.5%; Pred. No. 1,7e-198;  
Matches 1289; Conservative 0; Mismatches 280; Indels 12; Gaps 4;

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QY 100 CGGGGCAAGGCGGGGGGCTCCGGGAGAGGGGGGGGGTGGCCCTGTGCGCCCTCCG 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 CGGAAAGGCGGGGGGTGTTTCCACAGGTGTGGAAGGAGAGAGGGGGGCGCTTACG 90
QY 160 CCCGCGGGGTCAAGTGTGCGCCCTCCCTCGCGCCCTAGACCGCCCTGCGGGGCTATTAT 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 CCGCGGGGGGTAAACACGGCCCCCTCCCGCGCCCTGCGCGACTTTCATGCTATTTT 150
QY 220 GCGGGAACCGGACACCGGACACCGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ACCGCGGAGACACCGGACACCGGAGCTGGGGTGGCTGGCGGGGCGGAGACAGTCCG 210
QY 280 GCGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 339
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Db 211 ACCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 267
QY 340 TGGGAGGCGGTGTGTCAAGTGTGCGCGGGGTGCGCTTCAGAGCGGGGGGGGGGGGG 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 TGGGAGGCGGTGTGTCAAGTGTGCGCGGGGTGCGCTTCAGAGCGGGGGGGGGGGGG 327
QY 400 GCGCGCTTCCCGGACACTGTCTAGGGGACCGGCGCGGGGGGGGGGGGGGGGGGGGG 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 GCGCGCTTCCCGGACACTGTCTAGGGGACCGGCGCGGGGGGGGGGGGGGGGGGGGG 387
QY 460 GCGCGGGGGGAGTATTTCTTGCAGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 GCGGCGGGGAGTATTTCTTGCAGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 447
QY 520 TACCAAGTCCGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 TACCAAGTCCGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 507
QY 580 GAGGTGGCTTTTACAGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 GAGGTGGCTTTTACAGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 564
QY 640 TGGCGGGGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 TGGCGGGT---CGCGGAGCGGGCGGCTGGCCCGG---CTTTGGGCTTCAAGCTTGG 618
QY 700 CTTTTCAGATTTCCGAGAGCTCTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 759
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Db 619 CTCTTGAATTTCTGAGAGCTCGAGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 678
QY 760 GTATCTCTGTCTCATGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 GTATCTCTGTCTCATGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 738
QY 820 CGGAGGAGGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 CGGAGATGACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 798
QY 880 AATGGCTCAGCAAAATGCTGGAATCAACCGCGGCTGCGCTTCAATGACCGGTTTTC 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 AATGGCTCAGCAAAATGCTGGAATCAACCGCGGCTGCGCTTCAATGACCGGTTTTC 858
QY 940 GTGGTGAAGAGCGTGTGTATTTGTGGTTCCTTTGAGCTGTGAGCGCTTCCCTGTG 999
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTGGTGAAGAGCGTGTGTATCTCTGTGTCTCTCTTTGAGCTGTGAGTGTGTGGCC 918
QY 1000 TGTTCAGAGAGGCTATCTTCTTCAAGAGATGATGAATCAATCAATTTTGTGGCTAT 1059
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 TGTTCAGAGAGGCTATCTTCTTCAAGAGATGATGAATCAATCAATTTTGTGGCTAT 978
QY 1060 CTTCCCTTACTTTTGTGCGACTGGGCGAGCGCTGCGCGGAGGAGGAGGAGGAGGAG 1119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 979 CTGCTTACTTCTGTGGCGCTGGGCGAGGAGTGAAGCGGAGGAGGAGGAGGAGGAG 1038
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QY 1120 GCCATGTCACTGGCCATCTGTAGAGTCAATCCGATTTGGTGTGCTGTCTTCCGCACTTCAAG 1179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1039 GCTATGTCCCTGGCGCATCTTAAAGGCTATCCGATTTGGTGTGCTGTCTTCCGATCTTCAAG 1098
QY 1180 CTGTCCCGGCACTCAAAAGGGCTCAAAATCTTGGGGGAGAGCGCTTGGGGCTTCATGCT 1239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1099 CTGTCCAGGCACTTGAAGGGGTCTACAGATCTTGGGTGAGACACTGCGGGCTTCATGCT 1158
QY 1240 GAGCTGGGCGCTCTCATCTTTTCTCTTCATCCGTTGGTGTCTCTTTTCAGCGCGCTC 1299
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Db 1159 GAGCTAGTGTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1218
QY 1300 TACTTTCGGAAGTTGACCGGGGTGAGCTCCCATTTCACTACATCCCTGAGTCTCTG 1359
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Db 1219 TACTTTCGGAAGTTGACCGGGGTGAGCTCCCATTTCACTACATCCCTGAGTCTCTG 1278
QY 1360 TGGGCGGTGAGTCAATGATGACGTTGGGTATGGAACATGGGACCGGTCAGTGGGT 1419
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Db 1279 TGGGCGGTGATCAATGATGACGTTGGGTATGGAACATGGGACCGGTCAGTGGGT 1338
QY 1420 GGCAGATAGTGGGCTCTGTGTGCCATTTGCGGGGCTGCTGACTATTTCCCTGCCAGTG 1479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1339 GGCAGATAGTGGGCTCTGTGTGCCATTTGCGGGGCTGCTGACTATTTCCCTGCCAGTG 1398
QY 1480 CCGGTCAATGTCTCAATTTACGCTACTTTTATCACCAGGAGACAGAGGCGGAAGAGCT 1539
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1399 CCGGTCAATGTCTCAATTTACGCTACTTTTATCACCAGGAGACAGAGGCGGAAGAGCA 1458
QY 1540 GGGATGTTTCAAGCCATGAGGACATGACCTTGTGGGCCCATGAGGGGCAAGGGCAATGGG 1599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1459 GGGATGTTTCAAGCCATGAGGACATGACCTTGTGGGCCCATGAGGGGCAAGGGCAATGGG 1518
QY 1600 GGGGTGTGAGCGGGGAGTACCTGAGCTACCACTTCTGGGAGGAGGAGGAGGAGGAG 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1519 GGGGTGTGAGCGGGGAGTACCTGAGCTACCACTTCTGGGAGGAGGAGGAGGAGGAG 1578
QY 1660 CACCTGTACACCAAGTGTGA 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1579 CACATGTGTGACTGAGTGTGA 1599
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```

RESULT 2  
US-08-527-152-1  
Sequence 1, Application US/08527152  
Patent No. 5827655  
GENERAL INFORMATION:  
APPLICANT: Chandu, Kanianthara G.  
APPLICANT: Cahalan, Michael D.  
APPLICANT: Grissmer, Stephan  
APPLICANT: Goldin, Alan L.  
APPLICANT: Dehliels, Brent A.  
APPLICANT: Gutman, George A.  
APPLICANT: Masmuth, John J.  
TITLE OF INVENTION: Assay, Methods and Products Based On n  
NUMBER OF INVENTIONS: 5  
TITLE OF INVENTION: K+ Channel Expression  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hombach, Test, Albritton & Herbert,  
ADDRESSEE: Attn: W.H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/527,152  
FILING DATE: UNKNOWN  
CLASSIFICATION: 435



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/170,418  
FILING DATE: 20-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/558,568  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreyer, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-54444-2/RHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 150..1736  
US-08-527-152-1

Query Match 36.6%; Score 614.2; DB 1; Length 1994;  
Best Local Similarity 66.1%; Pred. No. 1.6e-110;  
Matches 960; Conservative 0; Mismatches 468; Indels 25; Gaps 4;

115 CCGGCGCTCCCGGAGAGGCGCGCGTCCGCTCCGCTCCGCGCGCGCGGAGTACA 174  
115 CCGGCGCTCCCGGAGAGGCGCGCGTCCGCTCCGCTCCGCGCGCGCGGAGTACA 174  
85 CCGGCGCTCCCGGAGAGGCGCGCGTCCGCTCCGCTCCGCGCGCGCGGAGTACA 144  
175 GTGCCCCCTCCCGCGCGCTAGCGCGCTCCGCGCTATTTTACGGCGGACCGGAC 234  
145 CACACATGACCGGTGGCGCGCGCGGAGCACCTGCTGAGCCAGAGCGCGGAGCGGTG 204  
235 ACCGACACCGGCGTGGGCGCGCGTGGGCGCACAGTGGTGGGCGCGCGGCGG 294  
205 GCGGCGCGCGCGCTCCAGAGGAGCGTGTGGCGAGTGGCGCGCGCGCGGT-GGACCGC 263  
295 TGGCGCGCGCGTGGAGCGCGCGGTGCCCGCGC-----CCCGTGGCGCTGCTGAGCGG 348  
264 TACGACGACATGCGCACCGCGCGGTGCCCGCGCGCGGAGCAAGATTGCTGCGGAGCGT 323  
349 CTGGCTGCTACAGTGGCGCGCGGTGGTGGAGACGCGCGCGCGCGCGCGCTTC 408  
324 GTGGTATCAACATCTCCGCGCGGTGGCGGTGAGACGACGCTCAAGACCTCTGCGACGTTTC 383  
409 CCGGACACTGCTGAGGAGCGCGCGCGCGCGCGCGCGCGCTTACGACGAGCGCGCGC 468  
384 CCGGAGACATGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 443  
469 GAGTATTTCTTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 528  
444 GAGTATTTCTTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 503  
529 GGTGGCGCGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588  
504 GGGGCGCGCGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 563  
589 TTCTACGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648  
564 TTCTACGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 623  
649 CCGCGCGAGCG 708  
624 GAGGAGAGCG 683  
709 TTTTCCGAGAGCTCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 768  
684 TATTCGAGAGCTCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 743

769 GTCTCATGCTGCTCTTCTGCTGAGAGCGTGGCTGACTTCCGCGAGCGCGGCG 828  
744 ATCTCATGCTGCTCTTCTGCTGAGAGCGTGGCTGACTTCCGCGAGCGCGGCG 800  
829 ACGGCGCTTCTGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 888  
801 -----TATCCG 851  
889 AGCGAATGCTGGAATTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 948  
852 TCGGCG 905  
949 ACGCTGATATTTGTTGTTCTCTCTTCTGAGCTGCTGAGCGCTGCTGCTGAGC 1008  
906 ACGTGTGATCATCTGCTCTCTCTCTGAGCTGCTGAGCGCTGCTGCTGAGC 965  
1009 AAGCTATCTTCTTCAAGAACGATGATGATGATGATGATGATGATGATGAT 1068  
966 AAGCGCGCTTCTTCAAGAACGATGATGATGATGATGATGATGATGATGAT 1025  
1069 TTTTGGCG 1128  
1026 TTTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085  
1129 CTGCGCATCTGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188  
1086 CTGCGCATCTGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145  
1189 CACTCAAGGCGCTGCAATCTTGGCGCGAGCGCTGCGCGCTGCTGCTGCTGCTG 1248  
1146 CATCTCAAGGCGCTGCAATCTTGGCGCGAGCGCTGCGCGCTGCTGCTGCTGCTG 1205  
1249 CTCTCATCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1308  
1206 CTCTCATCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1265  
1309 GAATGATGCGGCG 1368  
1266 GAGGAGAGCGACCGCTTCTTGGGCTTTTAAAGATATCCCGGATGCTTCTG 1325  
1326 GTAACATGACAACTGTTGTTGATGATGATGATGATGATGATGATGATGAT 1385  
1429 GTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488  
1386 GTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1445  
1489 GTCTCAATTTTCAAGCTATTTTATCACCGGAGAGCGGAGAGCGCTGGATGTT 1548  
1446 GTTTCACATTTCAAGCTATTTTATCACCGGAGAGCGGAGAGCGGAGAGCG 1505  
1549 AGCCATGTGACA 1561  
1506 ATGACAGCTGGACA 1518

RESULT 3  
US-09-178-109-3  
Sequence 3, Application US/09178109  
Patent No. 6395477  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang, Ling, Hui-Ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Polysium Channel Polynucleotides and  
TITLE OF INVENTION: Polypeptides and Uses Therefor  
FILE REFERENCE: ahp-98089  
CURRENT APPLICATION NUMBER: US/09/178,109  
CURRENT FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3

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Query Match	12.8%	Score 215.6	DB 4	Length 2064
Best Local Similarity	52.8%	Pred. No. 1.9e+33		
Matches 622; Conservative	0	Mismatches 499;	Indels 57;	Gaps 5;

OY	343	GAGGCGCGGGAGCTCAACGTCGGCGGGGCTGGCTTGTGAGACCGGGGCGGACGCTGGGC	402
Db	190	GAGCTGATTTGTCTTCAACGTCGAGTGGGGCGGAGTTTTCAGACTTGGAGGACCAAGCTGTGAG	249
OY	403	CGCTTCCGGACATCTGTCTAGTGGGGAGCCAGCGCGCGCGCGGCTGTCTAGACACACCG	462
Db	250	CGCTACCCGGACACCTTGCTGGGACAGACAGGAAGAGATTCTTCTCAAGAGGACAC-	308
OY	463	CGCCCGCAGATATTTCTTCACCGGGCACCGGCCAGCTTGTGACCGCTGTCTACTATAC	522
Db	309	--CAAGAGATCTTCTTCGACCGGGAGCCCGAGGTCTTCGGCTGGCTCTCAACTTCTAC	366
OY	523	CAGTCCGCTGGGGGCGCGCGCGGGCGGGGACAGTCGCTCGCTGACGTCTTCCGTGAAG	582
Db	367	C---GCACGGGGAAGCTGCACTACCCGGCTACGAGTGCATTTCTGTCTTAGACGACGAG	423
OY	583	GTCGCTCTTACAGGGGCTGGGGCGGGCGGCCCTTGGCAGCGCTCGGAGAGAGAGGGCTGC	642
Db	424	CTGGCTCTTACGGACATCTCCGGGAGATCATCGGGGAGTGTGCTGACGAGAGATACAG	483
OY	643	CCGGTGGCGCGCCAGCGCCCCCTTGGCCCCGCGGCTTGGCCCCGACGTGGCTGCTT	702
Db	484	GACCGCAAGGGGGAACGCGCAGAC-----GGCTCATG	516
OY	703	TTTCAGTTTCCCGAGACTCTCAAGCGCGCGCGGCTGCGCTGATGCTCCGTTGCTGTC	762
Db	517	GACACACACACCTCGGAGAACACACAGAGATCATGCTCCCTCAGCTTCGCGACGAC	576
OY	763	ATCTCTGCTCCATCGTGTGCTTCTGTGCTCGAGACGCTGCTCAGATCTCGGAGACGACGC	822
Db	577	ATGTGGCGGGCTTCGGAACCCCCACACAGAGAGCTGGCTGGCTGTCTTACTAGCTG	636
OY	823	GACGGCACGGGGCTTGTCTGTGTGACGCCGACCGCGCGGTTCCTCCGCTCCGCTGAT	882
Db	637	ACTGGCTTCTTCACTCGCTGTCTGTGCTATCACCAAGTGTGGAGACGGTGGCGCGCGC	696
OY	883	GGCTCCAGCCAAATGCTGTGAATTCACCCCGCGCTCCCTTAATGACCCGCTTCTGTG	942
Db	697	ACGGTCCCCGGGACAGAAAGAGCTGCCGTGCGGGAGAGCTACTCGGTGGCTTCTTCTGC	756
OY	943	GTCGAGACGCTGTGTATTGTGTGTTCTCTCTTGTGAGCTGCTGTAAGGCTCCTGTGCTGT	1002
Db	757	CTGGACACGCTGTGCGTCATGATCTTCACCGTGGAGTACTCTCTCGGCTCTTGGCGGCT	816
OY	1003	CCAAAGCAAGGCTATCTTCTTCAGAAACGTCGATGAACCTCATGTGATTGTGGCTATCTT	1062
Db	817	CCGACGCGTACCGCTTCACTCCGACGCTCATGAGATCATGAGTGTGGCCATCATG	876
OY	1063	CCCTACTTTGGGACATGGGGACCGAGCTGGGCCGCGAGAGGGGTGGGCGACGAGCC	1122
Db	877	CCCTACTACTCGGTGTGGTCAT-----GACCAACACAGCGAGAC	915
OY	1123	ATGTCACTGGCATTCTCTGAGAGTCAATCCGATTGGTGGCTTTCGCACTTTCGAAGCTG	1182
Db	916	GTCGCGGGGCTTCGTCGA---CGCTCGGGGTCTTCGGGTCTTAGAGATCTTCAAGTTT	972
OY	1183	TCCCGGCACTCAAGGGGCTGCAAAATCTTGGGGCAGAGGCTTCGGGCTTCATGCGTGA	1242
Db	973	TCCCGGCACTCCAGGGGCTGCGGATCTGGGGCTACACACTGAAGAGCTGTGCCCGAA	1032
OY	1243	CTGGGGCTCTCATCTTTTCTCTCTTCATCGGTGTGTGTCCTCTTTCAGAGGCGGCTGAC	1302
Db	1033	CTGGGGCTTCTCTCTCTCTCCGACACAGGCGCATCATCATCTTCTTCCACGTGATGTTT	1092

Qy	1303	TTTGGCAGATTTACCGGGAGACTCCCAATTTACATAGCATCCCGAGACCTCTGGAGG	1362
Db	1093	TATCCGAGAGGAGGCTCTCGGCGACGAAATTACAGCATCCCTCGTTTGGTAC	1152
Qy	1363	GGGTAGTACACATGACTTACAGTTGGCTATGAGACATGGACCCGTCACCTGTGGAGGC	1422
Db	1153	ACCATTTGCACATGACACACACTGGGATAGGAGACATGGTGCCTTAAGCATTTGCAAGG	1212
Qy	1423	AAGATTAGTGGGCTCTCTGTGTGCCAATTCGGGGCGTCTGACTAATTTCCCTGGCAGTGGCC	1482
Db	1213	AAGATCTCGGGCTCCATCTGCTCTCTTGAAGTGGGGTCTTGTCATTTGCCCTGCCATGCTCT	1272
Qy	1483	GTCATTGTCTCCAAATTCACACTACTTTATACACCGGGA	1520
Db	1273	GTGATTGTATTTCCAACTTACCGGATTTTACCAACACAA	1310

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RESULT
US-09-142-791A-3
; Sequence 3, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: Pct/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-3

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Query Match	12.8%;	Score 215.6;	DB 4;	Length 2072;
Best Local Similarity	52.8%;	Pred. No. 1.9e+33;		
Matches 622;	Conservative	0;	Mismatches 499;	Indels 57;
				Gaps 5;

QY	343	GAGGGGCGTGGTGGTCAACGTGGGGCGGGCTGGCTTTCAGAGAGGGGGGCGGCACGTGGG	402
Db	118	GAGCTGATTGTCTCTCAACGTGATGAGGGCGGAGTTCCAGACCTGAGAGACCACCGCTGGAG	177
QY	403	CGCTTCCCGGACACTGCTGCTAAGGGAGCCAGCGCGCGCGGCGCTTCTACGAGACGCG	462
Db	178	CGCTACCCCGGACACCTGCTGTGGCAGCAGGAGAGAGTCTTCTTCAACGAGGAGAC-	236
QY	463	CGCGCGGAGTCTTCTTGACGCCGACCGGCCAGAGCTTGACGCCGCGTCTACTACTAC	522
Db	237	- - - C A A G G A G T A C T T C T T G A C C C G G A C C C C G A G G T G T T C C G C T G C T G A C A C T T C T A C	294
QY	523	CAGTCCGGTGGCGGCTGGCGCGCGCGGCGACAGCTGCGCTGACAGCTTCTCTGGAAGAC	582
Db	295	C - - - G C A G G G G A A G C T G A C A T A C C C G C G T A C A G A G C A T C T C G C T C A C G A C G A G	351
QY	583	G T G G C C T T T A C G G G C T G G G G C G G G C C C T G G C A C G C C T G G C G A G A G A G G G C G T G C	642
Db	352	C T G G C C T T T A C G G C A T C T T C C C G G A A T A T C G G G A C T G C T T A C G A G G A T A A G	411
QY	643	C G G G T G C C G C C G A G C C C C C C T T G C C C G G C G C C T T T G C C C C G C C A G C A G T G A G G C G T T	702

Db	412	GACCGCAAGAGGGAGAAACGCCGAGC-----GGCTCATG	444
Qy	703	TTGCAATTTCCCAAGACTCTAGGCCGCGCGCTGCGCGTAAGTCTCCGTGCTGTC	762
Db	445	GACGACACAGACTCGAGAGAACCAACACGAGAGTCCATGCCCCCTCAGCTTCGCGACAGC	504
Qy	763	ATTCGTGTCACACGCGCTTCTGCTCGAGAGCGTACCAGATTCGCGGAGAGACCGC	822
Db	505	ATGTGGCGGGCTTTCAGAACCCCCACACACAGACGCTGCGCTTGCTTCTTACACTG	564
Qy	823	GACGGCACGGGGCTCTGCTGTCAGCCGACGCGCGCGGTGTTCCCGCTCCGCTGAAT	882
Db	565	ACTGCTTCTTCAACGCTGCTCGTGCATCACCAAGTGTGAGACGAGTCCGCGGCGC	624
Qy	883	GGCTCCAGCCAAATGCTTGGAATCCACCCCCTGCGCTTATATGACCGTCTTGCTG	942
Db	625	ACGGTCCCGGGCAGCAGAGGCTGCGTCCGGGAGACGCTACTGCGTGGCTTCTTGCG	684
Qy	943	GTCGAGACGCTGTGTATTTTGTGTTCTCTCTTTGAGCTGCTGTATCGGCTCTGCTGT	1002
Db	685	CTGGACACGGCGGCGCATGATCTTACCGGTGAGTACTCTCGGCTCTTCCGCGCT	744
Qy	1003	CCAAAGCAGGCTATCTTCTTCAAGAACGTGATGAACCTCATGATTTTGTGCTATCTT	1062
Db	745	CCGACGCGCTACCGCTTATCCGACGCTCATAGACATCATGAGTGTGGCCATCATG	804
Qy	1063	CCCTACTTGTGGCACTGGGACACGAGCTGGCCCGGACGAGGGGTGGGACAGAGCC	1122
Db	805	CCCTACTACTGCTGCTGTGCTAT-----GACCAACACAGAGSAC	843
Qy	1123	ATGTCACTGGCATCTCTGAGATCATCCGATTTGTGCTGCTTCCGATCTTCAAGCTG	1182
Db	844	GTCGCGCGGCGCTTGCA---CGTCCGGGCTTCCGGGCTTCAAGATCTTCAAGTTT	900
Qy	1183	TCCCGGACTTCAAAGGGCCCTGCAAACTTGGGGCAGAGCGCTTGGGCTCCATGCTGAG	1242
Db	901	TCCCGCCACTCCAGGGCCCTGGGAGCTCGGGCTTCACACTGMAAGTGTGCTCCGAA	960
Qy	1243	CTGGGCTCTCTCAATCTTCTTCCCTTCATCGGTGTGTCCTTCTTCCAGCGCGCTTAC	1302
Db	961	CTGGGCTTCTCTCTCTCTCTCCACACATGAGGCATCATCATCTTTGGCACATGATGTT	1020
Qy	1303	TTTGCCGAATTAACCGGGTGGACTCCCATTTCTACTAGCATCCCTGAAGTCTTCTGTTG	1362
Db	1021	TATCCCGAAGGGCTCTCGGCGACAACTTCACAAAGATCCCTGCTTTTGGTAC	1080
Qy	1363	GCGGTACTACCAATGACTAGTGTGCTATGAGACATGGACCCGTCACTGTGGGTGGC	1422
Db	1081	ACCATTTTCACTGACACACACTGCGATACGAGACATGCTCTTAAGACATTTGCAAGG	1140
Qy	1423	AAGATAGTGGGCTCTCTGTGTGCCATTTGGGCGCTGCTGACTATTTTCCCTGCGAATGCC	1482
Db	1141	AAGATCTTCCGCTCAATCTCTCTCTTGAATGCGTCTGTCATTTGCTTGCATGCTCCCT	1200
Qy	1483	GTCATGTCCTCAATTTCAAGCTCTTTATACCCGGGA	1520
Db	1201	GTCATTTCTTCAACTTATAGCCGGAATTTACCAACAGAA	1238
RESULT 5			
US-09-142-791A-1			
Sequence-1, Application US/09142791A			
Patent No. 6368823			
GENERAL INFORMATION:			
APPLICANT: Antoine Michel Alain Brill			
APPLICANT: Thierry Paul Gerard Calmeils			
APPLICANT: Jean-Francois Simon Pierre Falvire			
APPLICANT: Jean-Luc Jayre			
APPLICANT: Sabine Rouquet			
TITLE OF INVENTION: NOVEL COMPOUNDS			
FILE REFERENCE: GH-30012			
CURRENT APPLICATION NUMBER: US/09/142,791A			

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; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-142-791A-1

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Query Match	Similarity	12.8%	Score 215.6	DB 4	Length 2104
Best Local	Similarity	52.8%	Pred. No. 1.9e-33		
Matches	Conservative	0	Mismatches 499	Indels	Gaps
QY	343	GAGCGGCTGTCGTCACAGTGGCCGGGGCTTGCCTTCGAGACGCGGGCGCGACGCTGGGC	402		
Db	118	GAGCTGATTGTCCTCAACGATGAGTGGGGGAGTTCCAGACCTGGAGGACGCTGGAG	177		
QY	403	CGCTTCCGGGACACTCTGCTAGGGGACCCAGCGCGCGCGCTTCTAGACACAGCG	462		
Db	178	CGCTACCGGACACCTCTGCTGGGACAGCAGGAAGAGTCTTTCAMCAGGACAC	236		
QY	463	CGCCCGGATATTTCTTGACAGCGGACCGGCGCCACCTCTGACGCGCGTCTACTAC	522		
Db	237	--CAAGGATACTTCTTGACCCGGGACCCCGAGGTTGCTGCTGCTCAACTTCTAC	294		
QY	533	CAGTCGGTGGCGGCGCTGCGGCGCGCGGACGTCGCGCTCGAGCTTCTCTGGAAG	582		
Db	295	C--GCAGGGGAACTGCACTACCGCGGCTACGAGTGCATCTCTGCTACAGACAG	351		
QY	583	GTGGCTTCTACGGGCTGGCGCGCGCGGCTCTGACGCTGCTGGGAGAGAGGCTGC	642		
Db	352	GTGGCTTCTACGGGCTGCTCTCCGGAGATCATCGGGGACTGCTGTACGAGGATPAC	411		
QY	643	CGGTCGCGCCCGCGCGCCCTGCGCGCGCGCGCTTGCAGCGGACGCTGGCTGT	702		
Db	412	GACCGCAGAGGGAACACCGCGAGC-----GGCTCATG	444		
QY	703	TTTCGATTCCCGAGAGCTCTCAGGCGCGCGCGCTGCTCGCCGATCTCGTGTGTC	762		
Db	445	GACGACAACGACTCGGAGAACACAGAGAGTCCATGCTCTCGACTTCGCGACAGC	504		
QY	763	ATTCCTGTCCTCATGCTGTGCTTCTGCTCGAGACGCTGCCGACTTCCGACGACGCG	822		
Db	505	ATGTGGCGGCTTTCGAGAACCCCCACACACAGACGCTGGCCCTGCTCTTCACTACGT	564		
QY	823	GACGCGACGGGCTTGTGCTGCTCAGCGCGAGCGCGCGCTTTCGCTCGCTGTAAT	882		
Db	565	ACTGGCTTCTCATGCTGTGCTGCTGCTCATACACACAGTGTGGACAGGCTGCGTGGCG	624		
QY	883	GGCTCCAGCAATGCTCGGAATTCACCCCGCGCTTCAATGACCCGTTCTTCGTG	942		
Db	625	ACGTCCTCGGCGAGCAAGAGAGCTGCTGTCGCGGGAGCGCTACTCGGTGCTTCTTCG	684		
QY	943	GTGGAGAGGCTGTGATTTGTTGGTTCCTTTGAGTGTGTGTACGGCTCTGTGTCGT	1002		
Db	685	CTGGACAGCGCTGCTCATGATCTTTCACCGGTGAGTACCTCTCGGCTCTTCGCGCT	744		
QY	1003	CCAACCAAGGCTATCTTCTTCAAGACGATGATGAACCTCATGATTTGTGCTATCTT	1062		
Db	745	CCACACCGCTACCGTTCATCCGACGCTCATAGATCATGAGCTGTGGCTCATATG	804		
QY	1063	CCCTACTTTGTGCACTGGGACCGACGCTGGCCCGGACGAGGGGTGGGCGACGAGGC	1122		
Db	805	CCCTACTACTGCTGTGCTAT-----GACCAACACAGAGGAC	843		

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QY 1123 ATGTCACCTGGCCATCTCCAGAGTCATCCGATGTGCTGCTCTTCCGATCTTCAAGCTG 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 844 GTGTCCGCGCCTTCGTCAC---CGCTCCGGGTCTTCCGCGCTTCACAGATCTTCAAGTTT 900
QY 1183 TCCCGGACACTCAAAAGGCGCTGCAAAATCTTGAGGCGAGACGGCTTGAGGCTCCATCGTAG 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 901 TCCCGGACACTCCAGGCGCTGCGGATCTTGAGGCTACACACTGAAGAGCTGTGCTCCGAA 960
QY 1243 CTGGGCTCTCATCTTTTCTCTTCATGATGATGCTCTCTTTTCCAGGCGCTGTAC 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 961 CTGGGCTCTTCTCTCTCTCCCTACCATGAGCATTCATCTTTGGCAGCTGATGTTT 1020
QY 1303 TTGGCCGAAGTTGACCGGGGTGAGCTCCCATTTACATGATCCCTGATCTCTTGTTG 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1021 TATGCCAGAAAGGCTCTCTGCGGCGAGCAAGTTCAAAAGCATCCCTGCTGTTTGGTAC 1080
QY 1363 GCGGTACTCAACATGATACATGATGCTATGAGACATGCAACCGCTACATGTTGGGCG 1422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1081 ACCATTTGTACACATGACACACATGAGATACGAGACATGTCCTTAAGACGATTTGACGG 1140
QY 1423 AAGATAGTGGGCTCTCTGTGTCATTTGCGGCGCTGCTGCTATTTTCCCTGCGAGTCCC 1482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1141 AAGATCTTGGCTTCATCTCTCTCTCTGATGAGTGGCTCTGTCATTTGCTCCAGTCCCT 1200
QY 1483 GTCAATGTCTCAATTTTCACTTCTTTATACCGGGA 1520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1201 GTGATTTTTCACATTTAGCCGGATTTACACACAGAA 1238
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## RESULT 6

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US-09-178-109-1
; Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Chang Ling, Hwai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-09-178-109-1
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Query Match 12.8%; Score 215.6; DB 4; Length 2121;
Best Local Similarity 52.8%; Pred. No. 2e-33;
Matches 622; Conservative 0; Mismatches 499; Indels 57; Gaps 5;
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QY 343 GAGCGGCTGTCTCAACAGTGGCGGGCTGCTTCGAGACGGGCGCGACGCTGAGC 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 GAGCTGATTTGCTCCACAGTGAAGGGGAGGTTCCAGACCTGAGAGACACGCTGAG 249
QY 403 CGCTTCCCGACACTGCTGCTAGGAGACCAAGCGCGCGCGCTCTTACAGACGAGCG 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CGCTACCCGAGACCCCTGCGGGGAGGAGGAGGAGGATTTCTTCAAGAGGAGAC- 308
QY 463 CGCGGAGATTTCTTTCGACGCGGACCGGCCAGTTTCAGCGGCGCTCTACTACTAC 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 --CAAGAGATACCTTCTTCGACCGGAGACCGAGGTGTTCCGCTCCGCTCACTTCTAC 366
QY 523 CAGTCCGCTGGCGGCTGCGGCGCGCGCGACGCTGCTGACGCTTCTTCGAAAGAG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 C--GCACGGGGAAGCTGCTACACCGCGCTACGAGTGTCTCTGCTACGACGAGAG 423
QY 583 GTGGCTTCTACAGGCTGGGCGCGCGGCTGACAGCCTGCGCGAGAGAGGCGTGC 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 424 CTGGCTTTTACGGCATCTCCCGAGATCATCGGAGACTGCTCTACGAGATACAG 483
QY 643 CGGTTGCGCCGAGAGCGCCCTGCCCCGCGCTTCGCGCCGACGTGTGCTCTT 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GACGCAAGAGGAGAGAACCGCGAGC-----GGCTCATG 516
QY 703 TTGAGATTTCCGAGAGCTCTCAGGCCGCGGCTGCTGCGCTGATGCTCTGCTGTC 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 517 GACGACAAAGACTTGGAACACACAGAGATCTACGCTGCTGCTACCTTCCGCAACAC 576
QY 763 ATCTCTGCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 ATGTGGGCGGCTTTCGAAACCCACACACAGAGCTGCGCTGCTGCTTCTTACTACTG 636
QY 823 GACGCAAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 ACTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
QY 883 GGTTCACGCAATGCTGCAATTCACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 697 ACAGTCCCGGCGACAGAGAGCTCCGTCGCGGAGCGCTACTGCTGCTGCTGCTGCTGCT 756
QY 943 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 757 CTGAGACAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
QY 1003 CCAAGCAAGGCTATCTTCTTCAAGAGCTGATGACCTCATGATTTTGTGGTATCTT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 CCGAGCGGCTACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
QY 1063 CCTTACTTTGTGCGACTGCGACCGAGCTGCGCGGACGAGGAGGCTGCGGACGAGCC 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 CCTACTACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
QY 1123 ATGTCACCTGGCCATCTCCAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 916 GTGTCCGCGCCTTCGTCAC---CGCTCCGGGTCTTCCGCGCTTCACAGATCTTCAAGTTT 972
QY 1183 TCCCGGACACTCAAAAGGCGCTGCAAAATCTTGAGGCGAGACGCTTCCGCTCCATCGTAG 1242
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Db 973 TCCCGGACACTCCAGGCGCTGCGGATCTGCGGCTACACACTGAAGAGACTGTGCTCCGAA 1032
QY 1243 CTGGGCTCTCATCTTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
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Db 1033 CTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092
QY 1303 TTTTCCGCAAGTTCACCGGGGTGAGTCCCATTTTCACTGACATCCCTGAGTCTTGTGG 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1093 TATGCCGAGAAAGGCTCTCTGCGGACGAGTTCACAGACATCCCTGCTGCTTGTGGTAC 1152
QY 1363 GCGGTACTCAACATGACTACAGTTGGCTATGAGACATGCGACCGCTACATGTTGGTGGC 1422
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Db 1153 ACCATTTGTCCACATGACACACATGAGTGGATACGACATGCTTGAAGAGATTTGACAGG 1212
QY 1423 AAGATAGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482
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Db 1213 AAGATCTTCCGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 1483 GTCAATGTCTCAATTTTCACTACTTTTATACCGGGA 1520
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Db 1273 GTGATTTTTCACATTTAGCGGATTTTACACAGAA 1310
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## RESULT 7

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US-09-336-643A-9
; Sequence 9, Application US/09336643A
; Patent No. 639761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
```



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Db      178 CGCTACCCGAGACACCCCTGCTGGGAGACGAGAGAGTTCCTTCAACAGAGACAC- 236
Qy      463 CGCCGCGAGTATTTCTTCGACCCGCGACCGCCAGCTTCGACGCGCGTCTACTACTAC 522
Db      237 - -CAAGAGAGTCTTTCGACCCGCGACCCGAGGTTCGCTGCTCAACTTCTAC 294
Qy      523 CAGTCCGAGTGGGCGGCTGCGGCGCGCGACGTCGCGCTTCGAGCTTCCTGAGAGAG 582
Db      295 C---GCACGGGGAAGCTGCACTACACCGCGCTACAGATGCACTCTGCTACGAGAGAG 351
Qy      583 GTGGCCCTTTCACGGGCTGGGCGGCGCGCTTCGACGCTGCGCGAGAGAGAGGCTGC 642
Db      352 CTGGCTTTCACGCGCATCTCCGAGATCATCGGAGACTGCTCTACGAGAGATACAAG 411
Qy      643 CCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 702
Db      412 GACCCGAGAGAGAGAGAGAGCGCGAGC-----GGCTCATG 444
Qy      703 TTGAGATTTCCGAGAGCTCTCAAGCGCGCGCGCGCGCGCGCTTCGCTGCTGCTGTC 762
Db      445 GAGCAGACAGCATCTCGAGAGACACAGAGATCCATGCCCTTCGCTACGCTTCGCGCAACC 504
Qy      763 ATCTGCTCTCATCTGCTGCTCTTCTGCTCGAGAGCTGCTGCTGCTTCGCGAGAGACCG 822
Db      505 ATGTGCGCGCGCTTCGAGAGACCCGACACAGCAGCGCTGCGCGCTGCTTCTACTACGTG 564
Qy      823 GAGGAGCAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db      565 ACTGCGCTTTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
Qy      883 GCGTCCAGCCAAATGCTGAGAAATCCACCCGCGCTGCTGCTGCTGCTGCTGCTGCTG 942
Db      625 ACGGTCCCGGAGAGAGAGAGAGCTGCGCTGCGGAGAGCGCTACTGCGTTCCTTCTGCG 684
Qy      943 GTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Db      685 CTGAGACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
Qy      1003 CCAAGCAAGGCTATCTTCTTCAAGAGAGTATGAACTGATGCTGCTGCTGCTGCTGCT 1062
Db      745 CCCAGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
Qy      1063 CCTACTTGTGCGACTGCGGACCGAGCTGCGCGCGAGGAGGCTGCGCGAGAGAGCC 1122
Db      805 CCTACTACATCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Qy      1123 ATGTCACTGGCCATCTGAGAGATCATCGATGCTGCTGCTGCTGCTGCTGCTGCTG 1182
Db      844 GTGTCCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy      1183 TCCGCGGACATCAAAAGGCGCTGCAAAATCTTGGCGAGAGGCTTGGGCGCTCATCGGAG 1242
Db      901 TCCGCGGACATCTCAAGGCGCTGCGGAGATCTTGGCTACACATGAGAGCTGCTCCGGA 960
Qy      1243 CTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1302
Db      961 CTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Qy      1303 TTTTCCGAATTTGACGGGCTGAGCTCCCATTTCACTAGCATCCCTGATGCTCTGCTG 1362
Db      1021 TATGCCAGAGAGGCTCTCTCTGCGGAGCAGCATGCTCAAGCATCCCTGCTGCTTGGTAC 1080
Qy      1363 GCGGTATGTCACATGATAGTGGCTATGAGAGATGAGCATGCCGACATGAGGAGGCG 1422
Db      1081 ACCATTGTCACATGACACATGAGGATGAGAGATGAGGCTTAAGACATGAGAGG 1140
Qy      1423 AAGATATGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482
Db      1141 AAGATCTTGGGCTCATCTCTCTCTGAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCT 1200
Qy      1483 GTCAATGCTCAATTTCACTTCTTATCAGCGGGA 1520

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Db      1201 GTGATGTTTCCAACTTACCGGATTTACCACAGAA 1238
RESULT 9
US-08-288-405A-19
; Sequence 19, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandu, Gritscha
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herdert,
; ADDRESS: Attn: Walter H. Dregler
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; US-08-288-405A-19
Query Match 11.3%; Score 189.2; DB 1; Length 271;
Best Local Similarity 93.7%; Pred. No. 1.8e-28;
Matches 208; Conservative 0; Mismatches 7; Indels 7; Gaps 1;
Qy      1466 TTTCCCTGCGAGTGGCCCGCTGATGCTTCATTTTCACTTATACCGGAGACAG 1525
Db      1 TTTCCCGCGAGTCCCGTCTATTTGTCATTTTCACTTATACCGGAGACAG 60
Qy      1526 AGGCGGAAGAGGCTGGATGTTACGCCATGTGACATGACACCTTGTGGCCCACTGAGG 1585
Db      61 AGGCGGAAGAGGCTGGATGTTACGCCATGTGACATGACACCTTGTGGCCCACTGAGG 120
Qy      1586 G-----CAAGCGCATTTGGGGGCTGTGGAGGAGGAGTACCTGAGTACCACTCA 1638
Db      121 GNNCANCNANNNCATTTGGGGGCTGTGGAGGAGGAGTACCTGAGTACCACTCA 180
Qy      1639 CTCTGGCACCCCGCCAGAGAAACACTGCTGACCGAAGTGA 1680
Db      181 CTCTGGCACCCCGCCAGAGAAACACTGCTGACCGAAGTGA 222
RESULT 10

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US-07-955-916-5
: Sequence 5, Application US/07955916
: Patent No. 5397702
: GENERAL INFORMATION:
: APPLICANT: CAHALAN, Michael D.
: APPLICANT: CHANDY, Kanianthara G.
: APPLICANT: GRISMER, Stephen
: APPLICANT: GHANSHANI, Sanjin
: APPLICANT: GUTMAN, George A.
: APPLICANT: DETHELFS, Brent A.
: TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE
: TITLE OF INVENTION: DISEASES
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Walter H. Dreger
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/955,916
: FILING DATE: 19921002
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Dreger, Walter H.
: REGISTRATION NUMBER: 24,190
: REFERENCE/DOCKET NUMBER: A-54474-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 696 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-07-955-916-5

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Query Match	11.2%:	Score 187.4:	DB 1:	Length 696:
Best Local Similarity	61.8%:	Pred. No. 4.7e-28:		
Matches 368:	Conservative 0:	Mismatches 191:	Indels 36:	Gaps 3:
QY 944	TGAGACGCTGTGATTTGTTGGTCTCTCTTGGACCTGCTGGTAGCCCTCGTGTGTC			1003
Db 14	TCGAGGGGCTCTGTGTGGTCTGTGCTTACCTTGTGAATCTCTCATGGCTGTGATCTTGTGCC			73
QY 1004	CAAGCAGGCTATCTTCTTCAAGAACGATGAAACCTCATGATTTTGTGGCTATCTTTC			1063
Db 74	CCAACAAAGTGAGATTCAATCAAGAACCTGCTCAACATCATTTGATTTTGGCCATCTTGC			133
QY 1064	CCTACTTTGTGGCACTGGGGCACCAGCTGTGGCCCCGACGAGAGGGTGGGCCACGACGCCA			1123
Db 134	CTTTCTTACCTTGAGAGGTGGG-----GCTGAGGGGGCTGTCCCTCAAGCAGCCCAAGGAGC			187
QY 1124	TGTCACTGGGCATCTGTAGAGATCATCCGATTTGGTGGCTGTCTTCCGATCTTCAAGCTGT			1183
Db 188	TG---CTGGGCTTCTTGCGCGCTGTGCTCCGCTTGTGTGCGCATCTTGAAGCTGA 244			
QY 1194	CCCGGCACTCAAAAGGCGCTGCAGAAATCTTGGGCGACAGCGTTTCGGGCTTCCATAGCTGAGC			1243
Db 245	CCCGCACTTTGTGGGCGTCGGGCGTCTGGGCGACACAGGTGCTCGGAGCGACACCAAGAGT			304
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Query March	10.3%	Score 173.8	DB 1	Length 1805
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Db	879	TGGAGGGGCTGCGCTGGCTGCTGCTTACCTTGGATTTCTCATGGGTGTCGCTTCTGGC	938	
QY	1004	CAGCAGGCTATCTTCTTTCAGAACGCGATGAACCTCATGCATTTTGGCTATTCCTTC	1063	





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## RESULT 13

PCT-US94-08449A-1  
; Sequence 1, Application PC/TUS9408449A  
; GENERAL INFORMATION:  
; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESS: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08449A  
; FILING DATE: SUBMITTED HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2127 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA  
; PCT-US94-08449A-1

Query Match 9.6%; Score 161; DB 5; Length 2127;  
Best Local Similarity 48.8%; Pred. No. 7,1e-23;  
Matches 629; Conservative 0; Mismatches 630; Indels 30; Gaps 6;

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RESULT 14

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US-08-464-340A-3
: Sequence 3, Application US/08464340A
: Patent No. 5710019
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: GENERAL INFORMATION:
: APPLICANT: LI, ET AL.
: TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
: ADDRESSEE: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464, 340A
: FILING DATE: June 5, 1995
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/08449
: FILING DATE: 28 JUL 1994
:
: ATTORNEY/AGENT INFORMATION:
: NAME: FERRARO, GREGORY D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-415
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2483 BASE PAIRS
: TYPE: NUCLEIC ACID
: STRANDEDNESS: SINGLE
: TOPOLOGY: LINEAR
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: MOLECULE TYPE: CDNA
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US-08-464-340A-3

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Query Match	9.1%;	Score 152.8;	DB 1;	Length 2483;
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Oy	1123	ATGTCACTGGCCATCTCGAGAGTCATCCGATTGGTGCCTGTCTTCCGATCTTCAAGCTG	1182
Db	1537	GTCGACGAGGCGCGTGAG---GGCGTCGCGATCATGCGCATGCGCCGATCTTCAAGCTG	1593
Oy	1183	TCCGGGAGCTCAAAAGGCGCGCAAAATCTTGGGGCGAGACCTTGGGCGCTCCATGCGTGAG	1242
Db	1544	GCCCGCCACTCTCTCGGGCTTCGACAGCCCTCACCATTAGCCTTAAGCGACGCTTCAAGGAA	1653
Oy	1243	CTGGGCGCTCTCATCTTTTCCCTTCATCGGTGGTGGTCTTTTTCAGGCGCGCTAC	1302
Db	1654	CTGGGGCGTGGCTGATGTAACCTTGGGAGTGGGATCTTGCTCTCGAGCCCTGGGCTG	1713
Oy	1303	TTTGGCCAGATTGACGGGGTGACCTCCCATTTTACTAGCATCCCTGAAGTCTTCTGTGG	1362
Db	1714	ACCATGAGAGAGAGACCCTACCGAGACCCGTTTAAAGAAATCCCCAGCTCTTCTGGTGG	1773
Oy	1363	GGGTAGTCACCATGATACAGTTGGCTTGGAGCATGGACGCCGCTCATGTGGGAGGC	1422
Db	1774	GCATCATCACCATGACACCGTGGCTTAGGGGACATCTACCCCAAGACACAGCTGAGC	1833
Oy	1423	AAGATAGTGGGCTCTCTGTGTGCCATTGGGGGGCGTGCTACTATTTTCCCTGCCAGTGCC	1482
Db	1834	AAGTCAAGCGGGGCATCAGACTTCTGTGGGGTGTCATTGCCATCGCCCTGCCATTCAC	1893
Oy	1483	GTCATTGCTTCCAAATTTCACTACTTTTATCACCGGGAGACAGAGGGCGAAAGAGCTGGG	1542
Db	1894	CCCATCTCAACAACATTTGTACAGTACTACAAACAGCAGCGGTCCTGAGAACCGCGGCC	1953
Oy	1543	ATGTTCAGGCATGGAGCATGCGAGCGCTTGGGCGCACTGGAGAGAAAGGCCATGGGGGG	1602
Db	1954	AAGCAGCAGCTGGAGCTGATGAGAACTCAACTCCAGCAGCGGGGGCGAAGGCGAAGCGGG	2013

## RESULT 15

PCT-US94-08449A-3  
Sequence 3, Application PC/TUS9408449A  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: Potassium Channel Protein 1 and 2  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAPELLI, BYRNE, BAIN, GILFILLAN,  
ADDRESS: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08449A  
FILING DATE: SUBMITTED HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2483 BASE PAIRS











	DEFINITION
	Tetraodon nigroviridis genome survey sequence T7 end of clone 159H12 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL210432
VERSION	AL210432.1 GI:7869251
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetraodon nigroviridis. Tetraodon nigroviridis. Tetraodon nigroviridis.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE	1 (bases 1 to 900) Roest-Crollius,H., Fallon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Wincker,P., Brottier,P., Queller,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
AUTHORS	Unpublished
JOURNAL	2 (bases 1 to 900)
REFERENCE	Roeest-Crollius,H., Fallon,O., Dasilva,C., Fitzames,C., Fisher.C., Bouneau.L., Billault.A., Queller.F., Saurin.W., Bernot.A. and Weissenbach.J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
TITLE	Unpublished
JOURNL	3 (bases 1 to 900)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
JOURNAL	Submitted (12-APR-2000)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
FEATURES	Location/Qualifiers
source	1..900 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="159H12" /name="_lib"G"
BASE COUNT	206 a 242 c 283 g 166 t 3 others
ORIGIN	
	Query Match 21.9%; Score 368.2; DB 17; Length 900;
	Best Local Similarity 68.4%; Pred.No.2.4e-61;
	Matches 589; Conservative 1; Mismatches 224; Indels 47; Gaps 4;
OY	675 CCGCTTCGCCGGCCAGCCTGCTGCCTTTTGAGATTCCCAGACTCTCAGCCGCGG 734
Dd	
OY	899 CGAKTTYCAAGCGCGAGATCTGTGCTCTCTTGAGTAGCCGGAGACTCCAGCCGCGAG 840
Dd	
OY	735 CGTGTCCACCAGTAGCTCCGTCGTGTCATCATCCTGTCATCGTCTTGCTGCTGA 794
Dd	
OY	839 GGCGATCCGCGGGGTCTCCGTCCTGTATGTCATCTTCATTCATCTTTCGCTGGA 780
Dd	
OY	795 GACGCTGCCTGACTTCCGCGAGACCGGAGCGGCGGCGCTTGTCTGCAGCCGAGC 854
Dd	
OY	779 GACGCTGCCGGAGTTCAAGGAGCAAGAAGA-----GAACTGCAGCCGCGGG 733
Dd	
OY	855 CGGCCCCGGTGTTCGCCGCTCGGCTAATGCGTCCAGCCAATGCTGGAAATCCACCCG 914
Dd	
OY	732 GCACAATCCAGCGCAGCACGACGATTTC----- 702
Dd	
OY	915 CCTGCCCTTCAATGACCGGTTCTTGCTGTGSAGAGCGCTGATTTGGTTCTCCTT 974
Dd	
OY	701 ---GCTTTCAAGCAGACCCCTTTTTATGTGTGAGAGCGGTCTGCATCATCTGTTCTCTT 645
Dd	
OY	975 TGAGCTGCTGTATACCTCTCTGCTGTATGTCACAAAGGCTATCTCTTCAAAGAACGTAT 1034
Dd	
OY	644 TGAGATTTATAGTTCCTTCTTCGCCAGGCCCAAGCAACGGCTTCTTTAAAATAATCAT 585
Dd	
OY	1035 GAACCTCATCGATTTTGTGGCTATCTCTTCCTACTTTGTGGCATGGGACCGAGCTGGC 1094

D	b	584	GAACCTCATTAGACATCGTGTCCATTTTCGCTTAATTTCACTGTCCGACGAGACTGGC	525
O	y	1095	CCGGCAGCGAGGGGTGGGCCACAGCAGGCCATGTCACTGGCCATCTGAGAGTCATCCGATT	1154
D	b	534	CCAGCACACGAGGCACAAGGCGACAGAACCATTAS--TTCCGCATTCGAGAAATAATCCGCCT	466
O	y	1135	GSTGGTGTCCTTCCGCATCTTCAAGCTGTCCCGGACATCAAAAGGCGCTGCAAACTTGGG	1214
D	b	465	GGTCCGCTGTTCGCCATCTTCAATCTGTCCAGACACTGCACAAGGGCGTGCAGATCTGGG	406
O	y	1215	CCAGACGGCTTGGGGGCTCATATGCGTAGCTGGGCTCCCTCATCTTTTTCCTTCATCGG	1274
D	b	405	CCATATCCCTGGCGCGACAGATGAGGAGACTGGCCCTCTCATTTTCTTGTGGATCGG	346
O	y	1275	TGTGTCTCTTTTTCAGCGCCGCTCTACTTTGGCCGAGATTACCGGGTGCATCCCATTT	1334
D	b	345	CGTATCCTCTTTCACAGCGGCTACTTTCGCGAGGCGAGACGCCACACTCCCAATT	286
O	y	1335	CACATAGCATCCCTAGATCTTCTGTGTGGGCGGTATACACTGACTAGCTTGGCTATGG	1394
D	b	285	CACACGACATCCCCGACGGGTTGTGGTGGCTGTGGTAACCATAGACAGGTTGGGCTACGG	226
O	y	1395	AGACATGGACACCCGACACTGTGGGCGGCAAGATAGTGGGCTCTGTGTGCATTTGCGGG	1454
D	b	225	CGATTTGAAGCTATACAGGTCGTGGGAAAGATCTGTGGGCTCCGTGTGGCATTCGCGG	166
O	y	1455	CGTCTGACATATTTCCCTGCCAGTGGCCCGTCATGTCTCCAAATTCACACTACTTTATCA	1514
D	b	165	CGTGTAAACGATCGCGCTGGC-GTCCCGGTATCGTTCCAAATTTAATTTACTTTTACCA	107
O	y	1515	CCGGAGACAGAGGCGCAAGA	1515
D	b	106	CCGGAGACCGATTAACGAGA	86

RESULT 5  
LOCUS CENS03DKC/c

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 017A20 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL239205

VERSION AL239205.1 GI:7898340

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphae; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 839)  
Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Broitler,P., Quetier,F., Saurin,W. and Weissbach,J.  
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

.TITLE Unpublished

JOURNAL Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis unpublished

TITLE Genoscope.

JOURNAL Direct Submission  
AUTHORS Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.



## FEATURES

Location/Qualifiers

1. 839

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="017A20"

/clone\_1lb="g"

BASE COUNT 157 a 246 c 281 g 155 t

ORIGIN /note="Genoscope sequence ID : COB017BA10BP1-end : 77"

## Query Match

Best Local Similarity 20.4%; Score 342.8; DB 17; Length 839;

Matches 571; Conservative 0; Mismatches 247; Indels 60; Gaps 2;

```

QY 351 GGTGCTCAAGTGGCGGGCTGCGCTTCAGAGACGGGCGGCGACGCTGGGGCCGCTTCCC 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 839 GGTGCTCAAGTGGCGGGCTGCGCTTCAGAGACGGGCGGCGACGCTGGGGCCGCTTCCC 780
QY 411 GGACACTCTGTAGGGGACCGACGCGCGCGGCGCTTACAGACGACGCGCGCGCA 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 779 GGAGACCTCTGGGGAACCCAGAGAGAGATGCGCTACTTGACCCGCTCGCGAGCA 720
QY 471 GTATTTTGTGACCGGACCGCGCGCGCTTCAGACGCGCGCTTACTACTACAGTCGG 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 719 GTACTTCTTGGACCGGGAACCGCGCGCGCTTCAGACGCGCGCTTACTACTACAGTCGG 660
QY 531 TGGGCGGCTGCGGCGCGCGCGCGCTTCAGACGCGCGCTTCTCGAAGAGTGGCGCTT 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 659 CGGCGGCTGAGGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCTTCTCGAAGAT 600
QY 591 CTACGGGCTGCGGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCTTCAGAC 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 599 CTACGAGCTGGGATGAGGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCTTCAG 540
QY 651 GCCGAGCGCGCGCGCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCTTC 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 539 GGAGAGCGCGCGCGCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCTTC 480
QY 711 TCCGAGAGCTTCAGACCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCT 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 CCGGAGAGCTTCAGACCGCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCT 420
QY 771 CTCATGCTGCTTCTGCTTCAGACGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCG 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 CTCATGCTGCTTCTGCTTCAGACGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCG 360
QY 831 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 CGTGCAGAGTTCGCGCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCT 321
QY 891 CCAATGCTGGAATCCACCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCGCGCT 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 -----GCCCTACATCTGACGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCG 282
QY 951 GCTGTATTTGTTGTTCTTCTTTCAGACGCGCGCGCGCTTCAGACGCGCGCTTCAGAC 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 GCTGTATTTGTTGTTCTTCTTTCAGACGCGCGCGCGCTTCAGACGCGCGCTTCAGAC 222
QY 1011 GGTATCTTTTAAAGACTGATGAACCTGATGATTTTGTGCTATTCCTTCTTCTTCTT 1070
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 GGGGCGCTTCTTCAGAGACATGATGAACACATGACATGATGATGATGATGATGATGAT 162
QY 1071 TGTGGAGTGGGACGAGTGGGCGCGCGCGCGCGCTTCAGACGCGCGCTTCAGACGCG 1112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 CATCAGCTGGGACGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGG 102
QY 1113 CGAGCAGGCGCATGTCGCGCATTCCTGAGAGTATTCGATGATGATGATGATGATGAT 1172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 CGAGCAGGCGCATGTCGCGCATTCCTGAGAGTATTCGATGATGATGATGATGATGAT 42
QY 1173 CTTCAGGCTTCCGCGCATCAAGGCGCTTCAGAAATCT 1210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 CTTCAGGCTTCCGCGCATCAAGGCGCTTCAGAAATCT 4

```

## RESULT 6

A1324179/c

LOCUS

DEFINITION

A1324179 468 bp mRNA linear EST 23-DEC-1998  
 m183g06.x1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus cDNA  
 clone IMAGE:457594 3' similar to gb:X17622.cd41 POTASSIUM CHANNEL  
 PROTEIN KVL6 (HUMAN); gb:Y00305 Mouse MBK1 mRNA for mouse brain  
 potassium channel (MOUSE);, mRNA sequence.

## ACCESSION

A1324179

VERSION

KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

## TITLE

JOURNAL

COMMENT

The WashU-HMNI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMNI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LBNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:274482  
 This clone was previously sequenced on the 5' end only, this new  
 data is from the 3' end  
 High quality sequence stop: 453.

## FEATURES

source

Location/Qualifiers

1. 468

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:457594"

/clone\_1lb="Soares mouse placenta 4NDMP13.5 14.5"

/sex="unknown"

/tissue\_type="placenta"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: placenta; Vector: p773D-Pac (Pharmacia)

with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

15'.

TGTACCAATCTGAATGGAGCGCGCGCGGGAATTTT

T 3'; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p773 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT

ORIGIN

75 a 166 c 176 g 51 t

## Query Match

Best Local Similarity 20.0%; Score 336; DB 9; Length 468;

Matches 393; Conservative 0; Mismatches 75; Indels 2; Gaps 1;

```

QY 163 GCGGAGGTACAGTGGCCCTCCCTGCGCGCGCGCGCGCGCGCGCGCTATTTTACGC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 468 GCGGAGGTACAGTGGCCCTCCCTGCGCGCGCGCGCGCGCGCGCGCTATTTTACGC 409
QY 223 CGGACACCGACACCGGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCG 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 CGGACACCGACACCGGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCG 349

```

QY	283	GGTGGCGGGGGGTGGGGCGCCCATGAGACGGGGGAGTGGCCCGCCCGCCCGTGGGGGTGGTC	342
Db	348	GGTCCCGCGGGGTGGTGGCGGGCCATGAGCCAGGTGGTCCCGCGCCC--TGGGGCTGTTCG	291
QY	343	GAGCGGCTGGTGTCTCAACGTGGCGGGGTGCGCTTTCGAGACGCGGGCGGCGACGCTGGGC	402
Db	230	GAGCGGGTGGTGTCTCAACGTGGCGGGGTGGCGCTTTCGAGACCCCGCGGCGACGCTCGC	231
QY	403	CGCTTCCGGGACACTGTCTAGGGGAGCCAGCGCGCGCGGCGCTTTCAGACAGCAGCGG	462
Db	230	CGCTTCCGGGACAGCTGTGTGGGGAGCCGGTGGCGCGCAGCGCGCTTTCAGACAGCGGCGG	171
QY	463	CGCGCGGAGTATTTTGTGGACCGGACCGGCCAGCTTTCGAGCGCGTGTCTACTACTAC	522
Db	170	CGCGCGGAGTATTTTGTGGACCGGACCGGCCAGCTTTCGATGGGTGCTTACTACTACTAC	111
QY	523	CAGTCCGGTGGGGCGGCTGCGGGGCGCGCGCGGCGACAGTCCGCTGTGAGCTTTCCTGGAAAG	582
Db	110	CAGTCCGGGCGCGGCTGAGAGGCGCGCGCGGCGACCTCCCTCGAGCTTTCCTGGAGAG	51
QY	583	GTGGGCTTTCAGGGCTGGGCGCGGCGCGGCCCGACGACGCTGCGGAGGA	632
Db	50	GTGTCTTTCAGGGCTGGGCGCGGCGGCGGCTGGCGCGGCTCGGGAGGA	1

RESULT 7	
A1322534	
LOCUS	
DEFINITION	A1322534
	mhb3g06.yl Scores mouse placenta 4NbP13.5 14.5 Mus musculus cDNA
	clone IMAGE:57594 5' similar to gb:U17622_cds1 POTASSIUM CHANNEL
	PROTEIN KVL6 (HUMAN); mRNA sequence.

ACCESSION	A1322534	
VERSION	A1322534.1	GI:4056963
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE  
AUTHORS

Eulazipota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 522)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubaque, T., Gelsell, S., Kucab, T., Lacy, M., Le, M., Martin, J., Morris, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wille, T., Lennon, G., Soares, B., Wilson, K. and

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project unpublished (1996)		
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project		

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel.: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LINTL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:274482  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibbo  
High quality sequence stop:367.

FEATURES	SOURCE	Location/Qualifiers
		1..522
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="IMAGE:457594"
		/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
		/sex="unknown"
		/tissue_type="Placenta"
		/dev_stage="adult"
		/lab_host="DH10B"
		/note="Organ: placenta; Vector: pT7T3-Pac (Pharmacia)"

with a modified polylinker: Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dn) primer (5', TGTTACCAATCTGAGAGTGGAGGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was "constructed by Bento Soares and M.Fátima Bonaldo".

Query Match	19.7%	Score 331.4	DB 9	Length 522
Best Local Similarity	81.9%	Pred. No. 3e-54		
Matches 407; Conservative	0;	Mismatches 86;	Indels 4;	Gaps 2;

Oy 148 GTGCGCCCTTCGGCGCGGGGGTACACAATGCCCTCCTCGGCGCATAGCGGCCTGGCC 207  
| | | | | | | | | | | | | | | | | |  
Db 28 GCGCGCCCTTAGCGCGCGGGGTAAACACGCGCCCCCTCCCGCGGCGCTGGCGGGAATTTC 87

[illegible]

0x 328 cccctcggcgctgcgtgacacggagcttgctgaacgcmggccccgggcttcggcgtagacaggag 387  
Db 148 ACACGTCGGTTACCGGTGCGCCGGCGCCATGTGGCGCCATTGGAGGCACGCTCCGCGC GCC 207

Db 208 C--TTCGGCTGCTGCGAGCGGCTGCTGCTCAACGTGGCGGGGTTGCGCTTCGAGACCCGC 265

Oy 388 GCGCGCAGCGTGGGCGCGTTCCCGACACTTGTGCTAGGGGAACCCAGCGCGCGCGGGCGC 447

DB	Sequence	Position
266	GGCGCAGCGTCGGCGCTTCCGGGACACGCTGGGGGACCGGTGCGCCGACGGCGC	325
448	TTTCAGCAGCAGCGCGCGGAGATTCTTCGACCGGACCGGCGAGCTTCGACGCC	507

Db 326 TTCTCAGCAGGCGCGCGCGAGTATTTCTTCACGACACCGGCGCAGTTGGATGCG 385

Qy 508 GTGCTCTACCTACCACTCGGTGGGCGGCTGCGCGCGCGCGCGACGT--GCCGCTCG 565

[illegible][illegible]

RESULT 8  
B117089

LOCUS	B1117089	8/6 bp	mrna	linear	EST 26-JUN-2001
DEFINITION	602867188221 NIH_MGC_7	Homo sapiens	CDNA clone	IMAGE:5016164 5'	
	mrna sequence.				
ACCESSION	B1117089				

FUNCTION	DIFFUSION
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Enterobacteriaceae: Chordata: Vertebrata: Euteleostomi:

REFERENCE	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
AUTHORS	1 (bases 1 to 876)
TITLE	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCRD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory



adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[9][AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

Query Match 19.3%; Score 323.8; DB 17; Length 636;  
Best Local Similarity 72.0%; Pred. No. 9e-53;  
Matches 450; Conservative 0; Mismatches 172; Indels 3; Gaps 2;

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QY 940 GTGTGTGAGAGCGCTGTGTTGTTGTTGCTTCCCTTGGCGGCGTACGCGCTCCTGTC 999
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Db 636 GTGTGTGAGAGCGCTGTGTTGTTGTTGCTTCCCTTGGCGGCGTACGCGCTCCTGTC 577

QY 1000 TGTCCAGACGAGGCTATCTTCTTCAGACGTGATGAACTCATGATTTTGTGCTATC 1059
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Db 576 TGCCCGAGTAAGCGACCTCTCCAGAAATATCATGAACCTGATAGACATGTGGCCATC 517

QY 1060 CTTCCTCATTTTGTGGCAGCTGGGACCGGCGGCGGAGCGAGGGGTGGCCAGCAG 1119
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QY 1120 GCCATGTCATGGGCGCTGAGACGTCATCCGATGTTGGTGTGCTTCCGATCTTCAAG 1179
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QY 1240 GAGCTGGGCTCTCATCTTTTCTTCTTCAATGGTGTGCTCTTCTTCCAGGCGCGTC 1299
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QY 1300 TACTTTTCCGAGTGTGACGCGGCTGAGTCCCATCTTCCATGACCCCTGAGTCTTGG 1359
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QY 1360 TGGGCGGTAGTCAACATGATGATGATGAGACATGGGACCGGCTGATGAGT 1419
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QY 1420 GGCAGATAGTGGGCTCTGTGTGCGATTCGCGGCGTGC-TGACTATTTTCCCTCCAGT 1478
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QY 1479 GCCCGTCAATGTGTCCA--ATTTCAGCTACTTTTATCACCGGGGAGAGAGAGAGAG 1536
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RESULT 10  
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LOCUS 745 bp mRNA linear EST 18-MAR-2002  
DEFINITION UI-M-EOO-bwm-1-05-0-UI.r1 NIH\_BMAP\_EOO Mus musculus cDNA clone  
IMAGE:5697484 5', mRNA sequence.  
ACCESSION BM963332  
VERSION BM963332.1 GI:19546752  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
1 (bases 1 to 745)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES  
source  
Location/Qualifiers

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/db_xref="taxon:10090"  
/clone="IMAGE:5697484"  
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/tissue_type="whole brain"  
/dev_stage="embryo 15.5 dpc"  
/lab_host="DH10B (T1 phage resistant)"  
/note="Organ: brain; Vector: pYX-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then sequenced directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene discovery in the developing mouse nervous system', supported by National Institutes of Mental Health (NIMH), Hemlin Clin, Ph.D., program coordinator."
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BASE COUNT 139 a 216 c 202 g 188 t

Query Match 19.2%; Score 322.4; DB 14; Length 745;  
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Matches 453; Conservative 0; Mismatches 151; Indels 30; Gaps 1;

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QY 1013 CTATCTCTCTCAAGACGTATGAACTCATGCTTTTGGCTATCCCTCCACTTTTG 1072
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Db 61 CGGCTCTTCTTCCGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATG 120

QY 1073 TGGCAGTGGGACGAGCTGGCGGCGGAGGAGGCTG-----1110
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QY 1111 -----GGCAGACGAGGCGATGTCACTGGCATCTGAGATGATCCGATTGGTGGT 1162
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QY 1163 TCTTCGCACTTCACAGCTTCCCGGACACCAAGGCGCTGCAATCTTGGGACAGCG 1222
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Db 241 TGTTCGCAATCTTCAACCTCTCCCGCATTTCCAGAGGCTGCGAGATCGGTAAGACT 300

QY 1223 TTGAGGCGCTCATGCGAGCTGGGCTCTCATCTTTTCTTCTTCATGAGTGGTGGTC 1282
    |||||
Db 301 TACAGGCGTCAATGCGGAGACTGGGCTGCTCATCTTCTTCTTCATGAGTGGTATCC 360
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OY	1283	TCCTTTCACAGGCGCCTCTACTATTGGCGAAGTTGACCGGGTGGACATCCCATTTCCACTAGCA	1342
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OY	1343	TCCTCGAGTCCTCTTGTTGGGGGGAGTAGTCACCATGACTACAGTTGGCTATGAGACATGG	1402
Db	421	TCGCCAGATGCCCTTCTGGTGGGCGTGTGGTTTACATGACACCGGTAGATTATGGAGGACATGT	480
OY	1403	CACCGCTACGTGGTGGTGGCAAGATAGTGGGCTCTCTGTGGCCATTGCGGGCGGTGCTGA	1462
Db	481	ACCCCATACGCTTAGGGGGGACAGATTGTGGGCTCACTGTGGCCCATGTGTGGGGTCTCTGA	540
OY	1463	CTATTTCCTCGCAGATGGCCGCTCATTTGTCTCCAAATTTCACTACTTTTATACCGGGAGA	1522
Db	541	CCATTGCAATTACCGGTACCGGTCAATTGTCTCCAAATTTCAACTACTTTCACCCACCGAGGA	600
OY	1523	CAGAGGGGAGAGAGCGCTGGGATGTTCACCGCATGT	1556
Db	601	CGGAGCAGAGAGACAGAGGCCAGTATATACCCACATGT	634

RESULT 11			
LOCUS	BI764377		
DEFINITION	603046295F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186518 5',	772 bp	mRNA
ACCESSION	BI764377		linear
VERSION	BI764377		
KEYWORDS	EST.	GI:15755955	
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 772)		NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .		
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1465 row: n column: 23  
High quality sequence stop: 772.

## FEATURES

### source

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/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
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source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (pcory site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC library."

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Db	79	CTGGGCCACCGAACTGGCAGAGAGCAGCAGGGGGGAGAGAGCGGCCCAAGATGGCGACG	138
OY	1118	AGGCCATGTCTACGTGGCATTCCTGAGAGTCAATCCGATTTGGTGCTCTTCCGCATCTTCA	1177
Db	139	AGGGCATGTCCCTGGCCATCCCTCCGAGTCAATCCGCTGTCCGGGTGTTCCGCATCTTCA	198
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OY	1358	GSTGGGCGGTATGACCATGACTACAGTTGGTATGAGAGACATGGCACCCGCTACTGG	1417
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OY	1418	GTCGCAAAATAGTGGGCTCTGTGTGGCATTTGCGGGGTGCTGCACTAATTTTCCGTCCAG	1477
Db	438	GGGGCAAAATGTGGGGCTGCTGTGTGTGGCATTCGCCGGGGTCTTCACATGTGCTGCCGTG	497
OY	1478	TGCCCGTCAATGTCTCCAAATTTACAGTCACTTTTATCACCGGAGCAGAGGGCGAAGAGG	1537
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OY	1538	CTG	1540
Db	558	CGG	560

RESULT	12
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LOCUS	
DEFINITION	BMI28683 575 bp mRNA linear EST 12-MAR-2002
ACCESSION	U144F08.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
VERSION	CDNA Clone IMAGE:567646 5 similar to SW:CIK3_HUMAN P22001
KEYWORDS	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.3 ; mRNA sequence.
	BMI28683
	BMI28683.1 GI:17123227
	EST.

**SOURCE ORGANISM**

REFERENCE  
AUTHORS  
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Seacore, M., Brestelli, J., Grawohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wile, T., Martin, T., Bistlan, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, J., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T., Jackson, Y., and Powers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmeillon@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center For information on



FEATURES	Source
BASE COUNT	105 a 212 c 181 g 130 t
ORIGIN	
RESULT 14	
LOCUS	B0807519
DEFINITION	B0807519 628 bp mRNA linear EST 31-JUL-2002
ACCESSION	NISC_KK05510.y2 NCI_CGAP_Brn72 Macaca mulatta cDNA clone
VERSION	IMAGE:5330682.5, mRNA sequence.
KEYWORDS	B0807519
SOURCE	B0807519.1 GI:22031728
ORGANISM	EST. Rhesus monkey. Macaca mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca. 1 (bases 1 to 628) NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-tr@mail.nih.gov">cgapbs-tr@mail.nih.gov</a> DNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://infoimage.llnl.gov">infoimage.llnl.gov</a> Plate: L14M1839 row: E column: 19 Seq primer: M13RP1 reverse primer (ABI). Location/Qualifiers 1..628 /organism="Macaca mulatta" /db_xref="taxon:9544" /clone="IMAGE:5330682" /clone_lib="NCI_CGAP_Brn72" /rissue_type="hypothalamus" /lab_host="DH10B (phage-resistant)" /note="Organ: brain; Vector: pCMV-SPORT6, ccdb; Site:1; NotI; Site:2: EcoRV; Cloned unidirectionally. Primer: 0.150 dt. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI-CGAP library."

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QY 548	CGGCGCACGTCGCGCTCGACGCTCTTCTGGAAGAGTGGCTTCTACGAGGCTGGCGCGG	607		
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QY 608	CGGCGCTGCGACAGCGCTGGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	667		
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Db 183	CCGCGCGCGCTTGCGCCCGCGAGCTGAGTGGCTTTTTCGAGTTTCCGAGAGCTTCAGG	242		
QY 728	CCGCGCGCGCTTGCGCCCGCGAGCTGAGTGGCTTTTTCGAGTTTCCGAGAGCTTCAGG	787		
Db 243	CAGCGCGCGCTTGCGCCCGCGAGCTGAGTGGCTTTTTCGAGTTTCCGAGAGCTTCAGG	302		
QY 788	GCTTCGAGAGCTGCGCTGCTACTTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	847		
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Db 363	ACTCATCTGATGAGACCGCGGAACAGACAGCTGGGGGGCGCGCGCGGAGCTTCAG	417		
QY 908	CACCCCGCTGCTCTTCAATGACCGCTTCTTCTGCTGCTGAGAGCTGCTGATTTTGTGT	967		
Db 418	-----CTTTCGAGATCCCTTCTTCTGCTGCTGAGAGCTGCTGATCATCATCTGCT	464		
QY 968	TCTCCTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1027		
Db 465	TCTCCTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	524		
QY 1028	ACGTGATGACCTCATGATTTTGTGAGCTATCTTCCCTACTTTTGTGACACTGGGACCG	1087		
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LOCUS	020119 of library A from Tetradon nigriviridis, genomic survey			
ACCESSION	AL326301			
VERSION	AL326301.1			
KEYWORDS	GSI: genome survey sequence.			
SOURCE	Tetradon nigriviridis.			
ORGANISM	Tetradon nigriviridis			
REFERENCE	1 (bases 1 to 1060)			
AUTHORS	Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,			
TITLE	Bernot,A., Fizanes,C., Wincker,P., Brothier,P., Quetier,F.,			
JOURNAL	Saurin,W. and Weissenbach,J.			
REFERENCE	Human gene number estimate provided by genome wide analysis using			
REFERENCE	Tetradon nigriviridis DNA sequence			
REFERENCE	2 (bases 1 to 1060)			

Search completed: February 20, 2003, 11:45:25  
job time : 2806.74 secs

AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizes, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1060)  
AUTHORS Genoscope.  
TITLE Direct Submision  
JOURNAL Submitted (12-APR-2000)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.  
FEATURES  
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Matches 437; Conservative 0; Mismatches 198; Indels 4; Gaps 2;  
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QY 960 TTGTGTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019  
DB 68 TGCCTGTTCTTTTGTGAGCTGTGTGACATTTTGGCTGTGTCTAGCAAGAAATTT 127  
QY 1020 CTTCAGAGAGCTGATGACCTCATCTTGTGCTATCTTCCCTACTTGTGCTACT 1079  
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QY 1080 GGGCAGCAGCTGCGCCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1136  
DB 188 GGTACAGAAATTTCTACAAACACGAGAGAGAGCTCAGAGACAGACATGTCTTGGCCAT 247  
QY 1137 CTTGAGAGTATCCGATTTGCTGCTTCCGATCTTCAAGCTGTCCGACATCAA 1196  
DB 248 TCTGCCATCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307  
QY 1197 GGGCTGCAATCTTGGGCGAGACGCTTGGGCTCATGCTGAGCTGGGCTCTCAT 1256  
DB 308 GGGCTGCAATCTTGGGCGAGACGCTTGAAGAGATGCTGA-NTTGTGTTGCTCAT 366  
QY 1257 CTTTTCCTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316  
DB 367 TTTTTCCTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426  
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DB 547 GCTGTGCTCATGGGCGGCTGCTGCTATTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556  
QY 1497 TTTACGCTACTTTTATCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1535  
DB 607 CTTTACTACTTCTACACAG 645



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 ; Search time 133.056 Seconds  
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9410.374 Million cell updates/sec

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Perfect score: 556  
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	1341	24	ABL57038 Human potassium ch
2	556	100.0	1686	23	AA578540 DNA encoding novel
3	556	100.0	1747	22	AA513338 Human CDNA encodin
4	556	100.0	1792	24	AA537899 Human ion channel
5	532	95.7	691	24	AA528734 Human ion channel
6	436.6	78.5	1598	16	AA504953 Mouse Kvl.7 voltag
7	334.2	60.1	1836	22	AA521452 Human Kvl.5 DNA.
8	334.2	60.1	2867	24	AA595856 Gene #2354 used to
9	334.2	60.1	2867	24	ABL5917 Lung cancer relate

10	311.8	56.1	3147	24	AB199654 Mouse ischaemic co
11	273.4	49.2	2157	22	AA529512 Human endocrine po
12	273.4	49.2	2159	23	ABK43428 Human endocrine po
13	233.8	42.1	492	22	ABN06356 Human CDNA SEQ ID
14	233.8	42.1	492	22	AA528936 Human encoding for
15	233.8	42.1	492	22	AA529636 Human endocrine po
16	233.8	42.1	492	22	AA530165 DNA encoding rena
17	233.8	42.1	492	23	ABK43751 Human encoding novel
18	211	37.9	7642	24	AB133116 Human immune syste
19	209.2	37.6	2237	23	AB133285 Drosophila melanog
20	195	35.1	7642	24	AB133117 Human immune syste
21	190.2	34.2	8758	24	AB133119 Human immune syste
22	180.6	32.5	7488	24	AB133112 Human immune syste
23	180.2	32.4	998	22	ABK43164 Human breast cell
24	180.2	32.4	998	22	ABK43583 Human foetal liver
25	180.2	32.4	998	22	ABK23338 Human foetal liver
26	180.2	32.4	998	22	ABK01849 Human bone marrow
27	180.2	32.4	998	22	ABK27308 Human bone marrow
28	180.2	32.4	998	22	AA111882 Probe #1815 used t
29	180.2	32.4	998	22	AA133209 Probe #1811 used t
30	180.2	32.4	998	22	AA101820 Human genome deriv
31	180.2	32.4	998	24	ABK01828 Human breast cell
32	180.2	32.4	1340	22	ABK50280 Human foetal liver
33	180.2	32.4	1340	22	ABK68220 Human foetal liver
34	180.2	32.4	1340	22	ABK35230 Human bone marrow
35	180.2	32.4	1340	22	AAK16601 Human bone marrow
36	180.2	32.4	1340	22	AAK42356 Human bone marrow
37	180.2	32.4	1340	22	AA123127 Probe #13060 for g
38	180.2	32.4	1340	22	AA148435 Probe #17121 used
39	180.2	32.4	1340	22	AA108782 Probe #8773 used t
40	180.2	32.4	1340	24	ABK16411 Human genome deriv
41	180.2	32.4	1979	22	ABK54544 Human breast cell
42	180.2	32.4	1979	22	ABK55622 Human foetal liver
43	180.2	32.4	1979	22	ABK25318 Probe #3784 for ge
44	180.2	32.4	1979	22	AAK03850 Human brain expres
45	180.2	32.4	1979	22	AAK29317 Human bone marrow

#### ALIGNMENTS

RESULT 1	ABL57038 standard; cDNA; 1341 BP.
ID	ABL57038
AC	ABL57038:
XX	
DT	22-JUL-2002 (first entry)
XX	
DE	Human potassium channel 12189 partial cDNA.
XX	
KW	Potassium channel; ion transport; 12189; noctropic; anticonvulsant;
KW	neuroprotective; antiparkinsonian; hypotensive; neuroleptic;
KW	antidepressant; antimalaria; tranquilizer; anorectic; antidiabetic;
KW	antiarteriosclerotic; vasodilator; vulnerary; antiarrhythmic;
KW	cardiac; antiinflammatory; cytostatic; osteopathic; hepatotropic;
KW	antidiabetic; immunosuppressive; antiarthritic; antirheumatic;
KW	antipruritic; antihypertensive; antitumor; dermatological; antianemic;
KW	antiallergic; antiallergic; ophthalmological; immunomodulator;
KW	analgesic; virucide; human; gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1341
FT	/*tag= a
FT	/product= "12189"
FT	/partial
FT	/note= "The CDS does not include a start codon"
PN	W0200194390-A2.
XX	
PD	13-DEC-2001.

XX 06-JUN-2001; 2001WO-US18340.  
 PF  
 XX 06-JUN-2000; 2000US-209845P.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Curtis RAJ;  
 PI  
 XX WPI: 2002-401589/43.  
 DR P-PDB; ABB76166.  
 XX  
 PT New potassium channel family member polypeptide and polynucleotide,  
 PT useful for diagnosing, treating viral diseases, neurological, cardiac,  
 PT cellular proliferative or differentiative, bone, immune, liver and  
 PT metabolic disorders -  
 XX  
 PS Claim 1; Page 135-136; 158pp; English.

XX The present sequence is that of a partial cDNA for human 12189  
 CC (see ABB76166), a novel potassium channel family member. 12189  
 CC contains a potassium channel tetramerisation domain, an ion  
 CC transport protein domain and a core membrane region including 6  
 CC transmembrane domains. The invention provides human potassium  
 CC channel 52906, 33408 and 12189 nucleic acids and proteins, as well  
 CC as antisense nucleic acid molecules, recombinant expression vectors,  
 CC host cells, transgenic animals, fusion proteins, antigenic peptides  
 CC and antibodies. Also claimed are: a method for detecting the  
 CC presence of a 52906, 33408 or 12189 nucleic acid; a method for  
 CC modulating the activity of a 52906, 33408 or 12189 polypeptide using  
 CC a compound that binds the polypeptide; a method for identifying a  
 CC compound which modulates the activity of the polypeptide; a method  
 CC of treating or preventing an ion flux-related disorder using an  
 CC agent that modulates the activity or expression of a 52906 or  
 CC 12189 polypeptide or nucleic acid, especially a peptide.  
 CC phosphopeptide, small molecule, antibody, antisense molecule,  
 CC fibrocyte, a triple helix molecule, or a 52906 or 12189 nucleic  
 CC acid. The ion flux-related disorders include: potassium channel  
 CC associated disorders, such as neurological disorders and central  
 CC nervous system disorders such as cognitive and neurodegenerative  
 CC disorders e.g. Alzheimer's disease, Parkinson's disease, senile  
 CC dementia, Huntington's disease, Gilles de la Tourette's syndrome,  
 CC multiple sclerosis, progressive supranuclear palsy, epilepsy,  
 CC Jacob-Creutzfeldt disease, autonomic function disorders such as  
 CC hypertension and sleep disorders, neuropsychiatric disorders such  
 CC as depression, schizophrenia, mania, anxiety disorders or phobic  
 CC disorders, learning or memory disorders, amnesia or age-related  
 CC memory loss, attention deficit disorder, obsessive-compulsive  
 CC disorder, migraine or obesity; cardiac-related disorders such as  
 CC arteriosclerosis, ischemia reperfusion injury, restenosis, arterial  
 CC inflammation, tachycardia, congestive heart failure, myocardial  
 CC infarction and arrhythmia. The polypeptides and nucleic acids are  
 CC also useful as diagnostic targets and therapeutic agents for:  
 CC controlling cellular proliferative and/or differentiative disorders  
 CC e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma;  
 CC disorders associated with bone metabolism such as osteoporosis;  
 CC rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic  
 CC hypercalcaemia; immune disorders such as autoimmune disorders,  
 CC diabetes mellitus and psoriasis, including rheumatoid arthritis,  
 CC osteoarthritis and psoriatic arthritis, multiple sclerosis,  
 CC myasthenia gravis, autoimmune thyroiditis, ulcerative colitis,  
 CC psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma,  
 CC allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease,  
 CC chronic active hepatitis, autoimmune uveitis, scleroderma; liver  
 CC disorders including storage disorders such as Gaucher's disease,  
 CC glycogen storage disease, haemochromatosis and peroxisomal  
 CC disorders; viral diseases; pain; or metabolic disorders such as  
 CC obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.  
 XX  
 SQ Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Query Match 100.0%; Score 556; DB 24; Length 1341;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-146;

	Matches	556; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
OY	1	GTTCCTGTGGTGAGACGCTGTATTTGTTGGTTCCTTGGAGCTGTGACCCCT	60			
Db	594	GTTCCTGTGGTGAGACGCTGTATTTGTTGGTTCCTTGGAGCTGTGACCCCT	653			
OY	61	CTTGCTGTGTCACAGCAAGGCTATCTTCTTCACAGACGTGATGACCTCATCATTTTGT	120			
Db	654	CTTGCTGTGTCACAGCAAGGCTATCTTCTTCACAGACGTGATGACCTCATCATTTTGT	713			
OY	121	GGCTATCTTCCCTACTTTTGTGGCAGCTGGGACCGGACTGGCCGGACGAGGGGTGG	180			
Db	714	GGCTATCTTCCCTACTTTTGTGGCAGCTGGGACCGGACTGGCCGGACGAGGGGTGG	773			
OY	181	CCACGAGGACATGTCACCTGGGACATCTGAGAGTCATCCGATTGGTGGCTCTCCGCAT	240			
Db	774	CCACGAGGACATGTCACCTGGGACATCTGAGAGTCATCCGATTGGTGGCTCTCCGCAT	833			
OY	241	CTTCAAGCTGTCCCGGACATCAAGGGCCCTGCAATCTTGGGCCAGACGCTTGGGCTC	300			
Db	834	CTTCAAGCTGTCCCGGACATCAAGGGCCCTGCAATCTTGGGCCAGACGCTTGGGCTC	893			
OY	301	CATGCGTAGCTGGGCTCTCATCTTTTCTCTTATGCGTGGTCTCTTTTCCAG	360			
Db	894	CATGCGTAGCTGGGCTCTCATCTTTTCTCTTATGCGTGGTCTCTTTTCCAG	953			
OY	361	CGCCGTACTTTCCTCCAAAGTTGACCGGAGTGACCTCCATTTCACTAGCATCCCTGAGTC	420			
Db	954	CGCCGTACTTTCCTCCAAAGTTGACCGGAGTGACCTCCATTTCACTAGCATCCCTGAGTC	1013			
OY	421	CTTCTGTGGGCGGTAGTACCATGACTTACAGTTGGCTATGAGACATGACCCGTCAC	480			
Db	1014	CTTCTGTGGGCGGTAGTACCATGACTTACAGTTGGCTATGAGACATGACCCGTCAC	1073			
OY	481	TGTGGGTGGCAAGTATGAGGCTCTGTGTGGCATTTGGCGGCTGGTGAATTTTCCCT	540			
Db	1074	TGTGGGTGGCAAGTATGAGGCTCTGTGTGGCATTTGGCGGCTGGTGAATTTTCCCT	1133			
OY	541	GCCAGTCCCGTCATT	556			
Db	1134	GCCAGTCCCGTCATT	1149			
RESULT 2						
AA578540	standard; cDNA; 1686 BP.					
ID	AA578540					
XX	AA578540;					
AC	13-FEB-2002 (first entry)					
DT	DNA encoding novel human diagnostic protein #14344.					
XX						
DE	Human; chromosome mapping; gene mapping; gene therapy; forensic;					
XX	KW food supplement; medical imaging; diagnostic; genetic disorder; ss.					
KW	Homo sapiens.					
OS	WO200175067-A2.					
XX	11-OCT-2001.					
PD	30-MAR-2001; 2001WO-US09631.					
XX	31-MAR-2000; 2000US-0540217.					
XX	23-AUG-2000; 2000US-0649167.					
PR	(HYSE-) HYSEQ INC.					
XX	Dremanac RT, Liu C, Tang YT;					
XX	WPI: 2001-639362/73.					
DR	P-PDB; ABG14353.					

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

XX Claim 1, SEQ ID No 14344; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent upon human  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;

Query Match 100.0%; Score 556; DB 23; Length 1686;  
Best Local Similarity 100.0%; Pred. No. 5.2e-146;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTCGTGGTGAGACCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCT 60  
DB 1002 GTTCTTCGTGGTGAGACCTGTATTTGTTGCTTCCTTTGAGCTGCTGACGCT 1061  
QY 61 CCGGCTCTGTCAGACGAGCTATCTTTTCAGAACGTCATGACCTATCATTTTGT 120  
DB 1062 CCGGCTCTGTCAGACGAGCTATCTTTTCAGAACGTCATGACCTATCATTTTGT 1121  
QY 121 GGTATCTTCTCTACTTGTGTGACACTGGGACAGAGCTGGCCGGCAGAGAGGGGG 180  
DB 1122 GGTATCTTCTCTACTTGTGTGACACTGGGACAGAGCTGGCCGGCAGAGAGGGGG 1181  
QY 181 CCAGCAGGCGCATGTCACTGGCCATCTGTAGAGTCATCCGATTGGTCCGTCTCCGCAT 240  
DB 1182 CCAGCAGGCGCATGTCACTGGCCATCTGTAGAGTCATCCGATTGGTCCGTCTCCGCAT 1241  
QY 241 GTTCAAGCTGTCCCGGACATCAAAAGGCGCTGCAAACTTTGGGCGAAGCCTTGGGCGTC 300  
DB 1242 GTTCAAGCTGTCCCGGACATCAAAAGGCGCTGCAAACTTTGGGCGAAGCCTTGGGCGTC 1301  
QY 301 CATGCGTGAAGTGGGCGCTCTCATTTTTCCTTCATCGGGTGGTCTCTTTTCCAG 360  
DB 1302 CATGCGTGAAGTGGGCGCTCTCATTTTTCCTTCATCGGGTGGTCTCTTTTCCAG 1361  
QY 361 GCGCGTCTACTTGGCGAAGTTGACGGGGTGACCTCCATTTCATAGCATCCCTGAGTC 420  
DB 1362 GCGCGTCTACTTGGCGAAGTTGACGGGGTGACCTCCATTTCATAGCATCCCTGAGTC 1421  
QY 421 GTTCTGCTGGGGGTGATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 1422 GTTCTGCTGGGGGTGATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1481  
QY 481 TGTGGGTGCAAGATAGTGGGCTCTGTGTGCTGATTTGGGGGCTGCTGATTTTCCCT 540  
DB 1482 TGTGGGTGCAAGATAGTGGGCTCTGTGTGCTGATTTGGGGGCTGCTGATTTTCCCT 1541  
QY 541 GCCAGTCCCGTCATT 556

DB 1542 GCCAGTCCCGTCATT 1557

RESULT 3

AAS13338  
ID AAS13338 standard; cDNA; 1747 BP.

XX AAS13338;

XX 18-DEC-2001 (first entry)

XX Human cDNA encoding NOV4 protein.

XX Human: NOV4; ss: cytosolic; neurotrophic; neuroprotective; vulnerrary;  
KW cerebroprotective; antiparkinsonian; hypotensive; antisthmatic;  
KW antidiabetic; antipsoriatic; antinflammatory; immunosuppressive;  
KW antiatherosclerotic; dermatological; cancer; neurological disorder;  
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;  
KW immune disorder; autoimmune disease; respiratory disorder;  
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;  
KW cell growth regulation disorder; lesional psoriatic skin;  
KW atherosclerosis; abdominal aortic aneurysm.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 5'UTR 1..37

XX CDS 38..1717

XX 3'UTR 1718..1747

XX WO200168851-A2.

XX 20-SEP-2001.

XX 12-MAR-2001; 2001WO-US07735.

XX 10-MAR-2000; 2000US-0188277.

XX 10-MAR-2000; 2000US-0188316.

XX 14-MAR-2000; 2000US-0189139.

XX 14-MAR-2000; 2000US-0189140.

XX 17-MAR-2000; 2000US-0190231.

XX 17-MAR-2000; 2000US-0190401.

XX (CURA-) CURAGEN CORP.

XX Padigaru M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;

XX Majumder K, Li L;

XX WPI; 2001-570869/64.

XX P-PSDB; AAU08660.

XX Novel polypeptides and nucleic acids homologous to members of collagen,  
XX potassium channel, tuftelin family of proteins for diagnosing, treating  
XX cancer, atherosclerosis, neurological, skin and enamel defect disorders

XX Claim 9; Page 15-16; 128pp; English.

CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and  
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides  
CC and anti-NOVX antibodies are useful for treating or preventing a  
CC pathology associated with NOVX polypeptide in humans and for treating a  
CC syndrome associated with human disease e.g. disorders characterised by  
CC altered cell motility, proliferation and migration e.g. cancer,  
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.  
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's  
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,  
CC asthma, hypertension and seizure (NOV4), enamel defects, such as

CC amelogenesis imperfecta and disorders involving enamel defects,  
 CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic  
 CC neurological disorders, e.g. paraneoplastic limbic of brain-stem  
 CC encephalitis occurring during testicular cancer, diabetes, reproductive  
 CC health, metabolic and endocrine disorders, gastrointestinal disorders,  
 CC immune disorders and autoimmune diseases, respiratory disorders, bone  
 CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell  
 CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and  
 CC atherosclerosis, abdominal aortic aneurysm and neurological disorders  
 CC (NOV11). NOVX polypeptide is also useful for identifying an agent that  
 CC binds to it and a cell expressing NOVX polypeptide is useful for  
 CC identifying a therapeutic agent for use in treatment of a NOVX related  
 CC pathology. The antibodies and a polypeptide having 95% sequence identity  
 CC to NOVX polypeptide are useful for treating a pathological state in a  
 CC mammal. The present sequence encodes NOV4, a possible voltage gated  
 CC potassium channel.

XX  
 SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;

Query Match 100.0%; Score 556; DB 22; Length 1747;

Best Local Similarity 100.0%; Pred. No. 5, 2e-146;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTCGTGGTGGAGACGCTGTGTATTTGTTGCTCTTTGAGCTGCTGTAGCCCT 60  
 DB 970 GTTCTTCGTGGTGGAGACGCTGTGTATTTGTTGCTCTTTGAGCTGCTGTAGCCCT 1029  
 QY 61 CTTGCTGTGTCAGAGCAGGCTATCTCTTCAAGAACGTATGACCTCATGCAATTTGT 120  
 DB 1030 CTTGCTGTGTCAGAGCAGGCTATCTCTTCAAGAACGTATGACCTCATGCAATTTGT 1089  
 QY 121 GGGTATCTCTTCCCTACTTTTGGACATGGGACCGAGCTGGCCGGCAGGAGGGGTGG 180  
 DB 1090 GGGTATCTCTTCCCTACTTTTGGACATGGGACCGAGCTGGCCGGCAGGAGGGGTGG 1149  
 QY 181 CCAGCAGGCGCATGTCACTGCGCATCTGAGAGATCATCCGATTGGTGGCTTTCCGCAT 240  
 DB 1150 CCAGCAGGCGCATGTCACTGCGCATCTGAGAGATCATCCGATTGGTGGCTTTCCGCAT 1209  
 QY 241 CTTCAAGCTCTCCCGGACATCAAGAGGCGCTGCAAAATCTTGGGCGACAGCGTTGGGGCCTC 300  
 DB 1210 CTTCAAGCTCTCCCGGACATCAAGAGGCGCTGCAAAATCTTGGGCGACAGCGTTGGGGCCTC 1269  
 QY 301 CATGCGTAGCTGGGCGCTCTCTCATCTTTTCTTCATCGGTGGTGGTCTCTTTTCCAG 360  
 DB 1270 CATGCGTAGCTGGGCGCTCTCTCATCTTTTCTTCATCGGTGGTGGTCTCTTTTCCAG 1329  
 QY 361 CGCGCTCTACTTTGCGGAATTTGACGGGGTGGACTCCCATTTACTAGCATTCCTGTAGTC 420  
 DB 1330 CGCGCTCTACTTTGCGGAATTTGACGGGGTGGACTCCCATTTACTAGCATTCCTGTAGTC 1389  
 QY 421 CTTCTGGTGGCGGTAGTACCAATGACTACAGTTGGCTATGAGAGACATGACCCCGTCAC 480  
 DB 1390 CTTCTGGTGGCGGTAGTACCAATGACTACAGTTGGCTATGAGAGACATGACCCCGTCAC 1449  
 QY 481 TGTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCAATTTGGCGGCGTGTGCAATTTTCCCT 540  
 DB 1450 TGTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCAATTTGGCGGCGTGTGCAATTTTCCCT 1509  
 QY 541 GCCAGTCCCGTCATT 556  
 DB 1510 GCCAGTCCCGTCATT 1525

RESULT 4

AAD37899

ID AAD37899 standard; cDNA; 1792 BP.

XX

AC AAD37899;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human ion channel protein encoding cDNA.

XX Human: novel human protein; NHP: ion channel protein; forensic biology;  
 KW Pharmacogenomic; drug screening; mental disorder; biological disorder;  
 KW symptomatic manifestation; phenotypic manifestation; medical disorder;  
 KW gene; ss.  
 XX  
 OS Homo sapiens.  
 FH Key  
 FT CDS  
 FT 93..1463  
 FT /tag= a  
 FT /product= "Human ion channel protein"  
 FT /note= "This region is specifically claimed as  
 FT SEQ ID NO: 1 in claim 1 of the specification"

WO200231150-A2.

XX 18-APR-2002.

XX 10-OCT-2001; 2001MO-US31900.

XX 10-OCT-2000; 2000US-239623P.

XX (LEXI-) LEXICON GENETICS INC.

XX Fiddler CJ, Hilbun E, Gerhardt B, Turner CA;

XX WPI: 2002-452348/48.

XX P-PSDB; AAE23655.

XX Novel human ion channel polynucleotide encoding protein sharing

XX structural similarity with mammalian ion channel proteins, e.g.

XX potassium channels useful in therapeutic, diagnostic and

XX pharmacogenomic applications -

XX Disclosure; Page 36; 36pp: English.

XX The present invention relates to novel human proteins (NHPs), human ion  
 CC channel proteins and polynucleotides encoding such proteins. Sequences of  
 CC the invention are useful in therapeutic, diagnostic and pharmacogenomic  
 CC applications. They are useful for the identification of protein coding  
 CC sequences, for mapping a unique gene to a particular chromosome, as  
 CC additional DNA markers for restriction fragment length polymorphism  
 CC (RFLP) analysis and in forensic biology, for screening libraries,  
 CC isolating clones, preparing templates for cloning and sequencing, as  
 CC hybridisation probes, in microarrays or other assay formats, to screen  
 CC collections of genetic material from patients who have a particular  
 CC medical condition, to identify mutations associated with a particular  
 CC disease and also as a diagnostic or prognostic assay. NHPs are useful  
 CC for the detection of mutant human proteins or inappropriately expressed  
 CC proteins for the diagnosis of disease, for the generation of antibodies,  
 CC for screening for drugs effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of the  
 CC protein in the body, for identification of other cellular gene products  
 CC related to the protein and as reagents in assays for screening for  
 CC compounds that can be used as pharmaceutical agents in the therapeutic  
 CC treatment of mental, biological or medical disorders and diseases. The  
 CC present sequence is a cDNA encoding human ion channel protein.

XX  
 SQ Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other;

Query Match 100.0%; Score 556; DB 24; Length 1792;

Best Local Similarity 100.0%; Pred. No. 5, 3e-146;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTCGTGGTGGAGACGCTGTGTATTTGTTGCTCTTTGAGCTGCTGTAGCCCT 60  
 DB 716 GTTCTTCGTGGTGGAGACGCTGTGTATTTGTTGCTCTTTGAGCTGCTGTAGCCCT 775  
 QY 61 CTTGCTGTGTCAGAGCAGGCTATCTCTTCAAGAACGTATGACCTCATGCAATTTGT 120  
 DB 776 CTTGCTGTGTCAGAGCAGGCTATCTCTTCAAGAACGTATGACCTCATGCAATTTGT 835

OY 121 GGCATATCTTCCCTACTTTGTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGG 180  
 DB 836 GGCATATCTTCCCTACTTTGTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGG 895  
 OY 181 CCAGCAGGCGCATGTCATCTGAGAGTCATCCGATTTGTCCTTCCGAT 240  
 DB 896 CCAGCAGGCGCATGTCATCTGAGAGTCATCCGATTTGTCCTTCCGAT 955  
 OY 241 CTTCAAGCTGTCGGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGTC 300  
 DB 956 CTTCAAGCTGTCGGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGTC 1015  
 OY 301 CATGGGTGAGCTGGGCGCTCTCATCTTTCCTTTCATCGGTGTGGTCTCTTTTCCAG 360  
 DB 1016 CATGGGTGAGCTGGGCGCTCTCATCTTTCCTTTCATCGGTGTGGTCTCTTTTCCAG 1075  
 OY 361 CGCCGCTACTTGTGGCGAAGTTGACCGGGTGGACCTCCATTTCTACTAGATCCCTGAGTC 420  
 DB 1076 CGCCGCTACTTGTGGCGAAGTTGACCGGGTGGACCTCCATTTCTACTAGATCCCTGAGTC 1135  
 OY 421 CTTTGTGGTGGGCGTGTAGTACCATGACTAGTTGGCTATGGAGATGGACCCGCTCAC 480  
 DB 1136 CTTTGTGGTGGGCGTGTAGTACCATGACTAGTTGGCTATGGAGATGGACCCGCTCAC 1195  
 OY 481 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGGCTACTATTTCCTT 540  
 DB 1196 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGGCTACTATTTCCTT 1255  
 OY 541 GCCAGTGGCCGCTCAT 556  
 DB 1256 GCCAGTGGCCGCTCAT 1271

RESULT 5  
 AAD28734  
 ID AAD28734 standard; DNA: 691 BP.  
 AC AAD28734;  
 DT 07-MAY-2002 (first entry)

DE Human ion channel gene, ion-166.  
 KW Human; ion channel; neurological disorder; psychiatric disorder;  
 KW schizophrenia; attention deficit hyperactivity disorder; depression;  
 KW proliferation disease; migraine; ischaemia; neurodegenerative disease;  
 KW macular degeneration; Alzheimer's disease; congestive heart failure;  
 KW glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;  
 KW high blood pressure; restenosis; metabolic disease; neuroprotective;  
 KW obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;  
 KW alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 566..658  
 XX FT /tag= a  
 XX FT /product= "Human ion channel ion-166"  
 XX FT /note= "CDS does not include start and stop codon"  
 XX FT /partial  
 XX  
 XX WO200192303-A2.  
 XX PD 06-DEC-2001.  
 XX PF 25-MAY-2001; 2001WO-US16967.  
 XX PR 26-MAY-2000; 2000US-207119P.  
 XX PR 26-MAY-2000; 2000US-207152P.  
 XX PR 26-MAY-2000; 2000US-207257P.  
 XX PA (PHMA ) PHARMACIA & UPJOHN CO.

PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL, Goto LF;  
 DR WPI: 2002-147617/19.  
 DR P-PSDB: AAE18034.  
 XX  
 PT New human ion channel polypeptides and nucleic acids, useful for  
 PT treating or diagnosing neurological, psychiatric or neurodegenerative  
 PT diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or  
 PT Parkinson's disease  
 XX  
 PS Claim 1; Page 76; 126pp; English.

The invention relates to ion channel polypeptides designated as ion-x  
 (where x is 157-175) and their corresponding nucleic acids. The ion-x  
 sequences and their modulators are useful for the treatment of human  
 diseases and conditions such as neurological or psychiatric disorders.  
 These compounds are useful for treating schizophrenia, attention deficit  
 hyperactivity disorder, depression, anxiety, stroke, migraine, ischemia  
 or neurodegenerative disease (e.g. macular degeneration, Alzheimer's  
 disease, glaucoma, or Parkinson's disease). The compounds that modulate  
 ion channels can be used for treating of cardiovascular diseases (e.g.  
 congestive heart failure, arrhythmia, high blood pressure or restenosis),  
 metabolic diseases and disorders (e.g. diabetes or obesity), hormonal  
 disorders (e.g. polycystic ovarian syndrome or alopecia) and  
 CC proliferation diseases and cancers. The ion channels are also useful as  
 CC targets for discovering ligands or drugs to treat many diverse disorders  
 CC and defects. The ion-x sequences and their modulators may also be used  
 CC in diagnostic assays for such diseases or conditions. Ion-x nucleic  
 CC acids are used in gene therapy. The present sequence is a DNA encoding  
 XX human ion channel designated as ion-166.

Sequence 691 BP; 113 A; 207 C; 185 G; 186 T; 0 other;

Query Match 95.7%; Score 532; DB 24; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 2e-139;  
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTTGTGGTGGAGACGCTGTATTTGTTGGTCTCTCTTGGAGCTGTGACGCT 60  
 DB 160 GTTCTTGTGGTGGAGACGCTGTATTTGTTGGTCTCTCTTGGAGCTGTGACGCT 219  
 OY 61 CCGTGTCTGTCCCAAGCAGGCTATCTTCAAGAACGTGATGAACTCATGATTTGT 120  
 DB 220 CCGTGTCTGTCCCAAGCAGGCTATCTTCAAGAACGTGATGAACTCATGATTTGT 279  
 OY 121 GGCATATCTTCCCTACTTTGTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGG 180  
 DB 280 GGCATATCTTCCCTACTTTGTGGGCACTGGGACCGAGCTGGCCCGGACGAGGGGTGGG 339  
 OY 181 CCAGCAGGCGCATGTCATCTGAGAGTCATCCGATTTGGTGGCTTCCGAT 240  
 DB 340 CCAGCAGGCGCATGTCATCTGAGAGTCATCCGATTTGGTGGCTTCCGAT 399  
 OY 241 CTTCAAGCTGTCGGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGTC 300  
 DB 400 CTTCAAGCTGTCGGGCACTCAAGAGGCGCTGCAAAATCTTGGGCGAGAGCTTGGGCGTC 459  
 OY 301 CATGGGTGAGCTGGGCGCTCTCATCTTTCCTTTCATCGGTGTGGTCTCTTTTCCAG 360  
 DB 460 CATGGGTGAGCTGGGCGCTCTCATCTTTCCTTTCATCGGTGTGGTCTCTTTTCCAG 519  
 OY 361 CGCCGCTACTTGTGGCGAAGTTGACCGGGTGGACCTCCATTTCTACTAGATCCCTGAGTC 420  
 DB 520 CGCCGCTACTTGTGGCGAAGTTGACCGGGTGGACCTCCATTTCTACTAGATCCCTGAGTC 579  
 OY 421 CTTTGTGGTGGGCGTGTAGTACCATGACTAGTTGGCTATGGAGATGGACCCGCTCAC 480  
 DB 580 CTTTGTGGTGGGCGTGTAGTACCATGACTAGTTGGCTATGGAGATGGACCCGCTCAC 639  
 OY 481 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGGCTACT 532  
 DB 640 TGTGGGTGGCAGATAGTGGGCTCTGTGTGTCATTTGGGCGTGGCTACT 691

```

RESULT 6
AA04953
ID   AA04953 standard; cDNA; 1598 BP.
XX
AC   AA04953;
XX
DT   11-APR-1996 (first entry)
XX
DE   Mouse Kv1.7 voltage-gated potassium channel coding sequence.
XX
KW   Mouse Kv1.7 voltage-gated potassium channel;
KW   Insulin antagonist drug screening; Insulin agonist drug screening;
KW   non-Insulin-dependent diabetes mellitus; ds.
XX
OS   Mus musculus.
XX
FH   Key Location/Qualifiers
FT   CDS 1..1598
FT       /tag="a
FT       /note="specification states sequence is 1599.
XX       Incomplete stop codon given"
XX
PN   MO9523858-A1.
XX
PD   08-SEP-1995.
XX
PF   23-FEB-1995; 95WO-US02221.
XX
PR   10-AUG-1994; 9AUS-0288405.
PR   04-MAR-1994; 9AUS-0207401.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Chandry G, Chandry KG, Gutman GA, Kalman K;
XX
DR   WPI; 1995-320573/41.
DR   P-PSDB; AAR82937.
XX
PT   New voltage-gated potassium channel gene - used to identify
PT   material(s) which can increase insulin release e.g. for treating
PT   non-insulin dependent diabetes mellitus.
XX
PS   Claim 1; Page 22-23; 38pp; English.
XX
CC   The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-
CC   gated potassium channel. It may be used in drug screening for
CC   identification of therapeutics which modulate the channel and,
CC   therefore, modulate insulin secretion. Selective antagonists
CC   increase insulin release and thereby reduce hyperglycaemia
CC   associated with non-insulin-dependent diabetes mellitus.
XX
SQ   Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other:
Query Match 78.5%; Score 436.6; DB 16; Length 1598;
Best Local Similarity 86.7%; Pred. No. 1.7e-112;
Matches 481; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 2 TTCTGTGGTGGAGAGCGTGTATTTGTTGTTCTCCCTTGAGTGGCTGAGCGC 61
DB 853 TTCTTTGTGTGGAGAGCCCTGTATCTGTCTCTCCCTTGAGTGGCTGAGCATCG 912
QY 62 CTGCTGTCTCAAGCAAGGCTATCTTTCACAAAGCTGATGAACCTCATGATTTGTG 121
DB 913 GTGGCGCTGCCCTAGCAAGAGCTGTCTTCAAAATGTATGAACTAATGTGACTTCGTG 972
QY 122 GCTATCTCTCCCTACTTTTGTGGACATGGCACCAGCTGGCCCGGACGACGAGGGGTGGC 181
DB 973 GGCATCTCTGCTTACTTCTGCGGCGCTGGCAGAGTTACCCGCGACGCGGTGTGGGC 1032
QY 182 CACGACGACCATGTCATCTGGCATCCGAGAGTATCCGATGGTGGTGTCTTCCGATC 241
DB 1033 CACGCGGCTATGTCCCTGGCATCCAAAGGTCATCCGATGGTGGTGTCTTCCGATC 1092

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QY 242 TTCAGCTGTCCCGGCACTCAAAAGGCGCTGCAAAATCTTGGGCCAGACGCTTGGGCGCTCC 301
DB 1093 TTCAGCTGTCCAGGCAATTCGAAGGGGTCTACAGATCTTGGGTGACAGACTGCGGGCTCC 1152
QY 302 ATGCGTGAGCTGGGCGCTCTCATCTTTTCTTCTTCATCGGTGTGGTCTTTTCCAGC 361
DB 1153 ATGCGTGAGCTGAGTCTCCCATCTCCCTTCCTTCATATGGCGGTGGCTCTTTTCCAGC 1212
QY 362 GCGGTCTACTTTCGCGAAGTTGACCGGGGTGAGCTGCCATTTCACTAGCATCCCTGAGTCC 421
DB 1213 GCACTTACTTCTCTGAGTGGACCGGGTGGACACCATTTTCACGACATCCCGGAGTCC 1272
QY 422 TTCTGTGGGCGGTAGTCAACATGACTACAGTTGGCTATGAGACATGGCACCCGTCAC 481
DB 1273 TTTTGTGGGCGAGTGGTCACTGACATGACACAGCGTTGGCTATGGGACATGGACCCGTCAC 1332
QY 482 GTGGGTGGCAAGATAGTGGGCTCTGTGTGCCATTTGGGCGGCGTGTACTATTTCCCTG 541
DB 1333 GTGGGTGGCAAGATCGTGGGCTCTGTGTGCCATTTGGCAGGTGTGTCACCATCTCTCTG 1392
QY 542 CCAGTGCGCGTCATT 556
DB 1393 CTTGTGCTGTCAATT 1407

RESULT 7
AAH21452
ID   AAH21452 standard; DNA; 1836 BP.
XX
AC   AAH21452;
XX
DT   18-SEP-2001 (first entry)
XX
DE   Human Kv1.5 DNA.
XX
KW   Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
KW   activator; ds.
XX
OS   Homo sapiens.
XX
PN   WO200151519-A2.
XX
PD   19-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00055.
XX
PR   11-JAN-2000; 2000DE-1000651.
XX
PA   (AVENTIS PHARMA DEUT GMBH.
XX
PI   Leberer E, Leeuw T, Ritscher A;
XX
DR   WPI; 2001-442137/47.
XX
PT   Identifying inhibitors and activators of eukaryotic potassium channels,
PT   for use as pharmaceuticals, comprises using yeast cells that express
PT   heterologous, but no endogenous, potassium channels
XX
PS   Disclosure: Page 45-46; 78pp; German.
XX
CC   This sequence represents a novel method for identifying inhibitors or
CC   activators (A) of a eukaryotic potassium channel (KC) by applying a test
CC   compound to a mutant Saccharomyces cerevisiae cell in which: (1) the
CC   three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (11) a
CC   eukaryotic KC is expressed heterologously, where the effect of the
CC   compound on the eukaryotic KC is then determined. The method is used to
CC   identify inhibitors or activators (A) of a eukaryotic potassium channel.
CC   (A) are potentially useful as pharmaceuticals. The method is easily
CC   automated for parallel processing of many samples, using either different
CC   concentrations of test compounds and/or different levels of heterologous
CC   gene expression. It allows identification of compounds that inhibit human
CC   KC selectively. This sequence represents the human Kv1.5 encoding DNA

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CC described in the method of the invention.

xx Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;

xx Query Match 60.1%; Score 334.2; DB 22; Length 1836;

xx Best Local Similarity 75.8%; Pred. No. 1e-83;

xx Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

```
QY 2 TTCTTCGTGTGGAGAGCGTGTGTATTTGTGTCTCTCTGAGTGTGCGTACGCCCTC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 964 TTCTTATGTGTGAGACACGCTGTGTATGTGTCTCTGAGTGTGCGTACGCCCTC 1023
QY 62 CTGTCTGTCCAGAGCGCTATCTTCTTCAAGAACGTATGAACTCATCATTTTGTG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1024 TTGCGCTGTCCAGAGCGAGGTTCTCCGGAAACATCATGAACTCATCATTTG 1083
QY 122 GCTATCTTCCCTACTTTTGTGACATGGACCGACCGAGCGGCGGAGGAGGCG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1084 GGCATCTTCCCTACTTCAACCTGTGGGACCGAAGTGGCAGAGCAGCAGGAGG 1143
QY 182 -----CAGCAGGCGATGTCTACTGCGCATCTGCGCATCTGAGTCAATCCGA 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1144 GGAGAGGCGCGCCAGAAATGGGACAGGCGCATGTCCCTGCGCATCTCCGAGTCAATCCG 1203
QY 221 TTGTGCTGTCTTCCGATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAATCTTG 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1204 CTGTGCGGGGTGTCCGCACTTCAAGCTGTCCCGGACACTCCAAAGGCGCTGCAATCTTG 1263
QY 281 GGCAGAGCGCTTGGGCGCTTCATGCGTGAAGTGGGCGCTCTCTCTCTCTCTCTCT 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1264 GGCAGAGCGCTTGGGCGCTTCATGCGTGAAGTGGGCGCTCTCTCTCTCTCTCTCTCT 1323
QY 341 GGTGTGCTGTCTTTCAGAGCGCGTCTACTTTGGCGAAGTGAACGGGCGTCAATCCAT 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1324 GGGGTATCTCTTCTTCCAGTGTCCGTCTTGTGCAAGAGCTGACCAACGAGGAACCAT 1383
QY 401 TTCACTAGCATCCCTAGTCTTCTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1384 TTCTTACAGCATCCCTAGCGCTTCTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 1443
QY 461 GGAGACATGGACCGCTCACTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1444 GGGGACATGAGGCGCTCACTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 1503
QY 521 GGGGTGCTGACTATTTTCCCTGCGCAAGTGGCGCGTAT 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1504 GGGGTCTTCAACCATTTGCCCTGCTGTGCCCGTAT 1538
```

RESULT 8  
ABN95856  
ID ABN95856 standard; DNA; 2867 BP.

xx ABN95856;

xx 13-AUG-2002 (first entry)

xx Gene #2354 used to diagnose Liver cancer.

xx Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
xx metastatic liver tumour; cytostatic; expression profile; disease state;  
xx disease progression; drug toxicity; drug efficacy; drug metabolism.

xx Homo sapiens.

xx WO200229103-A2.

xx 11-APR-2002.

xx 02-OCT-2001; 2001WO-US30589.

xx 02-OCT-2000; 2000US-237054P.

xx

PA (GENE-) GENE LOGIC INC.

xx Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

xx WPI; 2002-426119/45.

xx Diagnosing and detecting the progression of liver cancer,

xx hepatocellular carcinoma or metastatic liver tumor in a patient,

xx involves detecting the level of expression of two or more genes in a

xx liver tissue sample

xx Claim 1; SEQ ID NO 2354; 298bp; English.

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient. Involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytosolic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

xx Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;

xx Query Match 60.1%; Score 334.2; DB 24; Length 2867;

xx Best Local Similarity 75.8%; Pred. No. 1.2e-83;

xx Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

```
QY 2 TTCTGTGTGTGAGAGCGTGTATTTGTGTCTCTCTTGTGAGCTGTGACGCCCTC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1198 TTCTTATGTGTGAGACACGCTGTGTATGTGTCTCTTGTGAGCTGTGACGCCCTC 1257
QY 62 CTGTCTGTCCAGAGCGCTATCTTCTTCAAGAGTGTATGAACTCATCATTTTGTG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1258 TTGCGCTGTCCCGCAGAGGAGGTTCTCCGGAATCATGAACTCATCATTTG 1317
QY 122 GCTATCTTCCCTACTTTTGGGCGTGTGGGCGAGCGTGGCGAGCAGAGGCGTGG 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1318 GGCATCTTCCCTACTTCACTGACCTGTGGGCGAGGAACTGGCAGAGCAGCAGGAGG 1377
QY 182 -----CAGCAGGCGATGTCTACTGCGCATCTCTGAGAGTCAATCCGA 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1378 GGAGAGGCGCGCCAGAAATGGGCGAGGCGCATGTCCCTGCGCATCTCCGAGTCAATCCG 1437
QY 221 TTGTGCTGTCTTCCGATCTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAATCTTG 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1438 CTGTGCGGGGTGTCCGCACTTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAATCTTG 1497
QY 281 GGCAGAGCGCTTGGGCGCTCATGCGTGAAGTGGGCGCTCTCTCTCTCTCTCTCTCT 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1498 GGCAGAGCGCTTGGGCGCTCATGCGTGAAGTGGGCGCTCTCTCTCTCTCTCTCTCTCT 1557
QY 341 GGTGTGCTCTTTCAGAGCGCGTCTACTTTGCGAAGTGTGACCGGAGTGGACTCCAT 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1558 GGGGTATCTCTTTCAGAGTGTCCGTCTACTTTCGAGAGGCTGACCAACCGGGAACCCAT 1617
QY 401 TTCACTAGCATCCCTAGTCTTCTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1618 TTCTTACAGCATCCCTAGCGCTTCTGTGTGGGCGGTAGTACCATGACTGACTGACTAT 1677
QY 461 GGAGACATGGACCGCTCACTGTGTGGGCGCAAGATGAGTGGGCGTCTGTGTGCAATTTG 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1678 GGGGACATGAGGCGCTCACTGTGTGGGCGCAAGATGAGTGGGCGTCTGTGTGCAATTTG 1737
QY 521 GGGGTGCTGACTATTTTCCCTGCGCAAGTGGCGCGTAT 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1738 GGGCTCCTCACCATTCGCTGCTGCGCTCAT 1772

RESULT 9  
ABL65917  
ID ABL65917 standard; DNA: 2867 BP.  
XX  
AC ABL65917;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Lung cancer related gene sequence SEQ ID NO:4254.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW Stomach; Lung; prostate; pancreas; carcinoma; adenocarcinoma;  
KW Cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001MO-US10838.  
XX  
XX 05-JUN-2000; 2000US-209473P.  
XX 18-SEP-2000; 2000US-209531P.  
XX 18-SEP-2000; 2000US-233133P.  
XX 20-SEP-2000; 2000US-233617P.  
XX 20-SEP-2000; 2000US-234009P.  
XX 20-SEP-2000; 2000US-234034P.  
XX 20-SEP-2000; 2000US-234052P.  
XX 22-SEP-2000; 2000US-234509P.  
XX 22-SEP-2000; 2000US-234567P.  
XX 25-SEP-2000; 2000US-234923P.  
XX 25-SEP-2000; 2000US-234934P.  
XX 25-SEP-2000; 2000US-235077P.  
XX 25-SEP-2000; 2000US-235082P.  
XX 25-SEP-2000; 2000US-235134P.  
XX 25-SEP-2000; 2000US-235280P.  
XX 26-SEP-2000; 2000US-235637P.  
XX 27-SEP-2000; 2000US-235638P.  
XX 27-SEP-2000; 2000US-235711P.  
XX 27-SEP-2000; 2000US-235720P.  
XX 27-SEP-2000; 2000US-235840P.  
XX 27-SEP-2000; 2000US-235863P.  
XX 28-SEP-2000; 2000US-236028P.  
XX 28-SEP-2000; 2000US-236032P.  
XX 28-SEP-2000; 2000US-236033P.  
XX 28-SEP-2000; 2000US-236034P.  
XX 28-SEP-2000; 2000US-236109P.  
XX 28-SEP-2000; 2000US-236111P.  
XX 29-SEP-2000; 2000US-236842P.  
XX 29-SEP-2000; 2000US-236891P.  
XX 02-OCT-2000; 2000US-237172P.  
XX 02-OCT-2000; 2000US-237173P.  
XX 02-OCT-2000; 2000US-237278P.  
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XX 02-OCT-2000; 2000US-237295P.  
XX 02-OCT-2000; 2000US-237316P.  
XX 03-OCT-2000; 2000US-237425P.  
XX 03-OCT-2000; 2000US-237598P.  
XX 03-OCT-2000; 2000US-237604P.  
XX 03-OCT-2000; 2000US-237606P.  
XX 03-OCT-2000; 2000US-237608P.  
XX 01-NOV-2000; 2000US-244867P.  
XX 01-NOV-2000; 2000US-245084P.  
XX  
XX (AVAL-) AVALON PHARM.  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;

XX  
DR WPI; 2002-188264/24.  
XX  
PT Screening for anti-neoplastic agent involves exposing cells to a  
PT chemical agent to be tested for anti-neoplastic activity, and  
PT determining a change in expression of a gene of a signature gene set -  
XX  
PS Claim 1; SEQ ID 4254; 44pp; English.  
XX  
XX The present invention describes a method (M1) for screening for an  
CC anti-neoplastic agent. The method involves exposing cells to a chemical  
CC agent to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening  
CC an anti-neoplastic agent, and can be used for producing a product which  
CC is the data collected with respect to the anti-neoplastic agent as a  
CC result of M1, and the data is sufficient to convey the chemical  
CC structure and/or properties of the agent. M1 can be used in the  
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilm's tumour.  
XX  
SQ Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;

Query Match 60.1%; Score 334.2; DB 24; Length 2867;  
Best Local Similarity 75.8%; Pred. No. 1.2e-83;  
Matches 436; Conservative 0; Mismatches 118; Indels 21; Gaps 1;

QY 2 TTCTCGTGGAGAGAGCGCTGTATTTGTTGCTTCTTGTAGCTGTACCGCTC 61  
DB 1198 TTCTTCATCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257  
QY 62 CTGCTGTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121  
DB 1258 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317  
QY 122 GCTATCCTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 181  
DB 1318 GCTATCCTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1377  
QY 182 -----CAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 220  
DB 1378 GAG 1437  
QY 221 TTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 280  
DB 1438 CTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1497  
QY 281 GCGCAG 340  
DB 1498 GCGCAG 1557  
QY 341 GGTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 400  
DB 1558 GGTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1617  
QY 401 TTCTCTGAGATCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 460  
DB 1618 TTCTCTGAGATCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1677  
QY 461 GAGAGATGAG 520  
DB 1678 GAGAGATGAG 1737  
QY 521 GGGCTGCTGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555  
DB 1738 GGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1772





PR 26-JUL-2000: 2000US-0220963.  
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 PR 08-SEP-2000: 2000US-0232080.  
 PR 08-SEP-2000: 2000US-0232081.  
 PR 12-SEP-2000: 2000US-0231968.  
 PR 14-SEP-2000: 2000US-0232397.  
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 PR 11-DEC-2000: 2000US-0254097.  
 PR 05-JAN-2001: 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-451936/48.

P-PSDB; AAU18283.

Isolated polypeptide for treating, preventing and/or prognosing disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnosis -

Claim 1; SEQ ID No 12; 604pp; English.

Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi.

CC ocular disorders such as corneal infection, endocrine disorders such as  
CC premature labour and infertility, gastrointestinal disorders such as  
CC Croom's disease, renal disorders such as glomerulonephritis and  
CC respiratory disorders such as asthma. The polypeptides can also be used  
CC to aid wound healing, to prevent skin aging due to sunburn, to maintain  
CC organs before transplantation, to regenerate tissues and in chemotaxis.  
CC The polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO

## Query Match

49.2%; Score 273.4; DB 22; Length 2157;

Best Local Similarity 75.4%; Pred. No. 1.2e-66; Mismatches 111; Indels 0; Gaps 0;

Matches 340; Conservative 0;

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OY 166 GGAGCGAGGGGAGGCGGAGCAGCAGCATGTCACATGCGCATTCAGATTCGATTTGT 225  
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OY 226 GCGTGTCTTCCGATCTTGAAGCTGTCGCGCATCAAGAGGCGCTCAATCTTGGGCA 285  
DB 134 AAGGCTCTCCGATCTTGAAGCTGTCGCGCATCAAGAGGCGCTCAATCTTGGGCA 193  
OY 286 GACGCTTCGGGCTCCATGCTGAGTGGGCTCTCATCTTTTCTCTTCATCGGTGT 345  
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OY 526 GCTGACTATTTCCCTGAGGCGGTAGTACCATGATGATGATTTGGCTATGAGA 556  
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KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200155318-A2.  
XX

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AC ABA06356;  
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DT 10-JAN-2002 (first entry)  
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DE Human cDNA SEQ ID NO: 22.  
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XX Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200154474-A2.  
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XX  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human endocrine polypeptide encoding cDNA SEQ ID NO 136.  
XX  
KW Endocrine protein; human; mouse; rabbit; goat; horse; food additive;  
KW cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasoprotective;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;  
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;  
KW ophtalmological; vulnerrary; gene therapy; autoimmune disease; neoplasm;  
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;  
KW cerebrovascular disorder; nervous system disorder; bacterial infection;  
KW fungal infection; viral infection; ocular disorder; endocrine disorder;  
KW gastrointestinal disorder; renal disorder; respiratory disorder;  
KW wound healing; skin aging; organ transplantation; food preservative;  
KW tissue regeneration; anti-fertility.  
XX  
OS Homo sapiens.  
XX  
PN W0200155364-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01308.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
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PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225265.  
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PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
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PR 08-SEP-2000; 2000US-0231413.  
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PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
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PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235836.  
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PR 29-SEP-2000; 2000US-0236367.  
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PR 02-OCT-2000; 2000US-0236802.  
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PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
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PR 20-OCT-2000; 2000US-0241786.  
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PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
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PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.







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## OM nucleic - nucleic search, using sw model

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(without alignments)  
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Perfect score: 556  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436.6	78.5	1599	1	US-08-288-405A-9
2	326.2	58.7	1994	1	US-08-527-152-1
3	179.4	32.3	696	1	US-07-955-916-5
4	168.2	30.3	1805	1	US-07-955-916-6
5	159	28.6	2064	4	US-09-178-109-3
6	159	28.6	2072	4	US-09-142-791A-3
7	159	28.6	2104	4	US-09-142-791A-1
8	157.8	28.6	2121	4	US-09-178-109-1
9	157.8	28.6	3424	4	US-09-336-643A-9
10	157.4	28.3	2104	4	US-09-142-791A-5
11	145	26.1	2483	1	US-08-464-340A-3
12	145	26.1	2483	5	PCT-US94-08449A-3
13	137.2	24.7	2127	5	PCT-US94-08449A-1
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15	130.8	23.5	196	1	US-08-288-405A-18
16	124.2	22.3	2293	4	US-09-336-643A-5
17	122.2	22.0	1927	4	US-09-336-643A-3
18	115	20.7	3102	4	US-09-336-643A-17
19	106.4	19.1	3080	4	US-09-336-643A-7
20	97.4	17.5	139	1	US-07-961-268-3
21	97.4	17.5	139	1	US-07-961-268-4
22	77	13.8	896	4	US-09-105-058C-1
23	57.6	10.4	2028	4	US-09-634-920-1
24	57.6	10.4	2734	3	US-09-135-021-79
25	57.6	10.4	2821	4	US-09-135-010A-115
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37	55	9.9	2565	4	US-09-105-058C-26	Sequence 26, Appli
38	55	9.9	2914	4	US-09-177-650-6	Sequence 6, Appli
39	53.8	9.7	93	1	US-08-288-405A-16	Sequence 16, Appli
40	53	9.5	702	4	US-08-843-417-3	Sequence 3, Appli
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42	53	9.5	6344	4	US-08-843-417-1	Sequence 1, Appli
43	53	9.5	6524	4	US-08-669-656A-1	Sequence 1, Appli
44	53	9.5	6527	4	US-08-669-656A-7	Sequence 7, Appli
45	53	9.5	7052	4	US-08-669-656A-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-288-405A-9  
; Sequence 9, Application US/08288405A  
; Patent No. 5559009  
; GENERAL INFORMATION:  
; APPLICANT: Chandy, Kananthara G.  
; APPLICANT: Kalman, Katalin  
; APPLICANT: Chandy, Grischa  
; APPLICANT: Gutman, George A.  
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
; ADDRESSEE: Attn: Walter H. Dreger  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/288,405A  
; FILING DATE: 10-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,431  
; FILING DATE: 04-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-59844-1/MHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELETYPE: 910 277299  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1599 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1599  
; US-08-288-405A-9

Query Match 78.5%; Score 436.6; DB 1; Length 1599;  
Best Local Similarity 86.7%; Pred. No. 2.8e-109;  
Matches 481; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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QY 122 GCTATCTCTCTCACTTTGTTGGCACTGGGCAACGAGCTGGCCCGGCAAGGAGGCTG 181  
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DB 1033 CAGCGGCTATGCTCCGCGCATCTCCAGATTTGGCTGTCTTCGCGATC 1092  
QY 242 TTCAAGCTGTCCGCACTCAAAAGGCGCTCAAAATCTTGGGCGCAGCTTCGGGCTCC 301  
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QY 302 ATGCGTGAAGCTGGGCTCTCTCATCTTTTCTCTTCATCGGTGTGCTCTTTTCAGC 361  
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DB 1333 GTGGGTGCGCAAGATGATGGGCTCTCTGTGTCATTTGGGCGCTGCTGACTATTTCCCTG 1392  
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DB 1393 CCAGTGGCGCTCAT 1407

RESULT 2  
US-08-527-152-1  
; Sequence 1, Application US/08527152  
; Patent No. 5827655  
; GENERAL INFORMATION:  
; APPLICANT: Chandu, Kanianthara G.  
; APPLICANT: Cahalan, Michael D.  
; APPLICANT: Grissmer, Stephan  
; APPLICANT: Goldin, Alan L.  
; APPLICANT: Dehiefs, Brent A.  
; APPLICANT: Gutman, George A.  
; APPLICANT: Masmuth, John J.  
; TITLE OF INVENTION: Assay, Methods and Products Based On n  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flenz, Hobach, Test, Albritton & Herbert,  
; ADDRESSEE: Attn: W.H. Dregler  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/527,152  
FILING DATE: UNKNOWN  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/170,418  
FILING DATE: 20-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/558,568  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-54444-2/MHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 150..1736  
US-08-527-152-1

Query Match 58.7%; Score 326.2; DB 1; Length 1994;  
Best Local Similarity 74.2%; Pred. No. 2.6e-79;  
Matches 412; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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DB 1191 ATGCGTGAAGCTGGGCTCTCTCATCTTTTCTCTTCAATCGGTGTGCTCTTTTCAGC 1250  
QY 362 GCGCTCTACTTTGCGCAAGTTGAACCGGCTGGGCTCCCATTTCCATCTACATCCCGATCC 421  
DB 1251 GCGCTCTACTTTGCGCAAGTTGAACCGGCTGGGCTCCCATTTCCATCTACATCCCGATCC 1310  
QY 422 TTCTGTGTGCGGCTAGTCAACCATGATCTACATTTGGCTATGGAGCAGCGCTGCTGCT 481  
DB 1311 TTCTGTGTGCGGCTAGTCAACCATGATCTACATTTGGCTATGGAGCAGCGCTGCTGCT 1370  
QY 482 GTGGGTGCGCAAGATGATGGGCTCTCTGTGTCATTTGGGCGCTGCTGACTATTTCCCTG 541  
DB 1371 GTGGGTGCGCAAGATGATGGGCTCTCTGTGTCATTTGGGCGCTGCTGACTATTTCCCTG 1430  
QY 542 CCAGTGGCGCTCAT 556  
DB 1431 CCAGTGGCGCTCAT 1445

## RESULT 3

US-07-955-916-5

Sequence 5, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHLEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE

DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-955-916-5

Query Match 32.3%; Score 179.4; DB 1; Length 696;

Best Local Similarity 62.0%; Pred. No. 1.1e-39;

Matches 354; Conservative 0; Mismatches 181; Indels 36; Gaps 3;

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DB 14 TCGAGGGCGTGTGTTGCTGCTGATTCCTTCATGCTGATGCTGATCTTCTGCG 73  
QY 72 CAGAGAGCGTATCTTCTTCAGAGAGTATGACCTCATCTTTTGGTGCATCTCT 131  
DB 74 CCAACAAGGTAGATTCATCAAGAACTGCTCATCTTGTGTTGGCCATCTCTG 133  
QY 132 CCTACTTTGAGCAGTGGGACGAGCTGGCCGAGGAGGAGGAGGAGGAGGAGGCA 191  
DB 134 CCTTCACTGAGAGTGGG-----GCTAGAGCGCTGTCTTCAGAGGAGGAGGAGG 187  
QY 192 TGTCACTGGCACTCTGAGAGTCAATCGATGAGTGTCTTCCGATCTTCAAGCTGT 251  
DB 188 TG---CTGGGCTTCGCGCGTCTGCTGCTGCGCATCTTCCAGGAGGAGGAGGAGG 244  
QY 252 CCGGAGACCAAGGCGCTGCAATCTTGGGCGAGACGCTTGGGCGCTTCATGCGTGA 311  
DB 245 CCGGAGACCTTGTGGCGTGGGCGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 304  
QY 312 TGGGCGCTCTCATCTTTTCTCTTCATGAGTGTGCTCTCTTTTCAGAGGCGCTGAG 371

## RESULT 4

US-07-955-916-6

Sequence 6, Application US/07955916

Patent No. 5397702

GENERAL INFORMATION:

APPLICANT: CAHALAN, Michael D.

APPLICANT: CHANDY, Kanianthara G.

APPLICANT: GRISMER, Stephen

APPLICANT: GHANSHANI, Sanjiv

APPLICANT: GUTMAN, George A.

APPLICANT: DETHLEFS, Brent A.

TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE

DISEASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/955,916

FILING DATE: 19921002

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54474-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1805 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-955-916-6

Query Match 30.3%; Score 168.2; DB 1; Length 1805;

Best Local Similarity 60.8%; Pred. No. 1.7e-36;

Matches 347; Conservative 0; Mismatches 188; Indels 36; Gaps 3;

QY 12 TGGAGAGCGTGTATTTGTTGCTTCCTTTGAGCTGCTGAGCCCTCGTGGTGTGTC 71  
DB 879 TCGAGGGCGTGTGTTGCTGCTGATTCCTTCATGCTGATGCTGATCTTCTGCG 938

Oy	72	CAACGAAAGGGATCTTCTTCATAAAGCGTAAGCAACTCATGTATTGTTGGGATATCC	131
Dd	939	CCAACAAAGGTGGGAATTCATCAGMAAGACTCCCTCATATATCTTAGCTTTTGCGCATTC	998
Oy	132	CTTACTTTGGGCACATGGGCAACCAGACTGCCCCGCCAGCGAGGGGTGGGCCAGCAGGCCA	191
Dd	999	CTTTCTTACCTGGAGGTGG--CCTAAGCGGGCTGTCTCTCAAAGCCGCCAAGAGAGT- -	1054
Oy	192	TGTCATGGGCAATCCGAGAGCATCCGATGGTGGGTGCTCTCCGATCTTCACAGCTGT	251
Dd	1055	------CTGGGCTTCTCGCGGCTGTCCGCTTGTGCGCATCTCGGCGCATCTTCACAGCTGA	1109
Oy	252	CCCGGCACTAAAGGGCGCTGCAAAATCTTGGGCCAGACGCTTGGGCTTCATGCGTGA	311
Dd	1110	CCCCCACTTCGTGGGCGCTGAGGGTCTTGAGGCACACGCTCGTCCGACACACAGAGT	1169
Oy	312	TGGGCGCCGACATCTTTTCTCTTCATGGGTGGTGTCTCTTTTCCAGCGCGCTACT	371
Dd	1170	TCTGCTGCTTATCATCTTCTCTGGCCCTGGAGGTGCTCATCTTTCACACATGATCT	1229
Oy	372	TTGCCGA-----AGTTGACCGGGGTGAGCTCCACTTTCACA	404
Dd	1230	ACGCCGAGAGGATAGGGGCGACAGCCCAATGACCCCAGCGCCAGCGAACACACACTT	1289
Oy	405	CTAGACATCCCTGAATCTTGTGGTGGGCGGTAGTACCACTGACTACAGTTGGCTATGAG	464
Dd	1290	AAAACATCTCCCATCGGCTTGTGGTGGGCTGTGGTACCACTGACGACACTGGGCTATGAG	1349
Oy	465	ACATGACCCCGGCTACTGTGGTGGCGCAAAATAGTGGGCTCTGTGGCATTCGGGCG	524
Dd	1350	ACATGTATCCCAAGAGGTGTCTTGGAATCGTGGTGGGACCTTGTGTGTGCTGCGTGTG	1409
Oy	525	TGCTGACTATTTCCCTCCACAGTCCCGCTCAT	555
Dd	1410	TGCTGACCATTCGATCCGCTCGCTCAT	1440

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RESULT 5
US-09-178-109-3
: Sequence 3, Application US/09178109
: Patent No. 6395477
: GENERAL INFORMATION:
: APPLICANT: Cockett, Mark I.
: APPLICANT: Dilks, Daniel W.
: APPLICANT: Chang Ling, Hual-Ping
: APPLICANT: Sokol, Patricia T.
: TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
: FILE REFERENCE: ahp-98089
: CURRENT APPLICATION NUMBER: US/09/178,109
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 2064
: TYPE: DNA
: ORGANISM: human
US-09-178-109-3

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Query Match	28.6%;	Score 159;	DB 4;	Length 2064;
Best Local Similarity	58.7%;	Pred. No. 5.6e-34;		
Matches 326;	Conservative	0;	Mismatches 205;	Indels 24;
				Gaps 2

QY	2	TTCTTCTGAGGAGACGCTGTGATATTTGTTGTTCTTCCTTTGAGCTGCGTACGCTC	61
Db	748	TTCTTCTGCTGGACAGCGCGTGGGTATGATCTTCAACCGTGAGTACTCTCTCGGCTC	807
QY	62	CTGCTCTGTCCAAACGACATCTTCTCTCAAGAACGTGATGAACCTCATGATTTTGTG	121
Db	808	TTTCGGGCTCCAGCGCTACCGCTTCTATCCGACAGCTCATGACATCATGAGCTGTG	867
OY	122	GCTATCTTCCCTACTTTGTGGACACTGGGACCGCAGCTGGCGCCGGACACGAGGGGTGGC	181

Db	868	GCATCATGGCCTA	CTACTACATCGGCTGTGTCAT-----GACCAAC	906
QY	182	CACGAGCCCATGT	CACTACTGCCATCTGAGAGTCATCCGATTGGTGCCTGTCTTCCGCATC	241
Db	907	AACGAGGACCTGT	CCGGCGCCTTCGCA--CGCTCCGGGCTTC	963
QY	242	TTTCAAGTGTC	CCCCGCGACATCAAGGGGCGTCAAAATTTGGGGCAGACGGCTTGGGCGCTCC	301
Db	964	TTTCAAGTTTTTC	CCGCGCACATCCAGGGCTCGGGATCTTGGCTACACATCAAGAGCTGT	1023
QY	302	ATGCGTAGCTGG	GGCCCTCATCTTTTTCCTTCATGAGTGTGATCTCTTTTCCAGC	361
Db	1024	GCTTCCGAACTG	GGGCTTTCTTCTTCTTCCCTACCATGGCATCATCATTTTTGCACCT	1083
QY	362	GCCCTCACTTTG	CCGAAGTTGACCGGGAGACTCCCATTTTCACTAGCATCCCTGAGTCC	421
Db	1084	GTGATGTTTATG	CCGGAAGGGCTCTCGGCCAGCAATTCACAAGCATCCCTGCTCG	1143
QY	422	TTTGTGTGGGG	GTATGCACCATGACTACAGTTGGCTATGAGAGACATGGACCCCTCACT	481
Db	1144	TTTTTGTACAC	ATTGTTTCCATTCACCATGAGCACTGGGTACGGAGACATGGTGGCTAAAGC	1203
QY	482	GTGGGTTGGCA	AGATAGTGGGCTCTCTGTGTGGCATTTGGCGGGGGTGTCTAGCTATTTTCCGTG	541
Db	1204	ATTTCAGGGGA	GAATCTTCGGCTCCATCTGTGCTTAAGTGGGGGCTGTGCTATTTGCCCTG	1263
QY	542	CCAGTGGCCG	CATTT 556	
Db	1264	CCAGTCCCTG	ATTT 1278	

```

RESULT 6 791A-3
: Sequence 3, Application US/09142791A
: Patent No. 6368623
: GENERAL INFORMATION:
: APPLICANT: Antoine Michel Alain Brill
: APPLICANT: Thierry Paul Gerard Calmels
: APPLICANT: Jean-Francois Simon Pierre Faivre
: APPLICANT: Jean-Luc Javre
: APPLICANT: Sabine Rouanet
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30012
: CURRENT APPLICATION NUMBER: US/09/142, 791A
: PRIORITY FILING DATE: 1999-02-02
: PRIOR APPLICATION NUMBER: PCT/EP98/01901
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: UK 9706377.0
: PRIOR FILING DATE: 1997-03-27
: PRIOR APPLICATION NUMBER: EP 97402971.2
: PRIOR FILING DATE: 1997-12-09
: PRIOR APPLICATION NUMBER: EP 97403007.4
: PRIOR FILING DATE: 1997-12-11
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1072
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
: US-09-142-791A-3

```

Query Match	28.6%	Score 159;	DB 4;	Length 2072;
Best Local Similarity	58.7%;	Pred. No. 5.7e-34;		
Matches 326;	Conservative	0;	Mismatches 205;	Indels 24;
				Gaps 2

Oy	2 TTTTTCGCGAGAGACGCCTATATTGTGGCTCCCTTGAGCCTGCAACGCCTC	61 
Dd	676 TTCTTCTGCCCTGCACACGGCGCTCATATCTTCAACGGTAGTAACCTCTGGGCTC	735 
Oy	62 CTGCTCTCTCCAACAAGGCTATCTTCTTCAAGAAGCTGATGAACCTCATGATTTGTG	121 
Dd	736 TTCGGGCTCCAAAGCGCTACCGCTATATCCGACGGCTCATGACCATCATGACGCTGTG	795 



OY	182	CACGAGGCATGTACATGGCGCATCTGAGAGTCATCCAGTTGGTGGTCTTTCGCCAATC	241
Db	907	AACGAGCACTGTCTCCGCGCCCTTGTCGA---GCTCCGGGCTCTTCCGCTCTTCCAGGATC	963
OY	242	TTCAACTGTGCCGCGCATCTCAAAGGGACTGCACAATCTTGGGCGAAGCGCTTGCGGCTCC	301
Db	964	TTCAAGTTTTCCGCGCACCTCCAGAGGGCTCGGGATCTCGGGCTACACACTGAAGAAGTGT	1022
OY	302	ATGCGTAGCTGGGACCCTTCATCTTTTTCCTTATGCTGCTGTGGTCTCTTTTCCAGC	361
Db	1024	GCCATCCAACTGGGGCTTTCTTCTCTCTCCCTCCATCCATGGCCATCATCTTTTCCCACT	1083
OY	362	GCGCTACTCTTGGCGAAGTGAACGGGGAGATCCCATTTTACATAGCATCCCGTAGTCC	421
Db	1084	GTCATGTTTTATTGCGCGAAGGGCTCCTCGGCGAGAACTTACAAAGCATCTTCCCTCTCG	1143
OY	422	TTTCGTGGGCGGTAGTACACATGACTACATGTTGGCTATGAGAGACATGGACCCCTCACT	481
Db	1144	TTTTTGTACACATTTGTACACATGACACACTGGAATACGGAAGACATGTTGCTTAAGACG	1203
OY	482	GTTGGGTGGCAAGATAGTGGGCTCTGTGTGCTGCCATTGGGGCGTGGCTACTATTTTCCCTG	541
Db	1204	ATTTCAGAGGAAGATCTTCGGCTCCATCTGTCTCTTGAAGTGGGCTCTGGTCAATTGCCCTG	1263
OY	542	CCAAGTGGCCGTCATT	556
Db	1264	CCAAGTCCCTGATTT	1278

```

RESULT 9
US-09-336-643A-9
: Sequence 9, Application US/09336643A
: Patent No. 6399761
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: No. 6399761el Human Potassium Channels
: FILE REFERENCE: SEQ-15P
: CURRENT APPLICATION NUMBER: US/09/336,643A
: CURRENT FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/0076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 3424
: TYPE: DNA
: ORGANISM: H. sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (257)...(2195)
: OTHER INFORMATION: K+HNOV12
: US-09-336-643A-9

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Query Match	28.4%;	Score 157.8;	DB 4;	Length 3424;
Best Local Similarity	57.5%;	Pred. No. 1.4e-33;		
Matches 319;	Conservative	0;	Mismatches 212;	Indels 24;
				Gaps 1

[illegible]

QY	122	GCTATCCCTCCCACTATTGGGACAGTGGGACAGCACTGGCCGGGAGGAGGAGTGGG	181
Db	1067	GCCATCTCGCCCTACTACATTTGGGCTTTT-----GGTGGCC	1107
QY	182	CAGCAGGCCCATGTCTACTGGCCATCTGAAGATCATCCGATTTGGTGGTGTCTTCCGATC	241
Db	1103	AAGAACGACGATGTCTGTGGCGCTTTGTACCCCTCGCTGTGTCCGGGTGTTTGGCATC	1162
QY	242	TTTCAAGCTGTCCCGGCACTAAAGGGCGCGCAATCTTGGGCGACAGCGTTGGGCTTC	301
Db	1163	TTTCAAGTTCTCCAGGCACTACAGGGCTTGAGGATTTCTGGCTACACACTCAAGAGCTGT	1222
QY	302	ATGGGTAGCTGGGCGCCCTCATCTTTTCTCTTTCATGCTGGTGGTCTCTTTTCCAGC	361
Db	1223	GGCTGTAGCTGGGCTTTCTCTCTTTTCCCTAACCATGGCCATCATATCTTTGCCACT	1282
QY	362	GCGCTACTTTGGCCGAGTTGACCGGGTGGAGTCCCATTTACTAGCATCCCTGATGCC	421
Db	1283	GTCATGTGTTTATGTGTGAAGGGCACAAACAAACACCACTTTACAGCACTCCCTGGGCC	1342
QY	422	TTTCAAGTGGGGGAGTACCATGACATGACATGAGTTGGGTATGAGAGCATGGGACCCGCTACT	481
Db	1343	TTTCTGGTATACCATTTGTCCACATGACCACAGCTTTGGCTACGGAGACATGGTGGCCAGCAC	1402
QY	482	GTTGGGTGGCAAGATAGTGGGCTCTGTGTGCCATTTGCGGGGTGCTGACTATTTCCCTG	541
Db	1403	ATTGCTGGCAAGATTTTCGGGTGCATCTGTCTCACTCAAGGGCGTCTGTGGTATTTCCCTG	1462
QY	542	CCAGTGGCGCGTCATT 556	
Db	1463	CTGTGGCAGTCAATT 1477	

```

RESULT 10
US-09-142-791A-5
Sequence 5, Application US/09142791A
Patent No. 6368823
GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Brill
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Falvire
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 2104
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-142-791A-5

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Query Match	28.38;	Score 157.4;	DB 4;	Length 2104;
Best Local Similarity	58.68;	Pred. No. 1.5e-33;		
Matches 325; Conservative	0;	Mismatches 206;	Indels 24;	Gaps 2

[illegible]











GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 05:50:07 ; Search time 920.625 Seconds  
(without alignments)  
9781.067 Million cell updates/sec

Title: US-09-804-014a-7\_COPY\_970\_1525

Perfect score: 556  
Sequence: 1 gtctctgtgtgtgagacgc.....ccctgcagtgccgcattc 556

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estba:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	301.2	54.2	636	17	AZ339279 1M0070M07
C 2	299.2	53.8	900	17	CNS028D3
C 3	284.8	51.2	745	14	BM963332
C 4	279.2	50.2	772	13	BM764377
C 5	271.8	48.9	559	12	BM812963
C 6	267.8	48.2	575	13	BM128683

Result No.	Score	Query Match	Length	ID	Description
C 7	264.6	47.6	593	13	BM128211
C 8	263.4	47.4	1060	17	CNS058R
C 9	256.4	46.1	1085	17	CNS035KP
C 10	246.8	44.4	629	17	AG163977
C 11	227.4	40.9	506	13	BI467889
C 12	225.4	40.5	697	10	BM541281
C 13	210.4	37.8	706	17	AG939522
C 14	201.4	36.2	434	10	BE654741
C 15	200.4	36.0	990	17	CNS04EVP
C 16	198.8	35.8	1058	14	BM924988
C 17	193.4	34.8	437	12	BE865003
C 18	192.8	34.7	457	9	AI694783
C 19	192.8	34.5	631	10	BM622001
C 20	189.6	34.1	400	12	BF108522
C 21	187	33.6	1355	14	BM906309
C 22	180.8	32.5	436	12	BF189101
C 23	179.8	32.3	1087	17	CNS02H90
C 24	171.4	30.8	668	14	BM187015
C 25	170.8	30.7	637	10	BM250655
C 26	168.2	30.3	2146	11	BC023222
C 27	165.2	29.7	876	13	BI117089
C 28	163.4	29.4	2265	11	BC019010
C 29	157.8	28.4	2265	9	BC019010
C 30	151.2	27.2	897	17	CNS02078
C 31	148.8	26.8	897	17	CNS02078
C 32	148.8	26.8	2314	11	BC030422
C 33	146.6	26.4	839	17	CNS03DKC
C 34	142	25.5	687	9	AI323497
C 35	141.2	25.4	687	12	AI323497
C 36	140.2	25.2	687	17	AI323497
C 37	139.6	25.1	687	12	AI323497
C 38	139.6	25.1	687	12	AI323497
C 39	139	25.0	687	17	AI323497
C 40	138	24.8	687	12	AI323497
C 41	137	24.6	687	12	AI323497
C 42	136.8	24.6	687	12	AI323497
C 43	136.8	24.6	687	14	AI323497
C 44	134.8	24.2	687	12	AI323497
C 45	132.2	23.8	687	10	AI323497

## ALIGNMENTS

RESULT 1  
LOCUS AZ339279/c 636 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0070M07R Mouse 10kb plasmid UGCM library Mus musculus genomic  
clone UGCM1M0070M07 R, DNA sequence.  
ACCESSION AZ339279  
VERSION AZ339279.1 GI:10413383  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 636)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
Plasmid Inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



QY	242	TTCAAGCTGTCCCGGACACTCAAAAGGCGCTGCAAAATCTTGGCCAGACGTTTGGGCGCTCC	301
Db	446	TTTCATCTCTTCAGACACCTCCAAAGGGGCTGCAGATCTCGGGCAATACCTCGCGCGACACG	387
QY	302	ATGCGTGAGCTGGGGGCTCCTCATCTTTTCCCTTCATCGAGGTGGTGGTCCCTTTTCCACG	361
Db	386	ATGAGGGAGACTGGCCCTCCTCTCATTTTCTTTCGTGATCGGGGTACATCCTCTTTCACAGC	327
QY	362	GCGCTCTACTTTTGGCGGAAGTTGACCGGGGAGACCTCCATTCTACTAGACATCCCTGAGTCC	421
Db	326	GCGGCTCTACTTGGCCGAGAGCGAGCAGCACCCACTCCCACTTACCAAGCATCCCGAGCGCG	267
QY	422	TTCTGTGTGGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCCGCTCACT	481
Db	266	TTCTGTGTGGGCTGTGTAAACATGACGAGAGGTGGGCTACGGCGGATATGTAAGCTTATCAG	207
QY	482	GTGGGTGGCAGAGATAGTGGGCTCTGTGTGTGCCATTGGCGGGGCGTGCTGATATTTCCCTG	541
Db	206	GTCGGTGGGAGAGATGTTGGGCTCTGTGTGCGCATCGCGGGCGGTGTAAACGATCGCGCTG	147
QY	542	CC 543	
Db	146	CC 145	

RESULT 3					
BM963332					
LOCUS	BM963332	745 bp	mRNA	linear	EST 18-MAR-2002
DEFINITION	UI-M-EO0-Bwm-1-05-0-UI.r1 NIH_BMAP_EO0 Mus musculus CDNA clone				
	IMAGE:5697484 5', mRNA sequence.				

ACCESSION	BM963332	GI:19546752
VERSION	BM963332.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.  
1 (bases 1 to 745)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: c9apb3s@iemail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: WCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
<http://image.liml.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pyX-5.

FEATURES	Location/Qualifiers
source	1. .745

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/organism="Mus musculus"
/strain="C57BL/6"
/db.xref="taxon:10090"
/clone="IMAGE:5657484"
/clone_1b="NIH_BMAP_E00"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/notes="Organ: brain; Vector: pYX-Asc; Site_1: Ecov I; Site_2: Not I. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecov I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag

```

sequence located between the Not I site and the polyA tail  
, is CAGCCACGAC. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institutes of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

Query Match	51.2%	Score 284.8;	DB 14;	Length 745;
Best Local Similarity	71.4%;	Pred. No. 7.1e-64;		
Matches 404; Conservative	0;	Mismatches 122;	Indels 30;	Gaps 1;

[illegible][illegible]

Db 241 TGTTCGAAATCTTCAAGCTCTCCGCCCAATCCAAAGGGCTGCACATCTCGGTAAAGACT 300

Db 291 TTGGGGCCCTCCATGCGTGAAGCTGGGGCCCTCTCAATCTTTTTCCTCTCAATGCGTGTGGTCC 350

Db 301 TACAGAGCGCTATGGGGAGGCTGGGGGCGGCGGCGTCAATCTTTTCTCTCTTCAATGGAGCTCAATC 360

QY 351 TCTTTCCAGGCGCGTCTACTTTGCCGAAGTTGACCGGGTSGACTCCCATTTCACTACA 410

Db 361 TCTTTTCCAGGCGCTGTCTACTTCGAGAGGCGTGATGATGTTGACTCGCTCTTCCCTACGA 420

OY 411 TCCCGACTCCTTTCGGGGCGGTAGCACCATGACTACAGTTGGCTATGGAGACATGG 470

Accession	Sequence	Position
Db	421 TCCAGATGCGCTTCGTGGGGCTGTGGTTACAATGACACGGTAGTTATATGGGACATGT	480
Qy	411 CACCGCTACTGTGTGGGTGGCAAGATAGTGGGCTCTGTGTGCCATTGGGGCGTCTGA	530
Db	481 ACCCGATACGGTAGGGGGCAAGATGTGGGCTCACTGTGGCCATTGTGGGGTCTCTCA	540
Qy	531 CTATTCCCTCCGATGGCCCGTCATT	556
Db	541 CCATGCTATTACCGGTACCGGTCATT	566

RESULT 4  
R1764377

LOCUS	BT664377	772 bp	mRNA	linear	EST 25-SEP-2001
DEFINITION	603046295F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:186518 5', mRNA sequence.				
ACCESSION	BT664377				
VERSION	BT664377.1	GI:15755955			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 772)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc.				





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 Db 428 TTAGTCTACTTTGCTGCTGATCATVCGGATACAAAGTTTCAAGTATCCCTGAGCA 487  
 QY 422 TTCTGTGGCGGTAGTACCATGACTACATGAGTGTGCTATGAGACATGACCCCTGACT 481  
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 BM128683  
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 DEFINITION 114f08.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
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 VERSION EST.  
 KEYWORDS human.  
 SOURCE human.  
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 575)  
 AUTHORS Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,R.,  
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas  
 M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T.,  
 Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center for information on  
 obtaining a clone please contact: Juliana Brown  
 (brownjefas.harvard.edu) This sequence now available from the IMAGE  
 consortium, for clone orders contact: info@image.llnl.gov  
 High quality sequence stop: 429.  
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 /tissue\_type="Islets of Langerhans"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
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 Site:2: Sal 1; Starting library constructed using  
 Superscript Plasmid Library Kit (Life Technologies). cDNA  
 made by oligo-dT priming. Size-selected by column  
 fractionation; average insert size 1.08 kb. Library was  
 amplified once on solid support and plasmid DNA from  
 library was prepared. The library DNA was normalized by  
 method #4 from Bionaldo, Lennon, and Soares 1996 Genome  
 Research 6:791-806; 0.5 microgram single-stranded library  
 plasmid DNA was mixed with 5 micrograms PCR product  
 representing library inserts and hybridized to an EcoT of  
 20. Single-stranded (unhybridized) plasmids were isolated

BASE COUNT 118 a 164 c 156 g 137 t  
 ORIGIN  
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 Best local Similarity 75.6%; Pred. No. 1.8e-59;  
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 Db 1 TGTGGCATCATCTTCTATTATTAACCTGTGGGTACGAGCTGGCGAAGACAGGCA 60  
 QY 178 GGGCCAGCAGCCATGCTCACTGAGCCATCCGAGAGCATCCGATGTGGTGTCCG 237  
 Db 61 TGCACACAGAGCCATGCTCTGGCCATCCGAGAGGTATCCGCTGTAGGGCTTCCG 120  
 QY 238 CATCTTCAAGCTGTCCCGGACATCAAGGCGCTGCAAACTTGGCGCAGCCTTGGGC 297  
 Db 121 CATCTTCAAGCTGTCCCGGACATCAAGGCGCTGCAAACTTGGCGCAGCCTTGGGC 180  
 QY 298 CTCATGCGGTGAGCTGGGCGCTCCTCATCTTTTCTTCTGATGCGTGTGCTTTC 357  
 Db 181 GTCCATGCGGGAGCTGGGATGCTCATCTTCTTCTTATTTGGGGTCACTTCTTC 240  
 QY 358 CAGCGCGCTACTTTCGCCAAGTTGACCGGGTGAAGTCCCATTTCTAGCATTCCTCG 417  
 Db 241 CAGCGCGCTACTTTCGCCAAGTTGACCGGGTGAAGTCCCATTTCTAGCATTCCTCG 300  
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 Db 301 TGCTTCTGTGTGGCGGTAGTACCATGACTACAGTTGGCTATGAGACATGGCACCGT 360  
 QY 478 CACTGTGGTGGCAAGATAGTGGGCTCTGTGCTCATTTGCGGCGCTGCTGACTATTTC 537  
 Db 361 GACCATGCGGGGCGCAAGATTTGTGGATCTCTGTGCTCATTTGCGGCGCTGCTGACTATTTC 420  
 QY 538 CTGCGCAGTCCCGCTATT 556  
 Db 421 ATTGCCAGTTCCTGTATT 439  
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 DEFINITION 110h09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
 cDNA clone IMAGE:5676160 5' similar to SW:CIK3\_HUMAN P22001  
 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL3 ; mRNA sequence.  
 ACCESSION BM128211 GI:17122763  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 593)  
 AUTHORS Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,R.,  
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas  
 M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T.,  
 Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:



[illegible]

Db	122	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614
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Db 350 TCTGTCTGTCTCAAGACGCTATCTTCTTGAAGACGTATGAACCTCATCATGATTTTGT 409

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QY 180 GCGACAGAGCCATGCTACT--GGCCATCTGAGAGTATCCGATTGGTGCCTGCTTCC- 236

Db 470 GCCANCAAGCCATGCTACTTGGCCATCTTGAAGATCCGATTGGTGCCTGCTTCCG 529

QY 237 GCATCTCAAGCTGTCGCCGACATCAAGG 267

Db 530 GAATCTTCAAGCTGTCCCGACATCAAG 560

RESULT 14  
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LOCUS  
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ACCESSION BE54741  
VERSION BE54741.1 GI:9980654  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 434)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
COMMENT Contact: Chn, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mestr@mail.nih.gov  
CDNA library preparation: M.B. Soares Lab Clone distribution:  
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It  
should be noted that Bento Soares is generating a small number of  
additional specialized non-redundant arrays of BMAP CDNAs whose  
availability will be considered under appropriate and limited  
collaborative arrangements  
Seq primer: M13 Reverse  
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Location/Qualifiers  
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from mouse spinal cord. The tag is a string of 5  
nucleotides present between the Not I site and the  
oligo-dT track. The library was constructed as described  
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806  
1996. Tissue provided by Ms. Annie Novakovich,  
Zivic-Miller Laboratories."

BASE COUNT 86 a 117 c 111 g 120 t

ORIGIN

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QY 278 TTGGGCCACGACCTTGGGACCTCCATGAGTGGGCTCCATCTTTTCTTC 337

Db 61 CTAGACAGACGCTGAGAGCTTCCATGCGGAGCTGGGGCTGCTATTTCTTCTTC 120

QY 338 ATCGGTGTGCTCTTCTTTCAGGCGGCTTACTTTGGCGAAGTTGACCGGGTGAATCC 397

Db 121 ATTGGGGTCATCTTTTCTTCCAGTGCATCTTACTTTGTGAGGACAGACCTTCTTCG 180

QY 398 CATTTACTACATCTTCTGAGTCTTCTGTTGGGCGGATGACCATGACTACAGTTGGC 457

Db 181 GGTTTTACAGTATCCCGAGTCCCTTGTGTGGCAGTAGTACCATGACAGCTTGTGT 240

QY 458 TATGAGACATGGGACCGGCTACTGTGGGTGGCAGATAGGGGCTCTGTGGCATC 517

Db 241 TATGCTATATGACACCCAGTACCATAGAGGACAAAGATTGTGGGCTCTTGTGGCATC 300

QY 518 GCGGGCGTGTGACTATTTCCCTGCCAGTGGCCGTCATT 556

Db 301 GCAGGTGTCTTGACCATGTCATGTCGAGTTCCTGTGATT 339

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ACCESSION AL287566  
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VERSION GSS: genome survey sequence.  
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ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  
1 (bases 1 to 990)  
Roest-Crolius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 990)  
Roest-Crolius, H., Jalllon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
JOURNAL  
REFERENCE 3 (bases 1 to 990)  
Genoscope.  
TITLE Direct Submission  
COMMENT Submitted (12-APR-2000)  
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetraodon>.  
FEATURES  
Location/Qualifiers  
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BASE COUNT 209 a 295 c 280 g 169 t 37 others

ORIGIN

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Matches 386; Conservative 16; Mismatches 122; Indels 32; Gaps 9;

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Db 2 TGGTTCCTTCCCTTGGCTGGTACGCTCCCTGCTG--TCCAAGCAAGGCTATCTTCTT 61
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OY 91 CAAGAACGT-GATGAACCTCATGCAATTTTGGCTATCCCTCCCTACTTTGTGCA--CT 147
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Db 62 CAGGAACATAGATGAACACCATGACATGTCGCMAMATCCCTAACTTCATACAGCT 121
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OY 148 GGGCACCGAGCTGGCCGGCA-----GCGAGGGGTGGCCAGC 185
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Db 122 GGGGAGGGAGCTGGCGAGGMAACAAGAGAGACAAAGGCGGTGGCGAGTA 181
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OY 186 AGGCCATGTCACATGGCATCCATGAGATCATCCGATTGGTGGCTTCCGATCTCA 245
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OY 305 CGTGAAGCTGGCC--TCTCATCTTTTCTTCTTCATCGTG--TGTCTCTTTTCCAGCG 362
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OY 363 CCGTCTACTTTGGCGAAGTTGACCGGGGTGACTCCCATTTCACTAGCATC--CCTGAGTCC 421
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Db 362 CTGTCTAMTTMCCGARGCCGARGAARACTCTTAMTTACACGACATACCCGAMGCC 421
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OY 422 TTCTGGTG--GGCGTAGTCACCATGACTACAGTTGGCTATGGAGACATGGCACCCGTCA 479
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Db 422 TTCTGGTGAGAGGTGTTTCATAGCAGCGGTGGGCMAGCGGACATRTACCGGTCA 481
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OY 480 CTGTGGGTGGCAAGATAGTGGCTCTGTGTGCCATTTGGGGCTGTGACTATTTTCC 539
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Db 482 CCATCGGTGGAGATGCTGGGACGCTGTGCCCATCGCCGGGCTGTGACCATCGCRC 541
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OY 540 TGGCAGTGGCCGTCAT 555
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Db 542 TGGCCGTACCMGTAT 557
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 20, 2003, 06:36:10 ; Search time 326 seconds

(without alignments)  
3861.555 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-USER=US09804014.ecgn1.1.1.0 -tname\_10022003\_161447\_27185 -NCP=6 -ICP=3  
-NO\_XLPXY -NO\_MMAP -LARGEOUTER -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
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14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2918	100.0	1747	22	AA513338	Human cDNA encoding
2	2418	82.9	1792	24	AA513338	Human ion channel
3	2373	81.3	1686	23	AA578540	DNA encoding novel
4	2288.5	78.4	1361	24	ABE57038	Human potassium ch
5	2203	75.5	1598	16	AA704953	Mouse Kv1.7 volta
6	1495.5	51.3	3147	24	AB199654	Mouse ischaemic co
7	1447.5	49.6	2867	24	AB959856	Gene #2354 used to
8	1447.5	49.6	2867	24	AB65917	Lung cancer relate
9	1425	48.8	1836	22	AAH21452	Human Kv1.5 DNA.
10	1365.5	46.8	2237	23	AB113285	Drosophila melanog
11	1089.5	37.3	7642	24	AB133117	Human immune syste
12	1028	35.2	7642	24	AB133116	Human immune syste
13	1021.5	35.0	7488	24	AB133113	Human immune syste
14	1016.5	34.8	8758	24	AB133119	Human immune syste
15	1014	34.7	691	24	AAH28734	Human ion channel
16	1000.5	34.3	7488	24	AB133112	Human immune syste
17	950.5	32.6	7500	24	AB133114	Human immune syste
18	937	32.1	994	24	AB019702	Oligonucleotide fo
19	937	32.1	994	24	AB019703	Oligonucleotide fo
20	925	31.7	8758	24	AB133118	Human immune syste
21	911.5	31.2	994	24	AB019704	Oligonucleotide fo
22	911.5	31.2	994	24	AB019705	Oligonucleotide fo
23	901.5	30.9	7500	24	AB133115	Human immune syste
24	756.5	25.9	3424	20	AA211901	Human potassium ch
25	746.5	25.6	2157	22	AA529512	Human endocrine po
26	746.5	25.6	2159	23	ABK43428	DNA encoding novel
27	746.5	25.6	2711	22	AAH21246	Human Kv4.1 cDNA.
28	746	25.6	2578	22	AAH99538	Human protein enco
29	745	25.5	2578	23	AAH99538	
30	739.5	25.3	2578	23	AAH99538	
31	734.5	25.2	2578	24	AAH99538	
32	733	25.1	2578	23	AAH99538	
33	732.5	25.1	1927	20	AA211898	Human potassium ch
34	730	25.0	1927	24	AA211898	
35	728	24.9	2064	24	ABH84401	Human Kv4.3 potass
36	728	24.9	2121	24	ABH84400	Human Kv4.3 potass
37	725	24.8	2121	21		
38	722.5	24.8	2351	22	AAH21247	Human Kv4.2 cDNA.
39	721	24.7	2072	19	AAV61572	Human Kv potassiu
40	721	24.7	2104	19	AAV61571	Human Kv potassiu
41	718.5	24.6	1716	23	AB129811	Drosophila melanog
42	709	24.3	2104	19	AAV61573	Human Kv potassiu
43	696	23.9	3102	20	AA211905	Human potassium ch
44	669	22.9	3102	23	AA211905	
45	651.5	22.3	3102	24	AA211905	

## ALIGNMENTS

RESULT 1  
ID AA513338 standard; cDNA; 1747 BP.

AC AA513338;  
XX

DT 18-DEC-2001 (first entry)

DE Human cDNA encoding NOV4 protein.

XX Human: NOV4; ss; cytosolic; nontropic; neuroprotective; vulnary;

KW cerebroprotective; antiparkinsonian; hypotensive; antistimatic;

KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;

KW antitherosclerotic; dermatological; cancer; neurological disorder;

KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;

KW immune disorder; autoimmune disease; respiratory disorder;

KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;

cell growth regulation disorder; lesional psoriatic skin;

KM		atherosclerosis; abdominal aortic aneurysm.
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..37
FT	CDS	/tag= a 38..1717
FT		/tag= b
FT	3'UTR	/product= "NOVA"
FT		1718..1747
XX		/tag= c
PN	MO20016851-A2.	
XX		
PD	20-SEP-2001.	
XX		
PF	12-MAR-2001; 2001WO-US07735.	
XX		
PR	10-MAR-2000; 2000US-0188277.	
PR	10-MAR-2000; 2000US-0188316.	
PR	14-MAR-2000; 2000US-0189139.	
PR	14-MAR-2000; 2000US-0189140.	
PR	17-MAR-2000; 2000US-0190231.	
PR	17-MAR-2000; 2000US-0190401.	
PA	(CURA-) CURAGEN CORP.	
PI	Padigaru M, Vernet CAM, Fernandes E, Shinkets RA, Spederna SK;	
PI	Majumder K, Li L;	
DR	WPI: 2001-570869/64.	
XX	P-PSTDB: AAU08660.	
PT	Novel polypeptides and nucleic acids homologous to members of collagen,	
PT	potassium channel, tufellin family of proteins for diagnosing, treating,	
PT	cancer, atherosclerosis, neurological, skin and enamel defect disorders	
PT	-	
PS	Claim 9; Page 15-16; 128pp; English.	
XX		
CC	The invention relates to isolated NOVX (NOVX1-11) polypeptides and	
CC	the polynucleotides that encode them. NOVX polypeptides, polynucleotides	
CC	and anti-NOVX antibodies are useful for treating or preventing a	
CC	pathology associated with NOVX polypeptide in humans and for treating a	
CC	syndrome associated with human disease e.g. disorders characterised by	
CC	altered cell motility, proliferation and migration e.g. cancer,	
CC	angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.	
CC	episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's	
CC	disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,	
CC	asthma, hypertension and seizure (NOV4), enamel defects, such as	
CC	amelogenesis imperfecta and disorders involving enamel defects,	
CC	including hypoplasia and hypominerallisation (NOVS-7), paraneoplastic	
CC	neurological disorders, e.g. paraneoplastic limbic of brain-stem	
CC	encephalitis occurring during testicular cancer, diabetes, reproductive	
CC	health, metabolic and endocrine disorders, gastrointestinal disorders,	
CC	immune disorders and autoimmune diseases, respiratory disorders, bone	
CC	disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell	
CC	growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and	
CC	atherosclerosis, abdominal aortic aneurysm and neurological disorders	
CC	(NOV11). NOVX polypeptide is also useful for identifying an agent that	
CC	binds to it and a cell expressing NOVX polypeptide is useful for	
CC	identifying a therapeutic agent for use in treatment of a NOVX related	
CC	pathology. The antibodies and a polypeptide having 95 sequence identity	
CC	to NOVX polypeptide are useful for treating a pathological state in a	
CC	mammal. The present sequence encodes NOVA, a possible voltage gated	
CC	potassium channel.	
XX		
SQ	Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other:	
Alignment Scores:		
Pred. NO.:	6,93e-148	Length: 1747
Score:	2918.00	Matches: 559

[illegible]



QY	176	SeSLVGLYVAIAgLeuAArgGArgProAlaHisValProleuNsPValPheLeuGIuGIuVal	199
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QY	196	AlaPheTYrGIuLeuGIuValaAlaAlaAlaLeuAlaArgLeuArgGIuNsPGLuGIuGlyCysPro	215
Db	372	GCGTTCACGGGGCTGGGGGGCGGGCGCTGGACAGCGCTGGCGGAGCGAGGGCTCCGG	431
QY	216	ValProProGIuArgProLeuProArgArgAlaPheAlaArgGIuLeuThrPheLeuPhe	235
Db	432	GTGGCGCGCCGAGCCCGCCCGTCCCGCGGGCGCTTCGCCCGCGACGTGGTGGCTCTTTC	491
QY	236	GIuPheProGIuSerSerGIuAlaAlaArgValLeuAlaValaValaSerValLeuValIle	255
Db	492	GAGTTTCCCCGAGACCTTCAGCGCGCGGGCGGTGTGTGGCTAGCTCTCCGGCTGGTCATC	551
QY	256	LeuValSerIleValaValPheCysLeuGIuThrLeuProAspPheArgAspAspArgAsp	275
Db	552	CTCGTCTCCATCGTCTGCTTCTGTGGCTGGAGCGGTGTGTACTTCCTCCGACGAGCGCGAC	611
QY	276	GIuThrGIuLeuAlaAlaAlaAlaAlaAlaGIuProValPheProAlaProLeuNsngIy	295
Db	612	GGCAGCGGGGCTTGCTGTGGTCGACGGCGGACCGGGCGCG--TTCCCGCTCGGTGGAATGGC	668
QY	296	SerSerGIuMetProGIuAspProArgIleuProPheNsPProPhePheValaVal	315
Db	669	TTCAGCCAAATGCTGTGAATACCAACCCGGCTGCTTCATATACCGGTCTTCTGGTGGGr	728
QY	316	GIuThrLeuCysIleCysTrpPheSerPheGIuLeuLeuValArgLeuLeuValCysPro	335
Db	729	GAGACGCTGTATTGTGTGTCTCTTGTAGCTGTGTAGCGCTCGGTGTCTCCAT	788
QY	336	SerIysAlaAlaIlePhePheIysAsnValMetAsnLeuIleAspPheValaAlaIleLeuPro	355
Db	789	AGCAAGGCTATCTTCTTCAGAAAGGTATGATACCTCATCTATTTGTGGCTATCTCTCC	848
QY	356	TyrPheValaAlaLeuGIuYrThGIuLeuAlaArgGIuArgGIuGIuGIuGIuGIuGIuGIu	375
Db	849	TACTTTGTGGACAGTGGGACCGAGCTGGCGGGAGGAGGGGTGGCGCACGAGCCATG	908
QY	376	SerLeuAlaAlaIleLeuArgValaIleArgLeuValaArgValPheArgIlePheIysLeuSer	395
Db	909	TCACGGGCCATCGTGAAGTATCCGATGGTGGTGTCTTCCGCAATCTTCAAGCTGTCC	968
QY	396	ArgHisSerIysGIuLeuGIuIleLeuGIuGIuThrLeuArgAlaSerMetArgIuLeu	415
Db	969	CGGCACATCAAAAGGCGCTGCAAATCTTGGCGACAGCGCTTGGCGCTCCATAGCTGAGCTG	1024
QY	416	GlyLeuLeuIlePhePheLeuPheIleGIuValaValLeuPheSerSerAlaValIyrPhe	435
Db	1029	GGCCTCCCTCATCTTTTCTCTTCTTATGGTGGTGGCTCTTCTTCCAGCGCGCTTCACTTT	1088
QY	436	AlaGIuValaAspArgValaAspSerHisPheThrSerIleProGIuSerPheTrpAla	455
Db	1089	GCCGAAGTTGACGGGGTGGAGCTCCCATTTACATAGCATCCCTAAGTCTTCTGTGGGG	1144
QY	456	ValValThrMetThrThrValGIuTYrGIuYrGIuAspMetAlaProValaThrValGIuGIuIys	475
Db	1149	GTAGTCACACATGACTACAGTTGGCTATGAGACATGACGACCCCTCATCTGGTGGTGCAG	1204
QY	476	IleValGIuSerLeuCysAlaIleAlaGIuValLeuThrIleSerLeuProValaProVal	495
Db	1209	ATATGTGGGCTCTCTGTGTGGCATTGGCGGGGTGTGCTGCTATTTTCCCTGGCAGTGGCCGTG	1266
QY	496	IleValSerAsnPheSerTYrPheTYrHisArgGIuThrGIuGIuGIuGIuGIuGIuGIu	515
Db	1269	ATTGTCTCCAAATTTCACCTACTTTTATCACCGGGAGACAGAGGGCCAAAGAGGTGGGAAG	1324
QY	516	PheSerHisValaAspMetGIuProCysGIuProLeuGIuGIuIyusAlaNsngIyGIuLeu	535
Db	1329	TTTCAGCCATGTGGACATGAGCGCTTGTGGCCCACTGGAGGGCAAGGCCAATGGGGGGCTG	1388
QY	536	ValAspGIuGIuValaProGIuLeuProProLeuThrPAlaProProArgIuGIuHisLeu	555

Db	1389	GTGACGGGAGGACTGAGCTAGCTACCACTTCACCTCTGGGCAACCCCAAGGAAACACCTG	1448
QY	556	ValThrGluVal	559
Db	1449	GTCAACCGAAGTG	1460
RESULT 3			
AAST78540	ID	AAST78540 standard; cDNA; 1686 BP.	
XX	AC	AAST78540;	
XX	AA	AAST78540;	
XX	DT	13-FEB-2002 (first entry)	
XX	DE	DNA encoding novel human diagnostic protein #14344.	
XX	KW	Human: chromosome mapping; gene mapping; gene therapy; forensic;	
XX	KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.	
XX	OS	Homo sapiens.	
XX	PN	MO200175067-A2.	
XX	PD	11-OCT-2001.	
XX	PF	30-MAR-2001; 2001WO-US08631.	
XX	PR	31-MAR-2000; 2000US-0540217.	
XX	PR	23-AUG-2000; 2000US-0649167.	
XX	PA	(HYSE-) HYSED INC.	
XX	PI	Drmnac RT, Liu C, Tang YT;	
XX	DR	WPI: 2001-639362/73.	
XX	DR	P-PSDB: ABG14353.	
PT	PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	PT	responsible for genetic disorders or other traits and to assess	
PT	PT	biodiversity -	
PS	PS	Claim 1; SEQ ID No 14344; 103bp; English.	
XX	XX	The invention relates to isolated polynucleotide (I) and	
XX	XX	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
XX	XX	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
XX	XX	and gene mapping, and in recombinant production of (II). The	
XX	XX	polynucleotides are also used in diagnostics as expressed sequence tags	
XX	XX	for identifying expressed genes. (I) is useful in gene therapy techniques	
XX	XX	to restore normal activity of (II) or to treat disease states involving	
XX	XX	(II). (II) is useful for generating antibodies against it, detecting or	
XX	XX	quantitating a polypeptide in tissue, as molecular weight markers and as	
XX	XX	a food supplement. (II) and its binding partners are useful in medical	
XX	XX	imaging of sites expressing (II). (I) and (II) are useful for treating	
XX	XX	disorders involving aberrant protein expression or biological activity.	
XX	XX	The polypeptide and polynucleotide sequences have applications in	
XX	XX	diagnostics, forensics, gene mapping, identification of mutations	
XX	XX	responsible for genetic disorders or other traits to assess biodiversity	
XX	XX	and to produce other types of data and products dependent on DNA and	
XX	XX	amino acid sequences. AAS64197-AAS94564 represent novel human	
XX	XX	diagnostic coding sequences of the invention.	
XX	XX	Note: The sequence data for this patent did not appear in the printed	
XX	XX	specification, but was obtained in electronic format directly from WIPO	
XX	XX	at ftp.wipo.int/pub/published_pct_sequences.	
XX	XX	Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;	
Alignment Scores:			
Pred. No.:	1	03e-118	Length: 1686
Score:	2373.00	Matches: 484	
Percent Similarity:	89.80%	Conservative: 0	

Best Local Similarity: 89.80% Mismatches: 18  
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 US-09-804-014a-8 (1-559) x AAS78540 (1-1686)

19 ProGlyThrGlyLysAlaGlnSerArgArgArgArgArgGlyArgAlaGly 38  
 132 CCGGGAGCTGGG-----GCTGGAGATGCCCTT 158  
 39 ArgAlaSerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyAlaThr 58  
 159 GGAGGCTCGGACGTAGACA-----GAGAGAGCTGGGCTGTGA 197  
 59 ValPro---ProProSerArgProSerArgProAlaGlyLeu-PheTyrAlaArgThr 77  
 136 GGGCTCTCCATGAAAGCTTGGGTACCGCTCGCGGCTATTTTACGCGGACACC 257  
 77 GAsPThrGlyHisArgAlaGlyAlaA----- 86  
 258 GGACACCGGACACCGGGCTGGGGCGGCG- GCGGCGGCGGCGGACGCGGCGGCGGCGG 316  
 87 -----ValGlyAlaThrArgArgPheAlaGlyArgGlyCysAlaAr 101  
 317 CGCACCGGGCGCGGGCTGGGGCCACACGTGCGGTGCGGGTCCGCGGCGGTGCGCGG 376  
 101 gHisGlyAlaAlaValProAlaAlaProCysGlyCysGlyAlaArgLeuValLeuAsnVa 121  
 377-CCATGGAGCGCGGTGCGCGCG-CCGTGCGGCTGCTCGAGCGGCTGCTCAACGT 434  
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 141 uGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArgArgGlyTyrPhePheAs 161  
 495 AGGGAGCCAGCGCGCGCGCTTCTACAGACGCGCGCGCTATTTCTTCCA 554  
 161 pArgHisArgProSerPheAspAlaValLeuTyrTyrTrpGlnSerGlyArgLeuArg 181  
 555 CCGGACCGGCGCGCTTGCAGCGCGTGTCTACTACTACAGTCCGGTGGGGGTGGCG 614  
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 615 GCGGCGGCGCGACGTGGCGCTGCAGCTCTCTCGAAGAGGTGGCTTCTACGGGTGGG 674  
 201 yAlaAlaAlaLeuAlaArgLeuArgGlnAspGlnGlyCysProValProProGlnArgPr 221  
 675 CCGGCGGCGCTGGCAGCGCTCGCGAGGAGGAGGCTCCCGGTGCGCGCGAGCGGCC 734  
 221 oLeuProArgArgAlaPheAlaArgGlnLeuTyrLeuLeuPheGlnPheProGlnSerSe 241  
 735 CCGCGCGCGCGCGCTTGGCGCGAGCTGTGGCTTTTGCAGTTTCCGAGAGCTC 794  
 241 rGlnAlaAlaArgValLeuAlaValValSerValLeuValIleLeuValSerIleValVa 261  
 795 TAGGCGCGGCGCGCTGCTGGCGTACTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCT 854  
 261 lPheCysLeuGlnThrLeuProAspPheArgAspAspArgAspGlyTyrGlyLeuAla 281  
 855 CTTCCTGCTCGAGAGCTCTGACTTCGCGACGACGCGAGCGGAGCGGCTTCTCTCG 914  
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 915 TCGAGCGGAGCGGCGCG- -TTCCCGCTCGCTGAGATGGCTCCAGCAATGCTCTG 971  
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 972 AATTCACCGCGCGCTTCAATGACCGCTTCTCGGTGCTGCTGCTGCTGCTGCTGCTG 1031  
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 1032 TTGGTTCTCTTGTAGACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1091

341 eLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuG 361  
 1092 CAAGAACGTGATGACCTCATGCTATTTGTGGCTATCTCCCTACTTTGTGGCACTGGG 1151  
 361 yThrGlnLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMetSerLeuAlaIleLeuAr 381  
 1152 CACCGAGCTGGCCCGGACGAGGCGGTGGCGCAGCAGCGCATGTCTACTGGCATCTCTGAG 1211  
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 1212 AGTCATCCATGTGGTGGCTGCTCCGATCTTCAAGCTGTCCCGCACTCAAGGCGCT 1271  
 401 uGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgIleLeuGlyLeuLeuIlePhePh 421  
 1272 GCATATCTTGGCGGACACGCTTGGGCTCCATGCTGAGCTGGGCTCTCATCTTTT 1331  
 421 eLeuPheIleGlyValAlaLeuPheSerSerAlaValTyrPheAlaGlnValAspArgVa 441  
 1332 CCTCTCATCGGTGTGCTCTTTTCCAGCGCGCTCACTTTGCCGAGTTGACCGGCT 1391  
 441 lAspSerHisPheThrSerIleProGlnSerPheTrpTyrAlaValAlaThrMetThrTh 461  
 1392 GGACTCCCATTCATCAGCATCTGATCTTGTGCTGGTGGCGGTGATCACCATGACTAC 1451  
 461 rValGlyTyrGlyAspMetAlaProValThrValGlyGlyLysIleValGlySerLeuCy 481  
 1452 AGTTGGCTATGGAGCATGGACCCCTCACTGTGGGTGGCAAGATGTGGGCTCTGTGG 1511  
 481 sAlaIleAlaGlyValLeuThrIleSerLeuProValProValIleValSerAsnPheSe 501  
 1512 TGGCATTTGGGGGTGCTGCTATTTCCGTGCGAGTGGCCGCTCATTTGCTCCAAATTGAG 1571  
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 1572 CTACTTTTATACCGGAGACAGAGGCGAGAGGCTGGAGATTTCAGCATGTGGACAT 1631  
 521 tGlnProCysGlyProLeuGlnGlyLysAlaAsnGlyGlyLeuValAspGlyGlu 539  
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RESULT 4  
 ABL57038  
 ID ABL57038 standard; cDNA: 1341 BP.  
 AC ABL57038;  
 XX  
 DT 22-JUL-2002 (first entry)  
 XX  
 DE Human potassium channel 12189 partial cDNA.  
 XX  
 KW Potassium channel; ion transport; 12189; nootropic; anticonvulsant;  
 KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;  
 KW antidepressant; antianemic; tranquilizer; anorectic; antimigraine;  
 KW antiarteriosclerotic; vasotropic; vulnerability; antiarrhythmic;  
 KW cardiant; antiinflammatory; cytoskeletal; osteopathic; hepatotropic;  
 KW antidiabetic; immunosuppressive; antiarthritic; antirheumatic;  
 KW antipsoriatic; antilyroid; antilucer; dermatological; antihaemic;  
 KW antisthmatic; antiallergic; ophthalmological; immunomodulator;  
 KW analgesic; virucide; human; gene therapy; gene; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 FH Key location/Qualifiers  
 FT 1..1341  
 FT CDS /tag= a  
 FT /product= "12189"  
 FT /partial  
 FT /note= "The CDS does not include a start codon"  
 PN WO200194390-A2.  
 XX  
 PD 13-DEC-2001.



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|||||
Db 958 GTCCTACTTGCCGAGATTGACCGGTGGAGTCCCATTTACATGACATCCCTGAGTCTTC 1017
QY 453 TTTPTTAlaValValThrmethrThrValGlyTyrGlyAspMetAlaProValThrVal 472
Db 1018 TGTGTGGCGGTGATGCACATGACTACAGTTGGTATGAGACATGGCACCCGCTACCTGTG 1077
QY 473 GLYGLYLeuValLeuValSerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuPro 492
Db 1078 GGTGGCAAAATAGTGGGCTCTCTGTGTGCCATTGGCGGCTGTGACTATTCTCGCCA 1137
QY 493 ValProValIleValSerAspPheSerTyrPheTyrHisArgGluThrGluGluGlu 512
Db 1138 GTGCCCGTCATGTCTCCCAATTTACACTATTATTATCACCGGAGACAGAGGCGCAAG 1197
QY 513 AlaGlyMetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyAlaAsn 532
Db 1198 GCTGGATGTTCAGCATGTGACATGACACCTGTGGCCACTGGAGGCAAGGCCAAT 1257
QY 533 GlyGlyLeuValAspGlyLeuValProGluLeuProProLeuThrPalaProProArg 552
Db 1258 GGGGGCTGTGTGACGGGAGGAGTACTGAGCTACCACTCCACTGTGGCACCACCCAGG 1317
QY 553 GluHisLeuValThrGluVal 559
Db 1318 AACACCTGCTCACCGAAGTG 1338

RESULT 5
AAT04953
ID AAT04953 standard; cDNA; 1598 BP.
XX
AC AAT04953;
XX
DT 11-APR-1996 (first entry)
XX
DE Mouse Kv1.7 voltage-gated potassium channel coding sequence.
XX
KW Mouse Kv1.7 voltage-gated potassium channel;
KW Insulin antagonist drug screening; Insulin agonist drug screening;
KW non-insulin-dependent diabetes mellitus; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..1598
FT /tag=a
FT /note="specification states sequence is 1599.
FT Incomplete stop codon given"
XX
PN W09523858-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02221.
XX
PR 10-AUG-1994; 94US-0288405.
PR 04-MAR-1994; 94US-0207401.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chandy G, Chandy KG, Gutman GA, Kaiman K;
XX
DR WPI: 1995-320573/41.
DR P-PSDB; AAR82937.
XX
PT New voltage-gated potassium channel gene - used to identify
PT material(s) which can increase insulin release e.g. for treating
PT non-insulin dependent diabetes mellitus.
XX
PS Claim 1: Page 22-23; 38pp; English.
XX
CC The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-
CC gated potassium channel. It may be used in drug screening for

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CC identification of therapeutics which modulate the channel and,
CC therefore, modulate insulin secretion. Selective antagonists
CC increase insulin release and thereby reduce hyperglycaemia
CC associated with non-insulin-dependent diabetes mellitus.
XX
SQ Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;
Alignment Scores:
Pred. No.: 1,24e-109 Length: 1598
Score: 2203.00 Matches: 452
Percent Similarity: 84.93% Conservative: 10
Best Local Similarity: 83.09% Mismatches: 61
Query Match: 75.50% Indels: 22
DB: Gaps: 8
US-09-804-014a-8 (1-559) x AAT04953 (1-1598)
QY 22 GLYLYSAlaGlnSerArgArgArgArgArgGlyArgAlaGlyArgAlaSer 41
Db 11 GGGAAAGCTCAAGAGATCCACGGAAAGCGCGGTGGCAGTGTTCACAGGTGGAA 70
QY 42 ArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValProPro 61
Db 71 CGCGACAGGCGCG-----CCCTTAGC-CCGCGGGGGTAAACACCGCCCTT 114
QY 62 ProSerArgProSerArgProAlaGlyLeuPheTyrAla-----Arg 75
Db 115 CCCCCGCGCCCTGGCCGG-----ACTTTCATGCTATTTTTTCACCGCCGACACCGG 165
QY 76 ThrProAspThrGlyHisArgAlaGlyAlaAlaValAlaGlyAlaThrArgArgPheAlaGly 95
Db 166 ACACCCGACAGTGGGGT-----GGCTGGGGGTGGGGGCGACAGCTCCGTCACCGGT 216
QY 96 ArgArgGlyCysAlaArgHisGlyAlaAlaValAlaProAlaAlaProCysGlyCysGlu 115
Db 217 CGCCCGGCGTGTGCGGCCATGAGCCACGCTGCCGCCGCC-----CTGCGCTCTCGAG 273
QY 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
Db 274 CGGCTGTGCTCAACGTTGGCGGGGTGGCTTGCTTGACAGACCGCGCGACGCTCGCGCG 333
QY 136 PheProAspThrLeuLeuGluGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArg 155
Db 334 TTCGCGGACACGCTGCGTGGGGGACCCGCGTGGCGGACCGCGCTTCAACAGCGCGGGCGG 393
QY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
Db 394 GCCGAGATTCTTTCGACACGACCGGCCGACGCTTGATGCGGTCTCTACTACAG 453
QY 176 SerGlyArgArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluVal 195
Db 454 TCGGGGCGCGGCTGAGACGCGCGGACGTCCTCCATCCTTCCGTGGAGAGGTG 513
QY 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysPro 215
Db 514 TCTTTCACGGGGCTGGGG---CGGCGGCTGGCGGCTGGCGGAGAGAGCGGCTCGCGG 570
QY 216 ValProProGluArgProLeuProArgAlaPheAlaArgGluLeuThrLeuLeuPhe 235
Db 571 GTC---GCCGAGCGCGCGCTGCC---CCGCCCTTGGCGGCTGAGCTGAGCTCTTC 624
QY 236 GluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSerValLeuValIle 255
Db 625 GAATTCCTGAGAGCTGCGAGGCTGGCGGCTGCTGCGCTGCTCCGACTGCTGATC 684
QY 256 LeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspAspArgAsp 275
Db 685 CTGGTCCCATGCTGGTCTTTGCTTCGACACACTGCAACACTTCCGCGACGACCGGAT 744
QY 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295
Db 745 GACCCGCGGCTCGCGCGGTAGCGGCTGACTGCTGCTCTGCTCGCTCGGCTCAATGCG 804

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Query Match: 49.61% Indels: 107  
 DB: 24 Gaps: 20  
 US-09-804-014a-8 (1-559) x ABN95856 (1-2867)

QY 2 GUAArgArGArGThrGlySerArg-----ArgGlnLysAspGlyGlnLysGly 17  
 DB 34 GAGAGGCGAGAGAGCGAGCGGCTTCTGACCTCAGGGCCAGGCGAGGGATGCCCGC 93  
 QY 18 Asp-----ProGlyThrGlyLysAlaGln-----Ser 26  
 DB 94 CAGCAACCCACGCTCTCCACAGAGAGGCGCGCGAGCTGGAGAGGAGACCTGACGCC 153  
 QY 27 ArgArgGlyArgArgArgArgGlyArgAlaGlyArg---AlaSerArgGlnArgAla 45  
 DB 154 AGGGGCGCGGAGAGCGTGAAGAGGGCGCGGAGCGGCTGAGTGGGGCGACATGCC 213  
 QY 46 -----ArgGlyArgProValAlaLeuArgProAla-GlyValThrValProProPr 62  
 DB 214 CTCTGCTCCGCGCATGAGAGATCGCTGCTGCTGGAGAACGGCGGCTCATGACC 273  
 QY 62 oSer-----ArgProSerArgProAlaGlyLeuPheThrValaArgThrProAs 78  
 DB 274 GTCAGAGAGAGCGCATGAGGCCCGGCGAGCTGCCGACAGGCCACAGGGGAGAGCTCCAG 333  
 QY 78 pThrGlnHisArgAlaGlyAlaAlaVal-----GlyAlaTh 90  
 DB 334 TGTCCCCGACGGCTGGGCTCAGCATGAGGCCCAAGAGCGGGCGCCAAAGGGCGCGGC 393  
 QY 90 rArgArgPheAlaGlyArgArgGlyCys----- 99  
 DB 394 GCGCAGAGAGACGGGAGCTGGGAGTGGCGCTTGGCTCCGCTGCCGACCCGGAGTG 453  
 QY 100 -----Al 100  
 DB 454 CGGCGCTTGGCTCCGCTGCCAGAGAGACTGCCAGGCGCTCGAGCGCGCCCTCCGAGAGC 513  
 QY 100 aArgHisGlyAlaAlaValProAla-----Al 109  
 DB 514 GAGAGAGAAAGAGCGATCCCGCTGGGACGCGTGGAGACACAGGCTTGGGACAGCG 573  
 QY 109 aProGlyGlyCysGlyArgLeuValLeuAsnValAlaGlyLeuArgPheGlnThrAr 129  
 DB 574 TCCCTGG---ACCAC-CAGGCGCTCCACATCATCTCCGCTTGGAGCGCA 629  
 QY 129 gAlaArgThrLeuGlyArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyAr 149  
 DB 630 GCTGGGACACCCAGGCGAGTTCACCAACACATCTCTGGGGACCCGCCCAAGCGCTGCC 689  
 QY 149 gPheTyrAspAspAlaArgArgGlyArgPhePheAspArgHisArgProSerPheAspAl 169  
 DB 690 GTACTTGCACCCCTGAGGAACGAGTACTTCTTGCACCGCAACGCGCCAGCTTCGACGG 749  
 QY 169 aValLeuTyrTyrGlnSerGlyArgLeuArgArgProAlaHisValProLeuAs 189  
 DB 750 TATCTCTACTACTACAGTCCGGGGCGCTCGGAGGCGCGTCAACGCTTCCCTGGA 809  
 QY 189 pValPheLeuGlnGluValAlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuAr 209  
 DB 810 CGGTTCGGGAGAGAGTACGCTTCTACAGCTGGGGAGAGCCATGGAGCGCTTCGG 869  
 QY 209 gGluAspGlnGlyCysProValProProGluArgProLeuProArgArgAlaAlaAr 229  
 DB 870 CGAGGATGAGGCGTTCATTAAGAAAGAGAGAGGCCCTGCTCGCAACGAGTTCACGG 929  
 QY 229 gGlnLeuThrLeuLeuPheGlnPheProGluSerSerGlnAlaAlaArgValLeuAlaVa 249  
 DB 930 CCAGGTGTGGCTTATCTTCAGATACCGGAGAGCTTGGGCGCGGCGGCATCGGCAT 989  
 QY 249 lAlaSerValLeuValLeuValSerIleValValPheCysLeuGlnThrLeuProAs 269  
 DB 990 CGTCTCGGCTTGTGTTATCTCTCATCTCATCATCCTTCTGCTTGGAGACCTCTGCTGA 1049

QY 269 pPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaGlyProValPh 289  
 DB 1050 GTTCAGGATGAAGACGTGCTCCGCCACACCTCCGCGCCGCCAGCCAGCTCCCGCG-- 1107  
 QY 289 eProAlaPro---LeuAsnGlySerSerGlnMet-----ProGlyAsnPro----- 303  
 DB 1108 -CCGCGCCCTGGGGCCACAGCGAGCGGGGTATGGCCCCCGCTCTGGCCCTACGGTGGC 1166  
 QY 304 -ProArgLeuPro-----PheAsnAspProPhePheValValGlnThrLeuCysIleCy 321  
 DB 1167 ACCGCTCTCTGCCAGAGACCTCGGCGACCCCTTCTATCTGTGAGACACAGTGGCTCAT 1226  
 QY 321 sTrpPheSerPheGlnLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePh 341  
 DB 1227 CTGGTTCACCTTCAGAGCTGCTCGCGCTTCTTCCCTGCCCGCCAGAGGACAGGTTCTC 1286  
 QY 341 eLysAsnValMetAsnLeuLeuAspPheValAlaIleLeuProThrPheValAlaLeuGl 361  
 DB 1287 CCGGACATCATGAAACATCATGATGTGGCCATCTTCCCTCACTTCATCAACCTGGG 1346  
 QY 361 yThrGlnLeuAlaArgGlnArg-----GlyValGlyGlnGlnAl 374  
 DB 1347 CACCGAATGAGAGAGAGAGAGAGGCGGAGAGAGGCGCCAGAAATGGGACAGAGGC 1406  
 QY 374 aMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLe 394  
 DB 1407 CATGTCCCTGGCCATCTCCGAGATCATCCCTGCTGCGGGTGTTCGCGATCTTCAAGCT 1466  
 QY 394 uSerArgHisSerLysGlyLeuGlnIleLeuGlnThrLeuArgGlnAspMetArgI 414  
 DB 1467 CTCCCGCACCTCCAAAGGGGTGAGATCTGGGAAACCTTGACAGGCTTCATGAGGGA 1526  
 QY 414 uLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTy 434  
 DB 1527 GCTGGGCTGCTCATCTTCTTCTTCTCATCGGGGTATCTCTTCCAGTGGCGCTA 1586  
 QY 434 rPheAlaGlnValAspArgValAspSerHisPheThrSerIleProGluSerPheThrPT 454  
 DB 1587 CTTCGAGAGGCTGCAACACAGAGGACCAATTTCTCTAGACCTTCCCTGCTTGTGTG 1646  
 QY 454 pAlaValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGl 474  
 DB 1647 GCGAGGTGTCACCATGACCACTGTGGCTACGGGACATGAGGCCATCATCTGTGGGG 1706  
 QY 474 yLysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPr 494  
 DB 1707 CAAGATGTGGGCGCTGATGTGTCATCGCGGGGTCTCACATTCCTCGCTGCGC 1766  
 QY 494 oValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGlnGlyGlnAlaGl 514  
 DB 1767 CGTCATGCTGTCCAACTTCACTTCTTACACCGGGAAACGGATCAGAGAGAGCGCGC 1826  
 QY 514 yMetPheSerHis-----ValAspMetGlnProCysGly-----Pr 526  
 DB 1827 AGTCTTAAAGAGAGAGAGGACACTCAGAGCCAGGG- GCCGGGCTGAGACAGAGAGTCC 1885  
 QY 526 oLeuGlnGlyLysIleAsnGlyLeuVal-----AspGlyLysVal 540  
 DB 1886 AGCGAAGAGTACAGGAGAGGAGATCTTCTTCAAGCTGGGGGAGACCTTGAGAAATG 1945  
 QY 540 lProGlnLeuProProProLeuThrPalapProProArgGlu 553  
 DB 1946 CAGACAGTGCCTCGAAGGG---CAGCTGCCCTTGAAGAA 1982

RESULT 8  
 ABL65917  
 ID ABL65917 standard; DNA: 2867 BP.  
 XX ABL65917;  
 AC ABL65917;  
 XX  
 DT 15-MAY-2002 (first entry)  
 XX Lung cancer related gene sequence SEQ ID NO:4254.



Db 690 GTACTTGACCCCTGAGAGACGACTTCTTGACCCGACCCGCGCACTTCAGCG 749  
 Qy 169 aValLeuTyrTyrGlnSerGlyGlyArgLeuArgProAlaHisValProLeuAs 189  
 Db 750 TATCCTTACTACTACAGTCCGGGGCGCGCTCGGAGCGCGGTCAACGCTCCCGA 809  
 Qy 189 pValPheLeuGluValAlaPheTyrGlyLeuGlyAlaAlaLeuAlaArgLeuAr 209  
 Db 810 CGTCTTCGCGACGATACGCTTCTACACAGCTGGGGAGAGCCATGTGAGCCCTTCG 869  
 Qy 209 gGluAspGluGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaAr 229  
 Db 870 CGAGAGTGAAGGGCTTCACTTAAGAAGAGAGAACCCCTGCTCCGCAACAGATTCCAGCG 929  
 Qy 229 gGlnLeuTyrLeuLeuPheGluPheProGluSerSerGlnAlaAlaAlaArgValLeuAlaVa 249  
 Db 930 CCAGCTGTGGCTTATCTTCGATATCCGAGAGCTCGGGGCCCGGGGCGCATCGGCAT 989  
 Qy 249 lValSerValLeuValIleLeuValSerIleValValPheCysLeuGluThrLeuProAs 269  
 Db 990 CGTCTCGCTGTGTATCTCATCTCATCTCATCTGCTGCTGGAGAGACCTGCTGA 1049  
 Qy 269 pPheArgAspArgArgpGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPhe 289  
 Db 1050 GTTCAGGAGATGACGTAGCTGCTCCGCCACCTCCGCGCCGCCACCAAGCTCCCGCG 1107  
 Qy 289 eProAlaPro---LeuAsnGlySerSerGlnMet-----ProGlyAsnPro----- 303  
 Db 1108 -CCGCGCCCTGGGGCCCAAGCGAGCGGGGTCATGCGCCCGCTGCTGGCCCTACAGTGCG 1166  
 Qy 304 -ProArgLeuPro-----PheAsnAspProPhePheValValGluThrLeuGlyIleCy 321  
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 Db 1227 CTGTTACCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286  
 Qy 341 eLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuG 361  
 Db 1287 CCGGACATCATGAACTCATCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1346  
 Qy 361 yThrGluLeuAlaArgGlnArg-----GlyValGlyGlnGlnAla 374  
 Db 1347 CACCGAAGCTGAGACAGACGAGCGGCGGAGAGCGCGGCGAGATGAGGCGAGCGAGCG 1406  
 Qy 374 aMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePhePhe 394  
 Db 1407 CATGTCCTGCGCATCTCCGAGTCAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466  
 Qy 394 uSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArg 414  
 Db 1467 CTCGCGGCACTCCAGAGGGGTGCGAGATCCGAGGCAACACTTGAGAGCGCTCCATGAGGA 1526  
 Qy 414 uLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaVal 434  
 Db 1527 GCTGGGGCTCTCATCTTCTCTCTCATCTGAGGATCATCTCTCTCTCTCTCTCTCTCTCT 1586  
 Qy 434 rPheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPhePhe 454  
 Db 1587 CTTCGCGAGAGCTGACCAACGAGGAGCACTTCTTAGACATCCCTGAGCTCTGCTGCTG 1646  
 Qy 454 pAlaValAlaThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGly 474  
 Db 1647 GGCAGTGTGATACCATGACACTGTGGGCTACGGGAGCATAGGCCCATCTGTGGGGG 1706  
 Qy 474 yLysIleValGlySerLeuGlySerLeuAlaIleAlaGlyValLeuThrIleSerLeuProVal 494  
 Db 1707 CAAGATCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1766  
 Qy 494 oValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGluValAla 514  
 Db 1767 CGTCACTGCTCTCAACTTCACTTCTTACACCGGGAAACGAGATCAGAGAGCGCGCG 1826

Qy 514 yMetPheSerHis-----ValAspMetGlnProCysGly-----Pr 526  
 Db 1827 AGTCTTAAGAGAGACAGGCGACTCAGAGCCAGG--CGCGGGCTGAGACAGAGACTCC 1885  
 Qy 526 oLeuGluGlyLysAlaAsnGlyLeuVal-----AspGlyGluVal 540  
 Db 1886 AGCGAAGGTCTAGGAGGAGGAGGATCTTGTCAAGCTGGGGGAGCCCTGGAGAATG 1945  
 Qy 540 lProGluLeuProProProLeuTyrPalaProProArgGlu 553  
 Db 1946 CAGACAGTGCCTCGAAGGG---CAGCTGCCCCCTAGAGAA 1982  
 RESULT 9  
 AAH21452  
 ID AAH21452 standard; DNA; 1836 BP.  
 AC  
 XX  
 XX  
 DT 18-SEP-2001 (first entry)  
 XX  
 DE Human Kvl.5 DNA.  
 XX  
 KW Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;  
 KM activator; ds.  
 XX  
 OS Homo sapiens.  
 PN WO200151519-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 05-JAN-2001; 2001MO-EP00055.  
 PR 11-JAN-2000; 2000DE-1000651.  
 XX  
 PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
 XX  
 PI Leberer E, Leeuw T, Ritscher A;  
 PT WPI; 2001-442137/47.  
 DR  
 XX  
 XX  
 PT Identifying inhibitors and activators of eukaryotic potassium channels,  
 PT for use as pharmaceuticals, comprises using yeast cells that express  
 PT heterologous, but no endogenous, potassium channels  
 PS Disclosure; Page 45-46; 78pp; German.  
 XX  
 CC This sequence represents a novel method for identifying inhibitors or  
 CC activators (A) of a eukaryotic potassium channel (KC) by applying a test  
 CC compound to a mutant *Saccharomyces cerevisiae* cell in which: (1) the  
 CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (11) a  
 CC eukaryotic KC is expressed heterologously, where the effect of the  
 CC compound on the eukaryotic KC is then determined. The method is used to  
 CC identify inhibitors or activators (A) of a eukaryotic potassium channel.  
 CC (A) are potentially useful as pharmaceuticals. The method is easily  
 CC automated for parallel processing of many samples, using either different  
 CC concentrations of test compounds and/or different levels of heterologous  
 CC gene expression. It allows identification of compounds that inhibit human  
 CC KC selectively. This sequence represents the human Kvl.5 encoding DNA  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 6, 61e-68 Length: 1836  
 Score: 1425.00 Matches: 323  
 Percent Similarity: 64.81% Conservative: 60  
 Best Local Similarity: 54.65% Mismatches: 146  
 Query Match: 48, 83% Indels: 65  
 DB: 22 Gaps: 15  
 US-09-804-014A-8 (1-559) x AAH21452 (1-1836)

QY	2	GIUARGARGARGHrGtGySerATGARGlnLYSAspGLYlnLYSGly-----	17
Db	48	CAGAGAGGGGAAATGAGAGCCGGGACGGCTGCGGCCAGGGCCACAGGGGAGAGCTTCAGTG	107
QY	18	---AspProGlyThrGlyLysAlaGlnSerATGATGCGlyATGATGATGATGATGATG	36
Db	108	TCCCCCAGCGGCTG-GGCTACGAGATGGGCCCAAGAGACCGGCGCCAAAGGGGGCGCGC	166
QY	37	AlaGlyArgLaseArgGlnATGATGATGATGATGATGATGATGATGATGATGATGATGATG	56
Db	167	-----AGAGAGACGGGAGACTCGGAGTGGGGCCCTGGCTCGCTCGGTCGGCGGAC--CCGGGA	219
QY	57	ValThrValProProPro-----SerATGProSerATGProAlaGlyLeu	71
Db	220	GTGGGGCCCTGGCTCGCTCGCTCGGACGAGAGCTGCCAGCGGCTGACGGCGGCT-----	273
QY	72	PheTyzAlaArgThrProAspThrGlnHisATGAlaGlyAlaAlaAlaGlyAlaThrArg	91
Db	274	-----CCGAGAGACGAGAGAGAAAGAGATCCGGGCTGGGCGACGGTGGAG	321
QY	92	ArgPheAlaGlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaLaProLaProCys	111
Db	322	GACGAGGCTGTGGGACGCGGCTCTCGACAC-----	354
QY	112	GlyCysGlyGlnArgLeuValLeuAsnValAlaGlyLeuArgPheGlnThrArgAlaArg	131
Db	355	-----CAGCGCTCCATCAACATCACTCGGGCTCGCTTGAAGAGCGAGCTGGGC	405
QY	132	ThrLeuGlyArgPheProAspThrThrLeuGlyAspProAlaArgATGATGATGATGATG	151
Db	406	ACCTCGCGGAGATGTCCTCCACACATCTCGGGGAGACCCGCGCAAGCTGGCTGGCTGATTC	465
QY	152	AspAspAlaArgArgGlyArgPhePheAspArgHisATGProSerPheAspAlaValLeu	171
Db	466	GACCCCTGAGGAACGAGTACTTTCGACCGCAACGCGCCAGCTTGACGATGATCTC	525
QY	172	TyTyrTyTyrGlnSerGlyGlyArgLeuATGATGATGATGATGATGATGATGATGATGATG	191
Db	526	TACTACTACAGTCCGGGGCGCGCTG---CGAGGGGTCAACTGCTCCCTGAGCTGTC	582
QY	192	LeuGlnGlnValAlaPheTyTyrGlyLeuGlyAlaAlaAlaAlaAlaArgLeuArgGlnAsp	211
Db	583	CGCGAGAGATACGCTTATCCAGCGTGGGAGACGAGCACTGATGACGCTTCGCGAGAT	642
QY	212	GlnGlyCysProValProProGlnATGATGATGATGATGATGATGATGATGATGATGATG	231
Db	643	GAGGGCTTACTTAAGAAG	702
QY	232	TrpLeuLeuPheGlnPheProGlnSerSerGlnAlaAlaAlaArgValLeuAlaValSer	251
Db	703	TGGCTTATCTTCAGATATCCGGAGACTGTGGGTCCGCGCGGACATGGCTATCGTCTCG	762
QY	252	ValLeuValLeuValSerLeuValPheCysLeuGlnThrLeuProAspPheArg	271
Db	763	GTCTTGATTACTCATCTCATCTCATCTCTGCTTGGAACCTGCTGATGATTCAGG	822
QY	272	AspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaAlaGlyProValPheProAla	291
Db	823	GATGAACGTAGCTGCTCGCACCTCGGGGCCCCACACACATCCCGCG---CCGCGC	879
QY	292	Pro---LeuAsnGlySerSerGlnMet-----ProGlyAsnProProArg	305
Db	880	CTGTGGGCGCACGACGGGATCATGGGCCCCCGCTGTGGGCTTACGATGGACACGCTC	939
QY	306	LeuPro-----PheAsnAspProPhePheValValGlnThrLeuCysIleCysTrpPhe	323
Db	940	CTGCGCAGAGACCTCGGCGACACCTCTTCACTGATGATGATGATGATGATGATGATGATG	999
QY	324	SerPheGlnLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsn	343
Db	1000	ACCTTTCAGGTGCTCGGCTTCTTCGCTTGGCCCCAGAGAGAGAGGATCTCCCGGAGAC	1058

QY	344	ValLeu1snLeu1leAspPheValAla1leLeuProTyPheValAlaLeuGlyThrc1u	363
Db	1060	ATCATGAACATCATCATGATGTGTGGCCATCTTCCCTACTTATCACTCCCTGGGACCCGAA	1119
QY	364	LeuAlaArg1naArg-----GlyValG1yGlnGlnAlaMetSer	376
Db	1120	CTGGCAGAGCAGGACGCCAGAGGGGGCGGAGAGGGCGCCACAAATGGGACAGGACCATGTGCC	1179
QY	377	LeuAla1leLeuArgVal1leArgLeuValArgValPheArg1lePheLysLeuSerArg	396
Db	1180	CTGGGCATCTCCCGAGTCATCCCGCTGTGTCGGGTCTCCGATCTTCAAGCTCTCCGCC	1239
QY	397	HisSerLysG1yLeuGln1leLeuGlyGlnThrLeuArgAlaSerMetArgG1uLeuGly	416
Db	1240	CACCTCAAGGGGGCTGCAGATCCCTGGGCAAGACCTTGCACAGCCCTCATGAGGAGCTGGGG	1299
QY	417	LeuLeu1lePhePheLeuPhe1leGlyVal1leuPheSerSerAlaValTyPheAla	436
Db	1300	CTGGCATCTTCTCTTCCTTTCATGGGGGTATCTCTTCTCAAGTACGCTGCTACTTCCGA	1359
QY	437	GluValAlaPargValaAspSerHisPheThSer1leProGluSerPheTyTPAlaVal	456
Db	1360	GAGGCTGACCAACCGAGGGAACCCATTTCTGTACATCCCTGACGAGCCTTCTGGTGGGCACTG	1419
QY	457	ValThrMetThrThrValG1yTyrg1yAspMetAlaProValThrValG1yG1yLys1le	476
Db	1420	GTCACCATGACCATGTGGGGCTACAGGGGACATGAGGCCCATCATGCTTGGGGGCAAGATC	1479
QY	477	ValG1ySerLeuGlyAla1leAlaG1yValLeuThr1leSerLeuProValProAla1le	496
Db	1480	GTTGGCTGCTGCTGTGTGCATTCGCGGGGGTCTTACCATTTGCCCTGCTGTGGCCCTATC	1539
QY	497	ValSerAsnPheSerTyrrPheTyrHisArgG1uThG1uG1yG1uAlaG1yMetPhe	516
Db	1540	GTCCTCAACTTCACACTCTCTTACACACCGGAGAACGATCAGAGAGAGCGGCACTCCTT	1599
QY	517	SerHis-----ValAspMetGlnProCysGly-----ProLeuGlu	528
Db	1600	AAGGACAGCAGGGCCTCTCAGAGCCAGAGG-GCCGGGGCTGGACAGAGCATGTCACGCGAA	1658
QY	529	GlyLysAlaAsnG1yG1yLeuVal-----AspG1yGluValProGlu	542
Db	1659	GGTCAAGCGGAGCAGGGGATCTTCTGCAGAGCTGGGGGACCTGTGAGAAATGCAGACAG	1718
QY	543	LeuProProPheLeuTyTPAlaProProArgGlu	553
Db	1719	TGCCCGAAGGGG---CAGCTGCCCCCTAGAGAA	1748
RESULT 10			
ABL13285	ID	ABL13285 standard; cDNA; 2237 BP.	
XX	XX	ABL13285;	
XX	XX	26-MAR-2002 (first entry)	
XX	XX	Drosophila melanogaster expressed polynucleotide SEQ ID NO 34337.	
XX	XX	Drosophila; developmental biology; cell signalling; insecticide;	
XX	XX	Pharmaceutical; gene; ss.	
XX	OS	Drosophila melanogaster.	
XX	PN	WO200171042-A2.	
XX	PD	27-SEP-2001.	
XX	PF	23-MAR-2001; 2001WO-US09231.	
XX	PR	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
XX	PA	(PEKE ) PE CORP NY.	

XX Venter JC, Adams M, Li PMD, Myers EM;  
XX WPI: 2001-656860/75.  
DR P-PSDB: ABB69182.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Claim 1; SEQ ID NO 34337; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from *Drosophila*. The invention  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB161716-AB130511), expressed DNA  
CC sequences (AB101840-AB161575) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, was obtained in electronic format directly from WIGO  
CC at ftp.wigo.int/pub/published\_pcr\_sequences.  
XX  
XX Sequence 2237 BP: 679 A; 477 C; 518 G; 563 T; 0 other; .  
SQ

Alignment Scores:

Pred. No.:	1,23e-64	Length:	223
Score:	1365.50	Matches:	294
Percent Similarity:	67.77%	Conservative:	55
Best Local Similarity:	57.09%	Mismatches:	99
Query Match:	46.80%	Indels:	67
DB:	23	Gaps:	9

US-09-804-014A-8 (1-559) X ABL13285 (1-2237)

Oy	30	ArgrArgrArgrArgrGlyAlaArgAlaGlyAlaArgAlaSerArgAlaArgAlaArgAlaArgPro	43
Db	222	CAGAGACGGACACAAACAGACAGAGGAGAGA--CGGAGACAGAGACGGAGG-----	269
Oy	50	ValAlaLeuArGProAlaGlyValThrValProProProSerArGProSerArGProAla	69
Db	269	-----	269
Oy	70	GlyLeuPheTyrAlaArgThrProAspThrGlyHisArg-AlaGlyAlaAlaValGlyAl	89
Db	270	-----GCTTTGGCCCAAAATGACAGACGTCAAGACGAGAGAGGGGGGGCTGTCATGGC--	321
Oy	89	aThrArGArGArGheAlaGlyArGArGglyCysAlaArgHisGlyAlaAlaValProAlaAl	109
Db	322	-----TTGGTGCGCGCA-----CCGCAACACTTTGAAACCCATCTCT--CA	359
Oy	109	aProCysGlyCysGlyuArGlyLeuValLeuAsnValAlaGlyLeuArGArgheGlyThrAr	129
Db	360	CGATCATGATTTCTGCGCAAGACGCGTATTAATATGTAAGCGGATTAAGGTTTATGACACA	419
Oy	129	gAlaArGThrLeuGlyArGArgPheProAspThrLeuLeuGlyAspProAlaArGArGlyAr	149
Db	420	ACTACGTACGTTAAATCATTCATCCCGGACACCGCTCTTGGGGGATCCAGCTCGGAGATTACG	479
Oy	149	gPheTyrAspAspAlaArGArGlyuTyrPhePheAspArgHisArgProSerPheAspAl	169
Db	480	GTACTTTGACCCGCTTAGAAATGAATTTTTTTTGACCGTAATGACGAGCGAGCTTCGATGC	539
Oy	169	aValLeuTyrTrTyrTrGlnSerGlyGlyAlaArgLeuArGArGProAlaHisValProLeuAs	189
Db	540	GATTTTATACATTAATACAGATGGTGGCCGACATACGAGACCGGTCATGTCCCTTTAGA	599
Oy	189	p-ValPheLeuGluGluValAlaPheTyrGlyLeuGlyAlaAlaAlaValAlaLeuAl	209
Db	600	CGGATTTTACGAGAAATTAATATTTTATGCAATTAGGTGATCAAGCAATTAATTAATTC	659
Oy	209	rGluAspGluGlyCysProValProProGluArGProLeuProArGArGArGAlaPheAla	229

[illegible]

DT	26-MAR-2002	(first entry)	
XX			
DE	Human immune system associated gene	SEQ ID NO: 1090.	
XX			
KW	Human; immune system disease; cytosine methylation; antiasthmatic;		
KW	antiartherosclerotic; anti-naeural; cytosolic; neotropic;		
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;		
KW	antirheumatic; antiarthritic; antidiabetic; antipsoriatic;		
KW	antitumour; cancer; eye disease; arteriosclerosis; anaemia;		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;		
KW	gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200200928-A2.		
XX			
PD	03-JAN-2002.		
XX			
PE	02-JUL-2001; 2001WO-EP07537.		
XX			
PR	30-JUN-2000; 2000DE-1032529.		
PR	01-SEP-2000; 2000DE-1043826.		
XX			
PA	(EPIC-) EPICENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
XX			
DR	WPI: 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful		
PT	for diagnosis and treatment of diseases associated with abnormal		
PT	cytosine methylation		
XX			
PS	Claim 1: SEQ ID NO 1090; 32bp + Sequence Listing; German.		
XX			
CC	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention.		
XX			
SO	Sequence 7642 BP; 1881 A; 279 C; 1925 G; 3557 T; 0 other;		
XX			
Alignment Scores:			
Pred. No.:	2,49e-49	Length:	7642
Score:	1089.50	Matches:	239
Percent Similarity:	58.10%	Conservative:	109
Best Local Similarity:	39.90%	Mismatches:	147
Query Match:	37.34%	Indels:	104
	24	Gaps:	11
US-09-804-014A-8 (1-559) x ABL33117 (1-7642)			
OY	3	ArgatgagtgThgClSerArGArGInLysASPgIGlulSGlYAsPProGlyThrgClY	22
DB	2934	CGAAAAACGAAACCGCGCCCGCAAAAAA	2905
OY	23	LysAlAGInSerArGArGInLysArGArGArG	33
DB	2904	AAACGAAAAACCGCAAAAAA	2845
OY	34	-----ArgGly	35
DB	2844	CCAAACCCAAACAAACATCGGACGCTTAACTACCAACAAACGATAAAGTGCAGCTCGAAA	2785
OY	36	ArgAlAGIyArGAlASerArGInArGAlArGClYArGPro-----ValAla	51
DB	2784	CGAAAAACGCAAAAAACCGCAAAAAA	2725

OY	52	LeuArpProAlaGlyValThrValProProProSerArg-----	64
Db	2724	TCCTTCCCGCGGCATTAACGACGACCGTCAACCTTTACGCGTCGCGCGCCCTCAAC	2665
OY	65	---ProSerArpProAlaGlyLeuPheTyAlaArgThrProAspPheGlyHisArgAla	83
Db	2664	CCGCACCGCGGCCACCC-----TCTCAAGCGCCACAGACMACAGCAGATAC	2617
OY	84	GlyAlaAla-----ValGlyAlaThrArgArgPheAlaGlyArgArgGlyLys	99
Db	2616	CCACACGCTAATAACACAGCAGCTACGGAAACCCGCCG-----AACCGGGAACATAC	2563
OY	100	AlaArghHisGly-----	103
Db	2562	GCCCGACATTAACCGTAATACCGAAAAACACACTACTAAACCGAAATATACCGATATATA	2503
OY	104	-----AlaAlaVal	106
Db	2502	AAAAACCCCGCTCAAAACGACTATAACGACGACGACTACGACCGCTACGAACCGCTAC	2443
OY	107	-ProAlaAlaProCysGly-----CysCysGlyArgLeuValLeuAsnVal	121
Db	2442	GCCCGCACTACCGACCGCGGAACGACAAACACTACTACGAAAAAGGGTATATCATCAT	238
OY	121	AlaGlyLeuArgPheGlyThrArgAlaArgThrLeuGlyArgPheProAspThrLeuLe	141
Db	2382	CTCCGAACTACGCTTCGAAACGCAACATAAACCCCTTACCAATTTCCCGAAACCGCTACT	2322
OY	141	uGlyAspProAlaArgArgGlyArgPheArgAspAlaArgArgGlyLysPheAs	161
Db	2322	AAACGACCCCAAGACGCACTAAATACTTCGACCGCTCCGCAACGAATACTCTTGGA	2263
OY	161	PArgHisArgProSerPheAspAlaValLeuTyTyTyTyGlnSerGlyArgLeuArg	181
Db	2262	CCGCACGCAACCAACTTCGACCGCACTCCTACTACTATCGAAACCGCATCCG	2203
OY	181	gArgProAlaHisValProLeuAspValPheLeuGlnGlyValAlaPheTyGlyLeuG	201
Db	2202	CCGACCGCATCACTACCCCATTCGCAATTTCTCCGAAAAAATCCGCTCTACCACTAAA	2143
OY	201	ValAlaAlaLeuAlaArgLeuArgGlyLysArgGlyCysProValProProGlyLysPr	221
Db	2142	CGAAAAAACCTTAAAAAATTCGCGCAAAACGAAACTTCTACGAAAAAATAAACGACC	2083
OY	221	OlouProArgArgAlaPheAlaArgGlnLeuTyTyPheLeuPheGluPheProGlnLysSe	241
Db	2082	CTTACCCCGCGCGACACTTCACACCGCAAAATATACTACTCTTCGAAATACCCGAAACTC	2022
OY	241	rGlnAlaAlaArgValLeuAlaValValSerValLeuValIleLeuValSerIleValVal	261
Db	2022	CGAACCGCAACCGAAACATCGCATCGATCCGTAATATCATCTCATCTCATATATCAT	1963
OY	261	lPheCysLeuGlnThrIleuProAspPheArgAspAspArgAspGlyTyhGlyLeuAlaAl	281
Db	1962	CTTCTACTATAAAACGGTACCGAAATTCGCGCGCAAAAAAAC-----TACC	1915
OY	281	aAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProGl	301
Db	1914	CGCCTCGACGTCGCAAAACATCATTCGAAACACCGACMACMACACGCTCGAAATCCCGGC	1855
OY	301	YasnProProArgLeuProPheAsnAspProPhePheValValGlyThrLeuCysIleCy	321
Db	1854	AAAAACCTCAAC-----TTCTCCGATCCCTTCCTCGTAATATAAAACGCTATACATCAT	1801
OY	321	StrPheSerPheGlyLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePh	341
Db	1800	CTAATTTCTCTTCACACTACTAATACGATCTTCGCTTATCTTACCAAAACACACTTCTC	1741
OY	341	eLysAsnValMetKsnLeuLeuLeuAspPheValAlaIleLeuProTyPheValAlaLeuG	361
Db	1740	CGGAACATCACTAAACCTAATCGCATTTAAACCATCATCATCTTATTTATACCTATAA	1681
OY	361	YThrGlyLeuAlaArgGlnArgGlyValAlaGlyGlnGlnAlaMetSerLeuAlaIleLeuAr	381

DB 1680 TACGGAACCTACCGAACGACAAACAATAACAACAACATATCTTAACCATCTTAAA 1621  
QY 381 ValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGly 401  
DB 1620 AATCATCCGGCTAATAAATCTTCCGATCTTCAAACTTCGGCCACATCCAAAACACT 1561  
QY 401 uGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhe 421  
DB 1560 ACAATTCCTCGAACCAACAAACGTTAAACGTAACGTAACGTAACGTAACGTAACG 1501  
QY 421 eLeuPheIleGlyValValLeuPheSerSerAlaValThrPheAlaGluValAspArg 441  
DB 1500 CCGTCTTATTAAATCATCTCTTCTCCAAACGCGATCTACTTACCGAAACAAACGACC 1441  
QY 441 IAspSerHisPheThrSerIleProGluSerPheTrpArgAlaValAlaThrMetTrp 461  
DB 1440 CACTTCGAATTTCAACACACATCCGATACCTCTTATAAACAATATAACCATACAC 1381  
QY 461 rValGlyTrpGlyAspMetAlaProValThrValGlyLysIleValGlySerLeuCy 481  
DB 1380 AATTAATTTACGACGATATACACCAATTAACCAATAAACAATAATTAATTAATCTCT 1321  
QY 481 sAlaIleAlaGlyValLeuThrIleSerLeuProValProValIleValSerAsnPhe 501  
DB 1320 TACCATCGCGGATATCTTAACCATCGCATTCACAAATTCGTAATTTTCCAACTTCA 1261  
QY 501 rTyPheTrpHisArgGluThrGluGlyGluAlaGlyMetPheSerHisVal 519  
DB 1260 TTACTTCTACCGACGAAACAAACAAACAAACATCCCATACATACATACACGTA 1206  
RESULT 12  
ABL33116  
ID ABL33116 standard; DNA: 7642 BP.  
XX ABL33116;  
AC 26-MAR-2002 (first entry)  
XX  
DE Human immune system associated gene SEQ ID NO: 1089.  
XX  
KW Human: immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antianemic; cyrostatic; noctropic;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;  
KW antineumatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200200928-A2.  
XX  
PD 03-JAN-2002.  
XX  
PE 02-JUL-2001; 2001WO-EP07537.  
XX  
PR 30-JUN-2000; 2000DE-1032529.  
XX  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2002-130909/17.  
XX  
PT Nucleic acid comprising fragment of chemically modified gene, useful  
XX for diagnosis and treatment of diseases associated with abnormal  
XX cytosine methylation -  
XX  
PS Claim 1; SEQ ID NO 1089; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 7642 BP; 2050 A; 279 C; 1786 G; 3527 T; 0 other;

Alignment Scores:  
Pred. No.: 4,89e-46 Length: 7642  
Score: 1028.00 Matches: 256  
Percent Similarity: 54.35% Conservative: 50  
Best Local Similarity: 45.47% Mismatches: 158  
Query Match: 35.23% Indels: 99  
DB: 24 Gaps: 10  
US-09-804-014A-8 (1-559) x ABL33116 (1-7642)  
QY 7 GlyserrArgArgGlnLysAspGlyGluLysGlyAspProGlyThrGly----- 22  
DB 4856 GGGCGGAGCGCGGAAAGGGCGGAGCGGAGAGAGAGGATTGGTTATCGTTGTC 4915  
QY 22 ----- 22  
DB 4916 GTTTTTTTTCGTCGATGAGCAGCGTTTAACTTTTTCGTCGTCGTCGTTT 4975  
QY 23 -----LysAlaGlnSerArgArg----- 28  
DB 4976 AGTTCGTTATTCGCGTTTATTTTATTTTATTCGTTTATTCGTTTATTCGTTTATTCGTT 5035  
QY 29 GLYARGARGARGARGARGGLYARGGLYARGGLYARGGLYARGGLYARGGLYARGGLYARG 48  
DB 5036 GGTGAATTACGTTACCGGA-----GTTCGTCGTAGTCGCGA 5074  
QY 49 ProValAlaLeuArgProAlaGlyValThrValProProSerArgProSerArgPro 68  
DB 5075 GTTGTCTCGATATGATGATCGTGTGT----- 5101  
QY 69 ALGlyLeuPheArgArgAlaArgThrProAspThrGlyHisArgAlaGlyAlaValGly 88  
DB 5102 CGGGGATATTT-----GTTGAGTCGGA 5125  
QY 89 AlaThrArgArgPheAlaGly-----ArgArg-GlyCysAlaArg 101  
DB 5126 GGTGTCGATGTCGAGGCGGTTTCGTTTAAAGCGGTTGCGGCGCGGTCGATCG 5185  
QY 101 gHisGlyAla-----AlaValProAlaAlaProCysGlyCysCys---GluArg 116  
DB 5186 TTACGAGTCGTTGCTGTTTATTTATTTGTCGTCGCGCGGAGATGATGTCGCGGCGC 5245  
QY 116 gLeuValLeuAsnValAlaLeuValLeuArgPheGluThrArgAlaArgThrLeuGlyArg 136  
DB 5246 CGTGTATTATTAATTTTTCGCGGTTTCGAGACGTAAGTATTTTTCGTTGTTAGTT 5305  
QY 136 eProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTrpAspAspAlaArg 156  
DB 5306 TTTCGAGACGTTGTGGCGATTTTAAAGCGCGATGAGTATTTTCGATTCGTTGCTAA 5365  
QY 156 gGluTrpPhePheAspArgHisArgProSerPheAspAlaValLeuTrpTrpTrpGln 176  
DB 5366 CGAGTATTTTTCGATCGTATCGGTTTACGTCGAGTATTTTATTAATTAATTAAGTT 5425  
QY 176 rGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluAla 196  
DB 5426 CGGGGTCGATTCGTCGCGGTTTAAAGCGGTTTATTCGATATTTTTCGAGAGATTCG 5485  
QY 196 aPheTrpGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluLysCysPro 216  
DB 5486 TTTTATTAATTTTCGCGAGAGGATTAAGAGAGTTTCGCGAGAGAGAGGTTTTCGCG 5545





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QY 215 ProValProProgluArgProleuProArgAlaPheAlaArgInleuTrpLeu 234
      :::::::::::::: :::: :::: :::: ::::
Db 2080 ATCAAAAAAAGGCGCTCTACCGGAAAAAATACCAACGCAATTAATCTACTC 2021
QY 235 PheIleuPheProgluSerSerGlnAlaAlaArgValIleuAlaValSerValIleu 254
      TTTCAAAATACCCGAAATCTCGAAACCGGCAAAATCAATCGGCAATCTCTCGTATATTC 2020
QY 255 IleuValSerIleuAlaValPheCysLeuIleuTrpLeuProAspPheArgAspAspArg 274
      ATCTCTATCTCTCATCTGATCTATCTTTTACTTAAACGCTCCCGCACTAAATTAACAAA 1901
Db 1960 ATCTCTATCTCTCATCTGATCTATCTTTTACTTAAACGCTCCCGCACTAAATTAACAAA 1901
QY 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaIleuProValPheProAlaProLeuAsn 294
      AACCTCACAGAAC-----ACGCTCACCGCATCGAACACACACATCATC 1856
Db 1900 AACCTCACAGAAC-----ACGCTCACCGCATCGAACACACACATCATC 1856
QY 295 GlySerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspProPhePheVal 314
      TACAAATTCACACATC-----TTACACAAACCCCTTCTCTCATC 1820
Db 1855 TACAAATTCACACATC-----TTACACAAACCCCTTCTCTCATC 1820
QY 315 ValGluThrIleuGlyCysIleCysTrpPheSerPheGluLeuLeuValArgLeuValCys 334
      GTAAAAACGCTATATATCATCTATCTCTCTCGAAGCAATTAATACGCTTCTGCGCTAC 1760
Db 1819 GTAAAAACGCTATATATCATCTATCTCTCTCGAAGCAATTAATACGCTTCTGCGCTAC 1760
QY 335 ProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeu 354
      CCCAAACAAACGAACTCTCTCAAAAACATCATTAACCTTAACATTAATACATCATCTAT 1750
Db 1759 CCCAAACAAACGAACTCTCTCAAAAACATCATTAACCTTAACATTAATACATCATCTAT 1750
QY 355 ProGlyThrPheValAlaLeuGlyThrGluLeuAlaArgGlnArg-----GlyValGlyGln 372
      CTTATTTTCATCAGCGCTTAACACCGAAATTAACCAAAAAAACCACCAAAAAACCA 1640
Db 1699 CTTATTTTCATCAGCGCTTAACACCGAAATTAACCAAAAAAACCACCAAAAAACCA 1640
QY 373 GlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePhe 392
      CAAACCAACCTCTCAACCATCTCAAAATCTCCGCTTAATTAATTAATTTTAAATCTTC 1580
Db 1639 CAAACCAACCTCTCAACCATCTCAAAATCTCCGCTTAATTAATTAATTTTAAATCTTC 1580
QY 393 LysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyIleuTrpLeuArgAlaSerMet 412
      AACTCTCTCCGCGCACTCTCAAAAACCTCAAAATCTTAACCAACCTCAAAATCAATATA 1520
Db 1579 AACTCTCTCCGCGCACTCTCAAAAACCTCAAAATCTTAACCAACCTCAAAATCAATATA 1520
QY 413 ArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyValIleValLeuPheSerSerAla 432
      AAAAAACCAAAACCTCAATCTCTCTCTCTCAATCAAGAAATCAATCTTAATTAATCA 1460
Db 1519 AAAAAACCAAAACCTCAATCTCTCTCTCTCTCAATCAAGAAATCAATCTTAATTAATCA 1460
QY 433 ValTrpPheAlaGluValAlaAspArgValAspSerHisPheTrpSerIleProGluSerPhe 452
      ATATACCTTTACCGGAAAGAAATAAATAAATCGACCTCTCCATATTCGCCGATACCTTC 1400
Db 1459 ATATACCTTTACCGGAAAGAAATAAATAAATCGACCTCTCCATATTCGCCGATACCTTC 1400
QY 453 TrpTrpAlaValAlaTrpMetThrThrValGlyTrpGlyAspMetAlaProValThrVal 472
      TAATAAACGATTAATTCATTAACCATTAATAATACGATTAACATACCTCATTAACAT 1340
Db 1399 TAATAAACGATTAATTCATTAACCATTAATAATACGATTAACATACCTCATTAACAT 1340
QY 473 GlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValIleuTrpIleSerLeuPro 492
      AAAAAACCAAAACCTCAATCTCTTAATACCTCAATTAATTAATTAATTAATTAATTAAT 1280
Db 1339 AAAAAACCAAAACCTCAATCTCTTAATACCTCAATTAATTAATTAATTAATTAATTAAT 1280
QY 493 ValProValIleValSerAsnPheSerTrpPheTrpHisArgGluTrpGluGlyGluGlu 512
      GTACTCTATCATATATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCAT 1220
Db 1279 GTACTCTATCATATATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCAT 1220
QY 513 AlaGlyMetPheSerHisValAsp 520
      CAACTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
Db 1219 CAACTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196

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RESULT 14  
ID ABL33119 standard; DNA: 8758 BP.  
XX ABL33119;  
XX 26-MAR-2002 (first entry)

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DE Human immune system associated gene SEQ ID NO: 1092.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antierleucosclerotic; antinaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antileukemic; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
PN WO200200928-A2.
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation.
XX
PS Claim 1; SEQ ID NO 1092; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 8758 BP; 2209 A; 217 C; 2178 G; 4154 T; 0 other;

```

Alignment scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatch:	Indels:	Gaps:
2,31e-45	8758	224	101	163	60	10
Score:	1016.50					
Percent Similarity:	59.52%					
Best Local Similarity:	41.03%					
Query Match:	34.84%					

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US-09-804-014A-8 (1-559) * ABL33119 (1-8758)
QY 3 ArgArgArgTrpGlySerArgArgGlnLysAspGlyLysGlyAspProGlyThrGly 22
      AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
Db 3576 AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
QY 23 LysAlaGlnSerArgArgGly-----Arg 30
      AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
Db 3517 AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
QY 31 ArgArgArgArgGlyArgAlaGlyArgAlaSerArgGlnArgAlaArgGlyArgProVal 50
      AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
Db 3457 AAAAAACCAAAACCTCAATTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTAAT 1196
QY 51 -----AlaLeuArgProAlaGlyValThrValProPro 61
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AC AAD28734;
DT 07-MAY-2002 (first entry)
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KW schizophrenia; attention deficit hyperactivity disorder; depression;
KW proliferation disease; migraine; ischaemia; neurodegenerative disease;
KW macular degeneration; Alzheimer's disease; congestive heart failure;
KW glaucoma; Parkinson's disease; cardiovascular disease; arrhythmia;
KW high blood pressure; restenosis; metabolic disease; neuroprotective;
KW obesity; hormonal disorder; polycystic ovarian syndrome; gene therapy;
KW alopecia; anxiety; stroke; neuroleptic; nootropic; cancer; diabetes; ds.
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OS Homo sapiens.
XX
FH key Location/Qualifiers
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FT /tag= a
FT /product= "Human ion channel Ion-166"
FT /note= "CDS does not include start and stop codon"
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XX WO200192303-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US16967.
XX
XX 26-MAY-2000; 2000US-207119P.
XX 26-MAY-2000; 2000US-207152P.
XX 26-MAY-2000; 2000US-207257P.
XX
XX (PAAA ) PHARMACIA & UPJOHN CO.
XX
XX Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL, Gotlow LF;
XX WPI; 2002-147617/19.
XX P-PDB; AAEL8034.
XX
XX New human ion channel polypeptides and nucleic acids, useful for
XX treating or diagnosing neurological, psychiatric or neurodegenerative
XX diseases, e.g. depression, anxiety, stroke, ischemia, or Alzheimer's or
XX Parkinson's disease
XX
XX Claim 1; Page 76; 126pp; English.

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 20, 2003, 06:33:10 : Search time 64 Seconds  
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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	756.5	25.9	3424	4	US-09-336-643A-9
4	737.5	25.3	1805	1	US-07-955-916-6
5	732.5	25.1	1927	4	US-09-336-643A-3
6	728	24.9	2064	4	US-09-178-109-3
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18	541	18.5	696	1	US-07-955-916-5	Sequence 5, Appl1
19	334	11.4	271	1	US-08-288-405A-19	Sequence 19, Appl1
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43	215	7.4	196	1	US-08-288-405A-18	Sequence 18, Appl1
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#### ALIGNMENTS

RESULT 1  
US-08-288-405A-9  
Sequence 9, Application US/08288405A  
Patent No. 5559009  
GENERAL INFORMATION:  
APPLICANT: Chandy, Kantanthara G.  
APPLICANT: Kalman, Katalin  
APPLICANT: Chandy, Grisca A.  
APPLICANT: Gutman, George A.  
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
ATTN: Walter H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,405A  
FILING DATE: 10-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,431  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-59844-1/WHD

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405A-9

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Score: 2203.00 Matches: 452
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RESULT 2
US-08-527-152-1
; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Cabalan, Michael D.
; APPLICANT: Grissmer, Stephen
; APPLICANT: Goldin, Alan L.

```

APPLICANT: Dethlefs, Brent A.  
 APPLICANT: Gutman, George A.  
 APPLICANT: Masmuth, John J.  
 TITLE OF INVENTION: Assay Methods and Products Based on n  
 TITLE OF INVENTION: K+ Channel Expression  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
 ADDRESSEE: Attn: W.H. Dreger  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/527,152  
 FILING DATE: UNKNOWN  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/170,418  
 FILING DATE: 20-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/558,568  
 FILING DATE: 27-JUL-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-54444-2/MHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1994 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 150..1736  
 US-08-527-152-1  
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 Pred. No.: 1.31e-106 Length: 1994  
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 DB 335 CATCTCGGGCTGGCTGGAGAGCGAGCTCAAGACCTCTGCACTTCCCGACACT 394  
 QY 140 uLeuGlyAspProAlaArGArGlyArGpHeuThrArGpHeuAspAlaArGArGlyuThrPhep 160  
 DB 395 GCTGGCGAGACCCCAAGCGGCGCATGGGAGTCTTGACCCACCTCGCAATGAGACTCTT 454  
 QY 160 eaSPArGHisArGProSerPheAspAlaValLeuTyTrpGlnSerGlyAlaGlye 180  
 DB 455 CGACCGCAACCGACCGAGCTTCGACCGCATCTCTACTACAGTCCGGGGCGGCAT 514  
 QY 180 uArGArGProAlaHisValProLeuAspValPheLeuGlnGluValAlaPheTyTrpGlye 200  
 DB 515 TCGCGGCGGCTGACGTGCCATGACATCTTCCGAGAGATCGCTTTTACAGCT 574  
 QY 200 uGlyAlaAlaAlaLeuAlaArGLeuArGLeuAspGlnGlyCysProValProProGluAr 220  
 DB 575 GGGTGAAGAGAGCCATGAAAGTCCGTGAGATGAGGCTTCCGCGGAGAGAGCG 634  
 QY 220 gProLeuProArGArGAlaPheAlaArGLeuTrpLeuPheGlnPheProGluSe 240  
 DB 635 ACCCTGCCCGCGCGTGCATCCAGCGCCAGGTGGCTGTCTTGAAATATCCGAGAG 694  
 QY 240 rSerGlnAlaAlaArGValLeuAlaValAlaSerValLeuValIleLeuValSerIleVa 260  
 DB 695 CTCGCGCGCGCGCGGCGCATGTCATGTGTAGCTGTGATTCATCTCATCTCATGT 754  
 QY 260 lValPheCysLeuGluThrLeuProAspPheArGAspArGArGlyThrGlyLeuAl 280  
 DB 755 CATCTTGTGCTTGGAGACGCTTCCGAGTTCGCGATGAGAAAGAC-----TA 802  
 QY 280 aAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetPr 300  
 DB 803 TCCCGCTCCCGCTGCAGAGAGCTGTGAGCTGCCAACACAGCAGCGGGGCGCC 862  
 QY 300 oGlyAsnProProArGLeuProPheAsnAspProPheValValGluThrLeuCysIl 320  
 DB 863 TTCTGAGGCTCC-----AGCTTCTCGGACCCCTTCTGTGTGAGACCTTGTGAT 916  
 QY 320 eCysTrpPheSerPheGluLeuLeuValArGLeuValCysProSerIysAlaIlePh 340  
 DB 917 CATCTGTGCTCTTGTGAGACTTGTGTGGCGGCTTGTGCTGCGCCAGTAAGCCACTT 976  
 QY 340 ePheTyAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyPheValAlaLe 360  
 DB 977 CTCAGAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1036  
 QY 360 uGlyThrGlnLeuAlaArGAlaArGAlaArGAlaGlyAlaGlnGlnAlaMetSerLeuAlaIle 380  
 DB 1037 GGGCACTGAGCTGGCTGACAGCAGACAGTAAGGAGGAGCCATGCTGCTGCGCATCT 1096  
 QY 380 uArGValIleArGLeuValArGValPheArGIllePheTyLeuSerArGHisSerIysGl 400  
 DB 1097 AAGAGTCATCCGCTTGTAGTAAAGGTTTCCGATCTTCMACTTCCCGCATTTCTAAAGG 1156  
 QY 400 yLeuGlnIleLeuGlyGlnThrLeuArGAlaSerMetArGLeuGlyLeuLeuIlePh 420  
 DB 1157 GCTCAGATCTCTGAGACAGAGCTGAAGCTTCATAGCGGAGCTGGGCTGCTCATATT 1216  
 QY 420 ePheLeuPheIleGlyValValLeuPheSerSerAlaValTyPheAlaGlyValAspAr 440  
 DB 1217 CTTCCTCTTCATTTGGGGTCACTCTTTCTTCACATGACGTTACTTGTGAGCAGACGA 1276













Db 940 -CGGGTCTCCGCTCTTCAGAGATCTTCAAGTTTCCCGCACCTCCAGGCGCTCGGAGT 998  
 QY 403 eLeuGIyGlnThrIleuArgAlaSerMetArgIleuGIyLeuIlePhePheLeuPh 423  
 Db 999 CCGTGGCTACACATGAGAGCTGTGCTCCGACACTGGGCTTTCTCTCTCCCTCAC 1058  
 QY 423 eLeuGIyValIleuPheSerSerAlaValIleuPheAlaIleuValAspValAsp 443  
 Db 1059 CATGGCATCATCATCTTGGCACCTGTATGTATTATGCCGGAAGGCTCTCCGCGCAG 1118  
 QY 443 HisPheThrSerIleProGIuSerPheTrpTrpAlaValIleuMetThrValGI 463  
 Db 1119 CAAGTTCACCAACATCCCTGCTGTTTGTACACCATGTTCACCATGACCACTGGG 1178  
 QY 463 YTrpGIySerMetAlaProValThrValGIyIleuGIySerIleuGIyAlaIleu 483  
 Db 1179 ATACGAGACATGTGCTTAAGACATTCAGGAAAGATCTTCATCTGCTCCCT 1238  
 QY 483 eAlaGIyValIleuThrIleSerIleuProValIleuValIleuSerAsnPheSerTrp 503  
 Db 1239 GAGTGGCGCTGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1298  
 QY 503 eTrpHisArg-----GluThrGIuGIyGIuGIuAlaGIyMetPheSerH 518  
 Db 1299 TTACCAACGAGATCAGAGAGCTGATAACGACAGGACAAAGAGCGCTGCTGCTG 1358  
 QY 518 sValAspMetGIuProCysGIyPro-----LeuGIuGIyValAlaAsnGIyI 534  
 Db 1359 GATTCGCTGTGGCCAAACAGCGAGTTGCAATCATACCTGCACAGACCGACGCGGT 1418  
 QY 534 YLeuValAspGIyGIuValIleuProIleuProIleuProIleuProIleuProIleu 554  
 Db 1419 CCTC-----AACGAGCGCTGAGCTG-----ACGGGACACCCCAAGAGAGCA 1463  
 QY 554 sLeu 555  
 Db 1464 CATG 1467

## RESULT 8

US-09-142-791A-3  
 ; Sequence 3, Application US/09142791A  
 ; Patent No. 6368823  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Antoine Michel Alain Brill  
 ; APPLICANT: Thierry Paul Gerard Calmels  
 ; APPLICANT: Jean-Francois Simon Pierre Faivre  
 ; APPLICANT: Jean-Luc Javie  
 ; APPLICANT: Sabine Rouanet  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GH-30012  
 ; CURRENT APPLICATION NUMBER: US/09/142,791A  
 ; CURRENT FILING DATE: 1999-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
 ; PRIOR FILING DATE: 1998-03-23  
 ; PRIOR APPLICATION NUMBER: UK 9706377.0  
 ; PRIOR FILING DATE: 1997-03-27  
 ; PRIOR APPLICATION NUMBER: EP 97402971.2  
 ; PRIOR FILING DATE: 1997-12-09  
 ; PRIOR APPLICATION NUMBER: EP 97403007.4  
 ; PRIOR FILING DATE: 1997-12-11  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2072  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-142-791A-3

## Alignment Scores:

Pred. No.: 3, 17e-44 Length: 2072  
 Score: 721.00 Matches: 176  
 Percent Similarity: 53.70% Conservative: 85  
 Best Local Similarity: 36.21% Mismatches: 153

Query Match: 24.71% Indels: 73  
 DB: 4 Gaps: 14  
 US-09-804-014a-8 (1-559) x US-09-142-791A-3 (1-2072)  
 QY 103 GYAlaAlaValIleuProAlaIleuProCys-----GlyCys 113  
 Db 56 GGATGGCGGTGGCCAACTCCCATTCGCCCTGGCGCGCGCGACAGAACAGCGGCAC- 114  
 QY 114 CysGIuArgLeuValIleuAsnValAlaGIyLeuArgPheGIuThrArgAlaArgThrLeu 133  
 Db 115 GATGACTATATGTCTCAACGAGTGGCGGAGGTTCACAGCTGGAGAGCAAGCTG 174  
 QY 134 GIuArgPhePheThrIleuGIyAspProAlaIleuArgGIyArgPheTrpAsp 153  
 Db 175 GAGCGCTACCCGACACCTGCTGGGAC--ACGAGAAAGAGATTCTTCAACAGAG 231  
 QY 154 AlaArgGIuTrpPhePheAspArgHisArgProSerPheAspAlaValIleuTrp 173  
 Db 232 GACACCAAGAGACTTCTTCGACCGGACCCGAGAGTGTCCGCGCTGCTCAACTTC 291  
 QY 174 YTrpGIuSerGIyValArgLeuArgArgProAlaHisValIleuAspValIleuGIu 193  
 Db 292 TACCGCACG---GGGAGCTGCACATACCGCGCTACGAGTGCATCTGCTACGACGAC 348  
 QY 194 GIuValAlaPheTrpGIyLeuGIyAlaAlaAlaLeuAla----- 206  
 Db 349 GAGCTGCGCTTACGCGCATCTCCCGAGATCAGGGAGCTGCTACGAGAGTAC 408  
 QY 207 -----ArgLeuArgGIu-----AspGIuGIyCysProValIleuPro 218  
 Db 409 AAGGACCGCAAGAGGAGAAAGCGCGAGCTCATGACAGCAAGACATCGGAGAACAC 468  
 QY 219 GIuArgProLeuProArgArgAlaPheAlaArgGIuLeuTrpLeuPheGIuPhePro 238  
 Db 469 CAGGAGTCCATGCTCGCTCAGCTTCCGACAGACATGTGGCGGCTTCGAGAACCC 528  
 QY 239 GluSerSerAlaAlaAlaArgValIleuAlaValIleuValIleuValIleuValSer 258  
 Db 529 CACACCGACAGCGTGGCGCTGCTTCTTACTACAGTGTGCTTCTTCATCGCTGTG 588  
 QY 259 ILeuValIleuPheCysLeuGIuThrLeuProAspPheArgAspArgAspGIyThrGIy 278  
 Db 589 GTCATCAACACAGCTGTGAGAGCGTCCG-----TGGCGCACG--- 627  
 QY 279 LeuAlaAlaAlaAlaAlaIleuProValIleuProAlaProLeuAsnGIySerGIu 298  
 Db 628 -----GTCCCGGACAGACAGAG 645  
 QY 299 MetProGIuAsnProProArgLeuProPheAsnAspProPhePheValIleuGIuThrLeu 318  
 Db 646 CTGCGCTGGCGGAG-----CGCTACTCGCTGCTCTTCTGCTGGACAGCGCG 696  
 QY 319 CysIleCysTrpPheSerPheGIuLeuLeuValArgLeuLeuValIleuProSerIleuAla 338  
 Db 697 TGGGTATGATGTCTTACCGGAGGATCTCTCGGCTTCTGCGGCTCCACGCGCTAC 756  
 QY 339 ILeuPheIleuAsnValIleuAsnLeuIleuAspPheValAlaIleuProTrpPheVal 358  
 Db 757 CGCTTCATCCGCGAGCTGATGACATCATGACGTGTGCGCATTCATGCTCTACATC 816  
 QY 359 AlaLeuGIyThrGIuLeuAlaArgGIuArgGIyValGIyGlnIleuIleuMetSerIleuAla 378  
 Db 817 -----GTCGTGCTATGACCAACAGAGAGCTGCCGCGCTTCTCACAGCTC--- 867  
 QY 379 ILeuArgValIleuArgLeuValArgValIleuArgIleuPheIleuSerIleuSerArgHisSer 398  
 Db 868 -----CGGCTCTCCGCGCTTCTTACAGATCTTCAAGTTTCCCGCACACTGC 912  
 QY 399 LysGIyLeuGIuIleuGIyGlnThrIleuArgAlaSerMetArgGIuLeuGIyLeuLeu 418  
 Db 913 CAGGCGCTCGGATCTGTGGCTACACATGAAAGCTGTGCTCCGAACTGGGCTTCTT 972

QY 419 IlePhePheLeuPheIleGlyValIleuPheSerSerAlaValTyrPheAlaGluVal 438  
Db 973 CTCCTCTCCCTCCACGATCCATCATCTTGGCCAGTGTATGTTTATGCGGAGAAC 1032  
QY 439 AspArgValAspSerHisPheThrSerIleProGluSerPheThrProAlaValThr 458  
Db 1033 GGCCTCTCGGCCAGCAAGTTCCACAGCATCTCCCTGCTTTGGTACCACTTGTCCAC 1092  
QY 459 MetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLysIleValGly 478  
Db 1093 ATGACCACTGGGATACGAGACATGTCCTTAAGACGATTCAGGAGAACCTTCGCGC 1152  
QY 479 SerLeuGlyAlaIleAlaGlyValIleuThrIleSerLeuProValProValIleValSer 498  
Db 1153 TCCATCTGCTCCCTGAGTGCGCTGCTGATCCCTGCGCACTCCCTGATGTTTCC 1212  
QY 499 AspPheSerTyrPheTyrHisArg-----GluThrGluGlyGluGluAla 513  
Db 1213 AACTTTAGCCGGATTACCCACCAATACAGAGCTGATTAACGACGAGGACAAAGAAC 1272  
QY 514 GlyMetPheSerHisValAspMetGlnProCysGlyPro-----LeuGluGly 529  
Db 1273 GCCCGCCTTGGCAGATCCGTCGTGGCCAAAGAGGAGCTTCGAATGATACCTGCACAGC 1332  
QY 530 LysAlaAsnGlyGlyLeuValAspGlyGlyValProGluLeuProProLeuThrProAla 549  
Db 1333 AACCGGACGGGCTCTC-----AACGAGCGCTGAGCTG-----ACGGGACCC 1377  
QY 550 ProProArgGluHisLeu 555  
Db 1378 CCAGAAAGAGGACCATG 1395

RESULT 9  
US-09-142-791A-1  
Sequence 1, Application US/09142791A  
Patent No. 6368823  
GENERAL INFORMATION:  
APPLICANT: Antoine Michel Alain Brill  
APPLICANT: Thierry Paul Gerard Calmels  
APPLICANT: Jean-Francois Simon Pierre Faivre  
APPLICANT: Jean-Luc Javre  
APPLICANT: Sabine Rouanet  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-30012  
CURRENT APPLICATION NUMBER: US/09/142,791A  
CURRENT FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: PCT/EP98/01901  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: UK 9706377.0  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: EP 97402971.2  
PRIOR FILING DATE: 1997-12-09  
PRIOR APPLICATION NUMBER: EP 97403007.4  
PRIOR FILING DATE: 1997-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: fastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 2104  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-142-791A-1

Alignment Scores:  
Pred. No.: 3,24e-44 Length: 2104  
Score: 721.00 Matches: 176  
Percent Similarity: 53.70% Conservative: 85  
Best Local Similarity: 36.21% Mismatches: 153  
Query Match: 24.71% Indels: 73  
DB: 4 Gaps: 14

US-09-804-014A-8 (1-559) x US-09-142-791A-1 (1-2104)  
QY 103 GlyAlaAlaValProAlaAlaProCys-----GlyCys 113

Db 56 GGATGCCGTTGGCCCACTGCGCCCTGGCCGCCGCCACAGAACAGCGGAG- 114  
QY 114 CysGlyuArgLeuValLeuAsnValAlaGlyLeuArgPheGlyuThrArgAlaArgThrLeu 133  
Db 115 GATGAGCTGATTTGCTCCCAACGTGAGTGGGAGGAGTTCAGACCTGGAGACAGCTG 174  
QY 134 GlyArgPheProAspThrLeuLeuGlyAspProAlaArgGlyArgPheTyrAspAsp 153  
Db 175 GACCGCTACCCGAGACACCTCTGGGAGC-----ACGGAGAGAGAGTTCTTCAACAGAG 231  
QY 154 AlaArgGlyuThrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 173  
Db 232 GACACCAAGAGATCTTCTGACAGCGGACCCGAGGTGTTCGCTGCGCTCACTTC 291  
QY 174 TyrGlnSerGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGly 193  
Db 292 TACCGGACG---GGAAAGCTGCACTACCCGCGCTACAGAGTCACTCTGCTACAGAGAC 348  
QY 194 GluValAlaPheTyrGlyLeuGlyAlaAlaAlaLeuAla----- 206  
Db 349 GACCTGCTCTTACAGGATCTCTCCGAGATCATCGGGAGCTGCTCTACGAGAGTAC 408  
QY 207 -----ArgLeuArgGlu-----AspGluGlyCysProValProPro 218  
Db 409 AAGGACCGCAAGAGGAGGAAGCCGAGCGGCTCATGAGACACAGACTCGGAGAACAC 468  
QY 219 GluArgProLeuProArgArgAlaPheAlaArgGlnLeuThrLeuLeuPheGluPhePro 238  
Db 469 CAGAGTCCATGCTGCTCGCTACAGTCCGCGCAGACCATGAGGGGCTTCGAGAACCC 528  
QY 239 GluSerSerGlnAlaAlaArgValLeuAlaValAlaValSerValLeuValIleLeuValSer 258  
Db 529 CACACCGACACGCTGCGCTGCTTCTACTAGCTGCTGCTTCACTGCTGCTGCTGCTG 588  
QY 259 IleValValPheCysLeuGlyuThrLeuProAspPheArgGlnAspArgGlyuThrGly 278  
Db 589 GTCATCCCAACAGCTGTGGAGAGCGTCCG-----TCGGCAGC--- 627  
QY 279 LeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGln 298  
Db 628 -----GTCCGGGCGCACAGAG 645  
QY 299 MetProGlyAsnProProArgLeuProPheAsnAspProPheValValGluThrLeu 318  
Db 646 CTGCGCGCGGAG-----CGCTACTCGGTGCTTCTTCCCTGCGACAGCGCG 656  
QY 319 CysIleCysThrPheSerPheGluLeuLeuValArgLeuLeuValCysProSerLysAla 338  
Db 697 TGCCTCATGATCTTACACGTTGAGGTACTCTCGGCTTTCGCGGCTCCACGCGCTAC 756  
QY 339 IlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheVal 358  
Db 757 CGCTTCATCGCAGCGTCATGAGCATATGAGCTGTGGCATCATGCCCTACTCATC 816  
QY 359 AlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMetSerLeuAla 378  
Db 817 -----GCTCTGTCATGACCAACAGAGAGGTGTCGCGCTTCTGACAGCTC--- 867  
QY 379 IleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSer 398  
Db 868 -----CGGCTTCCGCGCTTCAAGATCTTCAAGATTTTCCCGCATCTCC 912  
QY 399 LysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgIleuGlyLeuLeu 418  
Db 913 CAGGCGCTGGGATCCGCGGCTACACACTAGACAGCTGTCCCGACAGCGGCTTCT 972  
QY 419 IlePhePheLeuPheIleGlyValIleuPheSerSerAlaValTyrPheAlaGluVal 438  
Db 973 CTCCTTCTCCCTACACAGGATCATCATCTTGGCCAGTGTATGTTTATGCGGAGAAC 1032  
QY 439 AspArgValAspSerHisPheThrSerIleProGluSerPheThrProAlaValThr 458

Db	1033	GGCTCCCTCGGCCACAGCAAGTTCCACACACATCCCTGCTGCTTTGGTACACCAFTTGTCCACC	10922
Qy	459	MethThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGlyLysIleValGly	478
Db	1093	ATGACACACATCGGGATACGGAGACATGGTGCCTTAAGACGATTGGACGGGAAGATCTTGGGC	1152
Qy	479	SerLeuGlySalAlaIleAlaGlyValLeuThrIleSerLeuProValProValIleValSer	498
Db	1153	TCGATCTGCTCTTGGAGTGGCGCTGTCGTCATTGGCCCTGCAGATGCCCTGTGATTTGTTTC	1212
Qy	499	AsnHisSerIlyrPheYrThrHisArg-----GluThrGluGlyGluGluAla	513
Db	1213	AACTTTGACCGCGGATTTTACCACCGAATTCAGAGAGCTGATTAACGACGAGGCACAAAGAG	1272
Qy	514	GlyMetPheSerHisValAspMetGlnProCysGlyPro-----LeuGluGly	529
Db	1273	GCCCGCCTTGCCAGAGATCCGTGTGGCCAAACAGGACAGTTGGAATGCATACCTGCACAGC	1332
Qy	530	LysAlaAsnGlyGlyLeuValAspGlyGluValProGluLeuProProLeuThrPala	549
Db	1333	AAGGCGACAGCGGCTCCCTC-----AACGAGCGCTGTGAGACTG-----ACGGGCACC	1377
Qy	550	ProProArgGlnHisIleu	555
Db	1378	CCAGACAGAGGACACATG	1395
RESULT	10		
US-09-142-791A-5			
Sequence 5, Application	US/09142791A		
Patent No.	6368823		
GENERAL INFORMATION:			
APPLICANT:	Antoine Michel Alain Brill		
APPLICANT:	Thierry Paul Gerard Calmels		
APPLICANT:	Jean-Francois Simon Pierre Faivre		
APPLICANT:	Jean-Luc Jayre		
APPLICANT:	Sabine Rouanet		
TITLE OR INVENTION:	NOVEL COMPOUNDS		
FILE REFERENCE:	GH-30012		
CURRENT APPLICATION NUMBER:	US/09/142,791A		
CURRENT FILING DATE:	1999-02-02		
PRIOR APPLICATION NUMBER:	PCT/EP98/01901		
PRIOR FILING DATE:	1998-03-23		
PRIOR APPLICATION NUMBER:	UK 9706377.0		
PRIOR FILING DATE:	1997-03-27		
PRIOR APPLICATION NUMBER:	EP 97402971.2		
PRIOR FILING DATE:	1997-12-09		
PRIOR APPLICATION NUMBER:	EP 97403007.4		
PRIOR FILING DATE:	1997-12-11		
NUMBER OF SEQ ID NOS:	14		
SOFTWARE:	FastSeq for Windows Version 3.0		
SEQ ID NO 5			
LENGTH:	2104		
TYPE:	DNA		
ORGANISM:	HOMO SAPIENS		
US-09-142-791A-5			
Alignment Scores:			
Pred. No.:	2, 47e-43	Length:	2104
Score:	709.00	Matches:	178
Percent Similarity:	51.768	Conservative:	86
Best Local Similarity:	34.908	Mismatches:	159
Query Match:	24.308	Indels:	87
DB:	4	Gaps:	15
US-09-804-014A-8 (1-559) x US-09-142-791A-5 (1-2104)			
Qy	77	ProAspThrGlyHisArgAlaGlyAlaAlaValAlaGlyAlaThrArgArgPheAlaGlyArg	96
Db	36	CCGGGCTGGCGCCATCGGTGGGTGGCC-----	62
Qy	97	ArgGlyGlySalAlaArgHisGlyAlaAlaValProAlaAlaPro-CysGlyCys-----	113
Db	63	-----GGTGGCCCAATCTGCCCAATGCCCTCCGCGCCGCGCCGACAGAGA	104

[illegible]

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QY 455 aValaThMeThrThrValGlyTyrglyAspMetAlaProValThrValGlyGly 475
DB 1083 CATGTGCACCATGACCCAGATGAGATGATGCTGCTGATGAGTTCAGAGGAA 1142
QY 475 sTlLeValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValProVa 495
DB 1143 GATCTTCGCTCATCTGCTCTGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
QY 495 lIleValSerAspPheSerTyrrPheThrHisArg-----GluThrGluG1 510
DB 1203 GATTTGTTCCAACTTTAGCCGATTTACCCAGAAACAGAGCTGATTAAGCCAGGCG 1262
QY 510 yGluGluAlaGlyMetPheSerHisValAspMetGlnProCysGlyPro----- 526
DB 1263 ACAAAAGACGCCCGCTTCCAGATCCGTCGTGGCCAAACAGAGCGATTGCATGCA 1322
QY 527 -LeuGluGlyValAsnGlyLeuValAspGlyGlyValProGluLeuProProP 546
DB 1323 CCGTCACAGCAGCAGCAGCGGCTCTCC-----AACGAGCGCTGAGGCTG----- 1368
QY 546 oLeuTrpAlaProProArgGluHisLeu 555
DB 1369 -ACGGGACCCCGACAGAGAGCAGCATG 1395

RESULT 11
US-09-336-643A-17
Sequence 17, Application US/0933643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761 Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 3102
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (274)...(1705)
OTHER INFORMATION: K+hnov11
US-09-336-643A-17

Alignment Scores:
Pred. No.: 3,74e-42 Length: 3102
Score: 696.00 Matches: 202
Percent Similarity: 44.53% Conservative: 87
Best Local Similarity: 31.12% Mismatches: 172
Query Match: 23.85% Indels: 190
Gaps: 22

US-09-804-014A-8 (1-559) x US-09-336-643A-17 (1-3102)
QY 8 SerArgArgGlnLysAspGlyGlyLysGlyAspProGlyThrGlyLysAlaGlnSer--- 26
DB 124 AGACCCAGAACACCCAGCAGGCTGCGCCGCCAGCTAATGAGTACGAGAGGAGGCGCC 183
QY 27 ArgArgGlyArgArgArgArgGlyArgAlaGly-ArgAlaSerArgGlnArgAla-- 45
DB 184 CGCAGGCGCAGCGCGCTCTCGCCGACGCTGTTCCCTCCGCTTCAGGTGTAGCGCC 243

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QY 46 -----ArgGlyArgProValAlaLeuArgProAlaGlyValThrValProProSe 63
DB 244 CGCGCGCGCGCGCGCGCGCG-----CCTCCAGC 273
QY 63 rArgProSerArgProAlaGlyLeuPheTyrrAlaArgThrProAspThrGlyHisArgAl 83
DB 274 ATGACCGCGCAGA----- 286
QY 83 aGlyAlaAlaValGlyLarThrArgArgPheAlaGlyArgArgGlyCysAlaArgHisG1 103
DB 287 -----GCCGTGGGACGTGTGAGGCTTACCTGACGAGAGGAG-ATCCGC----- 333
QY 103 yAlaAlaValProAlaAlaProCysGlyCysGlyArgLeuValLeuAsnValAlaG1 123
DB 334 -----ATCATGTTGGCGCG 347
QY 123 yLeuArgPheGluThrArgAlaArgThrLeuGlyArgPheProAspThrLeuLeuGlyAs 143
DB 348 CTTCACAGAGAGGCTGCGCTGCGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
QY 143 pProAlaArgArgGlyArgPhe----- 150
DB 397 -----CGCCTGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
QY 151 -----TyrAspAspAlaArgArgGlyArgPheAspArgHisArgProSerPheAs 168
DB 450 CGATGACTACGACGACGCTCCAGCGGAGTCTTACTTCCAGCCAGCCGAGCTCTCC 509
QY 168 pAlaValLeuTyrrTyrrGlnSerGlyArgLeuArgArgProAlaHisValProLe 188
DB 510 CTAGCTGCTGCTCATTTATACACC--GGCAACCTTCAGCTCATGCTGCTGCTGCTGCTG 566
QY 188 uAspValPheLeuGluGluValAlaPheTyrrGlyLeuGlyAlaAlaAlaLeuAlaArgLe 208
DB 567 CTTCCTCTTACGACGACGATCGATCTGGGATCAACGAGCTTCTCATTT----- 618
QY 208 uArgGlyAspGluGlyGys-----ProValProProGluArgP 221
DB 619 -----GACTCTGCTGACGCTACGCTACGATGCGCGCAAGTACAGCCGAGCAGA 671
QY 221 o----- 221
DB 672 GAAGTGGAGCAGCAGAGTACGACGAGCAGCAGCAGCTTCTTCATGATGATCTTGC 731
QY 222 -----LeuProArgArgAlaPheAlaArgGlnLe 231
DB 732 CTTCACAGACGCGCTCCAAAGTTCATGATGGGACGCCCTCGGCAACTTCGAGCAGCT 791
QY 231 uTrpLeuLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaSe 251
DB 792 GTGCTGCGCTGACCAACCCGCGCTACGCTGACGAGGCTCTTCAACATCCCTGCTG 851
QY 251 rValLeuValIleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheAr 271
DB 852 CATCTGTGTGTGATGGGCTCATCACCAGTGTGCTCAATAGCCTGCGCCGATTTTCCA 911
QY 271 gAspAspArgAspLysThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAl 291
DB 912 A----- 912
QY 291 aProLeuAsnGlySerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspPr 311
DB 913 -----ATCCCTGACAGCAGGCAACCCCTGCGAGAGCAGCTAGG----- 951
QY 311 oPhePheValValGluThrLeuGlyIleCysTrpPheSerPheGluLeuLeuValArgLe 331
DB 952 -TTTGAATCTGGAGACATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
QY 331 uLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeuLeuAspPheVa 351
DB 1011 TGCTGTGGCCCTGACTTCTCAAGTCTTCAAGATGCGCTTAACCTTATTTAGCCCTCAT 1070

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QY 351 LAlaIleleuProtyrPheValAlaIleuGlythrGluIleuAlaArgAlaGlyValG1 371
Db 1071 GTCCATGTCCTCCCTTTACTACTCTGTGGTGAACCTG-----GTGGT 1115
QY 371 yGInGlnAlaMetSerLeuVala-----lIleuArgValAlaArgLeuValAr 387
Db 1116 GGAAGACACACCTACTTTAGCCAACTTGGGCAAGGGTGGCCAGAGCTCGAAGGCTGATCG 1175
QY 387 gValPheArglIlePheLysLeuSerArgHisSerLysGlyLeuGlnlIleuGlylTh 407
Db 1176 GATCTTCGCATCTTAAAGCTGGCCAGGACACTCCACTGGCTCCGCTGGGGGGCCAC 1235
QY 407 rLeuArgAlaSerMetArgGluIleuGlyLeuIleuPhePheLeuPheIleGlyVala 427
Db 1236 TTGTAATACAGCTACCAAGAAATAGAGGTGCTTTGCTTACACTCTCCGGGGGATTC 1295
QY 427 lLeuPheSerSerAlaValAlaYrPheAlaGluValAsparGValAspSerHisPheThrSe 447
Db 1296 CATCTTCTCCGTGGTGGCCCTACACCACTTGAAGAAAGAGAG---AACGAGGGCCTGGCCAC 1352
QY 447 rIleProGluSerPheTrpTrpAlaValAlaThrMetThrThrValGlyTrGlyAspMe 467
Db 1353 CATCCCTGCCTGCTGGGGGGGGCTCCCTCAGTATGACACACAGGGGGGTACGGGGATGT 1412
QY 467 tAlaProValThrValGlyGlyLyslIleValGlySerLeuGlySalaIleAlaGlyValle 487
Db 1413 GTCGCCAGGACACAGGCGCAAGAAAGCTGACTGCTCTGCTGCATCTTGGAGAGCATCTT 1472
QY 487 uThrIleSerLeuProValAlaProValAlIleValSerAsnPheSerTrpPheYrHisArgG1 507
Db 1473 CGTGGTGTCTGCTGCCCATCCTACCTTGATCTTCATATAAGTTCTTCCACTTTTACCGGGCCA 1532
QY 507 uThrGlyGlyGluGluAla-----GlyMet----- 515
Db 1533 AAAGCAACTTGAGAGTGCATGCGCAGCTGTGACTTTGGAGATGGAATGAAGAGAGTCCC 1592
QY 516 -----PheSerHis-----Va 519
Db 1593 TTCGGCTCAATTAAAGGACTATTATGCCCATTAAGTTAAATCCCTATGCAAGCCTGAC 1652
QY 519 lAspMetGlnProCysGlyProleuGluGlyLysAlaAsn-----Gl 533
Db 1653 GAACATATAGACAGAGACTCACCAAGTAAGTATTCCTTCCCTACAGTTAGCGGGG 1712
QY 533 yGlyLeuVal-----AspGlyLeuValProGluLeuProProProLeuTrpAlaProP 551
Db 1713 AGGACTGTGCACCCCTCCACCC-CACATTGCTAGAGCTGCTTGTGGCTCTGGGACACACC 1771
QY 551 oArgGluHisLeuValThrGluVal 559
Db 1772 CAGG---CACCTTATGTTATGGTG 1793

RESULT 12
US-08-464-340A-3
Sequence 3, Application US/08464340A
Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARBILLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1

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	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US-08/464,340A	
	FILING DATE: June 5, 1995	
	CLASSIFICATION: 435	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: PCT/US94/08449	
	FILING DATE: 28 JUL 1994	
	ATTORNEY/AGENT INFORMATION:	
	NAME: FERRARO, GREGORY D.	
	REGISTRATION NUMBER: 36,134	
	REFERENCE/DOCKET NUMBER: 325800-415	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 201-994-1700	
	TELEFAX: 201-994-1744	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 2483 BASE PAIRS	
	TYPE: NUCLEIC ACID	
	STRANDEDNESS: SINGLE	
	TOPOLOGY: LINEAR	
	MOLECULE TYPE: CDNA	
	US-08-464-340A-3	
	Alignment Scores:	
	Pred. NO.: 7,35e-39 Length: 2483	
	Score: 649.50 Matches: 204	
	Percent Similarity: 44.05% Conservative: 81	
	Best Local Similarity: 31.53% Mismatches: 208	
	Query Match: 22.26% Indels: 156	
	DB: 1 Gaps: 19	
US-09-804-014A-8 (1-559) x US-08-464-340A-3 (1-2483)		
OY 3 ArgArqArqr-----GlySerArqArgInLysAspIgLylULySgLYASP 18		
Db		
Db 357 CGCAGGAGCGCCAGACTGAACGGCGGAGCGGCCGCAGCCAGCCGGTGATGCCCGC 416		
OY 19 ProGIrThrgILySLagInserArqArgglYArqArqArqArqAgLyArqAlagLy 38		
Db 417 GCCGAGCGCGCGCGCGCCCAAGCCCCCGCGGTTCCTCCGCGGCGCCCGATGCCACC 476		
OY 39 ArgAlaserArqInArgAlaArqglYArqProValAlaleuarqProAlagLyALThr 58		
Db		
Db 477 CGAGCCCGC-----CCGCGCGGATGC 500		
OY 59 ValPro-----ProPro-----SerArgProSerArqProAla 69		
Db ::::		
Db 501 CTCGCCCGCGCGCGCCCGCACGACTGCCCGCTGTGACGCGCCCTTCCCGCAGCGC 560		
OY 70 GlyLeuPheTyrrAlaArqThrProAspThrcILyHis----- 81		
Db		
Db 561 GGCGCGCGCGCGCTCTCCCGACGAGATACACGACGACGGGTGGCACCCCGCGACCCAA 620		
OY 82 -----ArgAlagLyAlalaValAgLyAlaThrArg 91		
Db 621 CGAACACGCGCGCAGCTCTCAGCGGGCGCGCGGAGCGCTCGAGGGCGCGCACGG 680		
OY 92 ArgPheaIagLyArqArgGLyCyAlaArqHisIsLyAlaValAlProAlaIaProcys 111		
Db 681 GAGATGAGCGGTCGGGGAGCGCGACCTCCCGGACCGCGGCACGACCTCCGCTGC 740		
OY 112 GlyCyscsgLIarq-LeuValleuAsnVaIalagLyLeuArqPhegILunhrArqAlaAr 131		
Db 741 CAGGAGCACAATAGAGATAGTCGTCACCAOITGGGGGGGTGGCGCAGGTGCTGTAAGGGA 800		
OY 131 gThrLeugLyArqPheProAspThrLeuLeuGLyASP-----ProAlaArqArgLyAr 149		
Db 801 CCTCTCTAGTCAGTACCTTGAGACCGCGCTGGCGACCTCATCAACGTCTGGCTGGGG 860		
OY 149 gPhe-----TyraSPAlaArqArgILyurYrPheP 160		
Db ::		
Db 861 CTACGACACCATTTCTTCCCTGTGTCGACGACTACGACCCCGGACAGCGATTTCTACTT 920		

Oy	160	eaasrAHHIsarproserPheaspalaValLeuYrYrTyrGlnSerIylGlyArgLe	180
Db	921	TgACAGGGAGCCCGGAGCGCTTCACAGTGTCATCGAGGTACTATTGGGAGAGTCCA	980
Oy	180	uaIrgArProAlaHisValProLeuAspValPheLeuGluGluValAlaPheTrgIyle	200
Db	981	CATGAAGAAGGCATCTGCCCATC---TGCCTCAAGAAGAGATGGACTTCTGGAAAGT	1037
Oy	200	wGIyAlaAlaAlaLeuAlaArgLeuArgLysAspGluGlyCysProValProProGluAr	220
Db	1038	GGACCTCAAGTTCTG-----GACGACTGTGGCAAG-CGACCTGAGCG	1081
Oy	220	gProLeu-----	222
Db	1082	AGAACCGGAGAGACTGGAGAGATGCGCGCCGCTGACACTCTCGAGCACGTGG	1144
Oy	223	-----ProArg-ArgAlaPheAlaArgLInLeuTrpleuLeuPheg	236
Db	1142	GCGTGAGCGCGCGGAGGGCGGCTGGCGCGCTGCCAGAAAGTCCGTGGAAgTTCCtgg	1200
Oy	236	IurPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuValIlle	256
Db	1202	AGAAAGCCGAGTCTCTCTGCCCCGCGGGGTGGTGCCAGAGCTCTCTTCCTGCTCATTC	1261
Oy	256	eUaValSerlLeValAlaPheCysLeuGlnIurPheuProspPheargAspaBapArgAspg	276
Db	1282	TTCGTCGTCTCGGTGTATGTGATGGACACCATCCCAGAACTGCAG-----	1306
Oy	276	IyThrgIyLeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlys	296
Db	1309	-----GTCCGAGCGC-----	1322
Oy	296	erSerGlnMetProGlyAsnProProArgLeuProPheAsnAspProPhePheValG	316
Db	1321	-----GAGGGCGAACCGGGTGAGCACCCGACGCTGGAGAAC-----GTGG	1360
Oy	316	IuThrLeuGysIlieCysTrpPheSerPheGluLeuLeuValArgLeuLeuValCysPros	336
Db	1361	AGAGCGCGTGATGGCTGGTTCACCTGGAGTACTGCTGGCGCTTCTCTGTCACCCA	1420
Oy	336	erIySaIalIePhePheIyAsnValMetAsnLeuIleAspPheValAlaIleLeuProt	356
Db	1421	ACAAGCTGCACTTGGCGCTCTCCTTCATGAACATTGTGGACGCGTGGGCATCTCCCT	1480
Oy	356	yrrPheValAla-----LeuGlyThrIuleuAlaArgGlnArgGlyG	371
Db	1481	TCTACGTAGCGCTCACGCTCACGACCTCGGTGCCGATGATGAGCTGACCAACGTG-	1538
Oy	371	IyGlnGlnAlaMetSerLeuAlaIleLeuArgAlIleArgLeuValArgValPheArgI	391
Db	1540	--CAGCAGGCC-----GTGAGGGCGGTGGGATCAAGCCATCGCGCGCA	1583
Oy	391	IepHeIyLeuSerArgHisSerIyGlyLeuGlnIleLeuGlyGlnThrLeuArgAlas	411
Db	1583	TCTTCAGCTGGCCCGCCACTCTCGGGCTGTGAGACCTCACACTRAGCCCTCAAAGCA	1642
Oy	411	erMetArgIuleuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSers	431
Db	1643	GCTTCAGGAAGACTGGGCTGCTGCTCATGACTGTGCAGAGGGATNCTCGTCTCTCG	1702
Oy	431	erAlaValTyrrPheAlaGluValAspArgValAspSerHisPheThrSerIleProGlus	451
Db	1703	CCCTGGGCTACACCATGAGCAGAGCCATCCAGAGACCTGTTTAGAACATACCCCAAGT	1762
Oy	451	erPheTrpTrpAlaValValThrMetThrPhrAlaGlyIyryGlyAspMetAlaProValT	471
Db	1763	CCTTCTGTGTGGCATATATACCATGACACCGTGGCTACGGCGCACTTACCCCAAGA	1822
Oy	471	hrValGlYglYsIleValGlYserLeuCysAlaIleLaGlyValLeuThrIleSerI	491
Db	1823	CCAGCGTGAGCAAGCTCAACGGCGGCATCAGCTTCTGTGTGTGTGTGTCATTTGCCATCGCC	1882
Oy	491	eUrProValProValIleValAsnProPheSerTyrrPheTyrrHisArgGluThr-----	508

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Db      1883  TGCCATTCACCCCATCATCAAACTTTGTCCAGSTACTACAAACAGACCGCGCTCTCG 19
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Oy      509  -----
Db      1943  AGACCCGCGCCAGCAGACGACCTGACCTGACTCACTCCAGCAGCGGGGCGAG 20
              |||:::  |||:::|||||  |||
Oy      510  IYGIUGIUALIAGIymtPherSerHisValAspMetGlnProCysGlyProLeuGluGly 53
              |||:::  |||:::|||||  |||
Db      2003  GCAAGACCGGGGGGTCCCGCAGTGGACGACCTCCCTCCAGACCT---GCGGGG 20
              |||:::  |||:::|||||  |||
Oy      530  YSAIAaangIyGlyLeuValaLaspGlyIuValIProGluLeuProProProLeuTPAlap 55
              |||:::  |||:::|||||  |||
Db      2060  AG-----GAGCGCCCGAG-CTCGACACACCGCGGTGAAGCTC 20
              |||:::  |||:::|||||  |||
Oy      550  roPArGtGluHisLeu 55
              |||:::  |||:::|||||  |||
Db      2095  TCCACAGCGCACACTT 2111
              |||:::  |||:::|||||  |||

RESULT 13
PCT-US94-08449A-3
? Sequence 3, Application PC/TUS9408449A
? GENERAL INFORMATION:
? APPLICANT: LI, ET AL.
? TITLE OF INVENTION: Potassium Channel Protein 1 and 2
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
? ADDRESSEE: CECCHI, STEWART & OLSTEIN
? STREET: 6 BECKER FARM ROAD
? CITY: ROSELAND
? STATE: NEW JERSEY
? COUNTRY: USA
? ZIP: 07068
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 INCH DISKETTE
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: WORD PERFECT 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US94/08449A
? FILING DATE: SUBMITTED HERewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: FERRARO, GREGORY D.
? REGISTRATION NUMBER: 36,134
? REFERENCE/DOCKET NUMBER: 325800-105
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ. ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2483 BASE PAIRS
? TYPE: NUCLEIC ACID
? STRANDEDNESS: SINGLE
? TOPOLOGY: LINEAR
? MOLECULE TYPE: CDNA
PCT-US94-08449A-3

Alignment Scores:
Pred. No.: 7.35e-39 Length: 2483
Score: 649.50 Matches: 204
Percent Similarity: 44.058 Conservative: 81
Best Local Similarity: 31.538 Mismatches: 208
Query Match: 22.268 Indels: 156
DB: 5 Gaps: 19

US-09-804-014A-8 (1-559) x PCT-US94-08449A-3 (1-2483)
Oy      3  ArgArGArGtHr-----GlySerArGArGtGlnLysAspGlyGluYsgIyAsp 18

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357 CCAGAGAGCCGAGCTGAAGCGCGCGCCGCCAGCCAGCCGGGTGAGTCCCGG 416
19 ProglYThrGlyLysAlaInSerArgArgGlyArgArgArgArgGly 38
417 GCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 476
39 ArgAlaSerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThr 58
477 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 500
59 ValPro-----ProPro-----SerArgProSerArgProAla 69
501 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 560
70 GlyLeuPheThrAlaArgThrProAspThrGlyHis----- 81
561 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 620
82 -----ArgAlaGlyAlaAlaValAlaGlyAlaThrArg 91
621 GCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 680
92 ArgPheAlaGlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCys 111
681 GAGATGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
112 GlyCysCysGlyArg-LeuValLeuAsnValAlaGlyLeuArgPheGlyThrArgAlaArg 131
741 CAGCGACGACATAGAGATGCTGTCACACGTGGGGCGCGCGCGCGCGCGCG 800
131 gThrLeuGlyArgPheProAspThrLeuLeuGlyAsp-----ProAlaArgArgGlyArg 149
801 CCTCCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 860
149 gPhe-----TyrAspAspAlaArgArgGlyThrPhePhe 160
861 CTACGACACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 920
160 eAspArgHisArgProSerPheAspAlaValLeuArgGlyThrGlnSerGlyArgGly 180
921 TCACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980
180 uArgArgProAlaHisValProLeuAspValPheLeuGlnGluValAlaPheThrGlyLe 200
981 CATGAAGAGAGGCGATCTGCCCATC---TGCCTTCAAGAACGACATGACTTCTGGAAGT 1037
200 uGlyAlaAlaAlaLeuAlaArgLeuArgGlyAspGlnGlyCysProValProProGlnArg 220
1038 GACCTCAAGTTCCTG-----GACGACTGTTCAGAGAG--CCACCTCAGCG 1081
220 gProLeu----- 222
1082 ACAAGCGCGAGAGCTGAGAGAGATCGCGCGCGCGCGCGCGCGCGCGCG 1141
223 -----ProArg-ArgAlaPheAlaArgGlnLeuThrPheLeuPheG 236
1142 GCGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1201
236 lupPheProGlnSerSerGlnAlaAlaArgValLeuAlaValSerValLeuValIleL 256
1202 AGAAGCGCGCGAGTCTGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 1261
256 euValSerIleValAlaPheCysLeuGlnThrLeuProAspPheAlaGAspAspArgAspG 276
1262 TCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1308
276 lYThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlyS 296
1309 -----GTGCTGAGCGCG----- 1320
296 eSerGlnMetProGlnAsnProProArgLeuProPheAsnAspProPhePheValAlaG 316
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1321 -----GAGGCGAACCGCGGTGAGACACCGACGCTGAGAGAAC-----GTGG 1360
316 luthrLeuCysIleCysTrpPheSerPheGlnLeuLeuValArgLeuLeuValCysPro 336
1361 AGAGCGGTGACATTTGGCTGGTTCACCTGGAGTACTGGCTGGCTTTCTGTCA 1420
336 eLysAlaIlePhePhePheLysAsnValMetAsnLeuIleAsnPheValAlaIleLeuPro 356
1421 ACAAGCTGACACTTCGGCGTCTCTTCATATGACATTGTGGACGTCGTCGCTCCCT 1480
356 yrePheValAla-----LeuGlyThrGlnLeuAlaArgGlnArgGlyValG 371
1481 TCACCTGAGCCCTCACGCTCACGACCTGGGTGTCGCGCATGATGAGCTGACCAAGT- 1539
371 LysGlnIleAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgI 391
1540 --CAGCAGCGC-----GTGCAAGCGCTGGAGATCATGCGATCGCGCGCA 1582
391 lPheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlnGlyInThrLeuArgAla 411
1583 TCTTCAAGCTGGCGCGCGCGCACTCTCGGCGCTGAGACCTCACCTTGGCTCAACGCG 1642
411 eMetArgGlnLeuGlyLeuLeuIlePhePheLeuPheIleGlyValLeuLeuPheSer 431
1643 GCTTCAAGGAACCTGGCGCTGCTCATGATACCTGAGCGATGGGTATCTTCTCTCTG 1702
431 eAlaValArgPheAlaGlnValAlaAspArgValAlaSerHisPheThrSerIleProGln 451
1703 CCTGGGCTACACCATGAGAGCAGACCATTCACAGACCTGTATTAAAGCATCTCCAGT 1762
451 ePheThrTrpAlaValAlaIleThrMetThrValGlyArgGlyAspMetAlaProValArg 471
1763 CTTTCTGGTGGCGATCATCATCAGATGACACCGCTGAGCGCGATCTACCCCAAGA 1822
471 hValGlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSer 491
1823 CCACGCTGAGCAAGCTTCAACGCGCGCGCATCAGCTTCTGTGTGATGTCATTTGCCAT 1882
491 euProValProValIleValSerAsnPheSerArgPheArgHisArgGlyThr----- 508
1883 TGCCATTCACCCCATCATCAACACTTGTGATGATACAAACAGACGCGCTCTG 1942
509 -----GluG 510
1943 AGACCGCGCGCAAGCAGAGCTGAGCTGATGAACTCAACTCAACACAGCGGGGAG 2002
510 lYglnGlnAlaGlyMetPheSerHisValAspPheGlnProCysGlyProLeuGlnGlyL 530
2003 GCMAAGCGCGGGGCTCCCGCAGTGAAGCTGAGAACCTCCCTCCAGAGCCT---GCGGGA 2059
530 yAlaAsnGlyGlyLeuValAspGlyGluValProGlnLeuProProPheLeuThrAlaP 550
2060 AG-----GAGGCGCGAG--CTGACAGACGCGGCTGAAGCTC 2094
550 roProArgGlnHisLeu 555
2095 TCCACACGACGACACTT 2111

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RESULT 14  
 US-08-464-340A-1  
 ; Sequence 1, Application US/08464340A  
 ; Patent No. 5710019  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LI, ET AL.  
 ; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA

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? ZIP: 07068
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 INCH DISKETTE
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: WORD PERFECT 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/464,340A
? FILING DATE: June 5,1995
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: PCT/US94/08449
? FILING DATE: 28 JUL 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: FERRARO, GREGORY D.
? REGISTRATION NUMBER: 36,134
? REFERENCE/DOCKET NUMBER: 325800-415
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2127 BASE PAIRS
? TYPE: NUCLEIC ACID
? STRANDEDNESS: SINGLE
? TOPOLOGY: LINEAR
? MOLECULE TYPE: CDNA
? US-08-464-340A-1

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## Alignment Scores:

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Pred. No.: 3,75e-36 Length: 2127
Score: 611.50 Matches: 174
Percent Similarity: 44.60% Conservative: 74
Best Local Similarity: 31.29% Mismatches: 204
Query Match: 20,964 Indels: 105
DB: 1 Gaps: 14

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US-09-804-014A-8 (1-559) x US-08-464-340A-1 (1-2127)

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DB 196 GGGAGGAGGAAGCGCGCGCGCGCAACTCCGAGCGGGGAGCGCGCGGAACTTGAG 255
QY 37 ALAGLYARGALASERARGGLNARGALARGGLY----- 47
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DB 256 GCC-----CGAGGAGGATGGAAGGCCCAAAATGACCCCTTACCGGAGACA 303
QY 48 -----ARGPROVALALALEUARGPROALAGLYVALTHYVALPROPROP- 65
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DB 304 ATTCTGACTACGACTACAGCGCGCTGAGCTGCACCTCGACGCTTCCACCGCGCT 363
QY 66 SERARGPROALAGLYLEUPHETRYALARGTHYPROASPTHREGLYHISARGALAGLYALA 85
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DB 364 TCC-----TCCCGCAGCGCC 378
QY 86 ALAVALGLYALATHRARGARGPHEALAGLYARGARGGLYCYSALAARGHIS--GLYALA 104
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 379 AGCGCATCAAGCGCGCGCTTACCGCGCGCGAGCGCGCTGCGCGCGCAGATGAGCCCC 438
QY 105 ALAVALPROALALAPROCYSGLYCYSGLIARGLEUVALLEUASNVALALAGLYLEU 124
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DB 439 GCCAGGCGTGTCAAGCGCGAGAGCGCGCGC-CGTGCGATCTCATCAACGTAAGCGGCATC 497
QY 125 ARGPHGLIUTHRARGALARGTHREGLYARGPHEPROASPTHRELEUGLYASPRO 144
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DB 498 AAGTACTCGCTCGCTCGAGCACGCTGAGACGAGTCCCGCTGACGCGCGCTGCGCACCTC 557
QY 145 ALAARGARGGLYARGPHE-----TYRASPASPALAARG 155
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DB 558 AAGGCTTGACCAACTTCGACGACATCTCAACGTGTGCGATGACATACGACGTCACCTGC 617
QY 156 ARGGLIUTYRPHSPHSPARGHISARGPROSERPHEASPALAVALLEUTYRITYRGLN 175
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DB 618 AACGAGTTCTTTCGACCCGCAACCCGCGGCGCTTCGCGCATCTTCGACCTTCGCGC 677
QY 176 SERGLYIARGLEUARGARGPROALANISVALPROLEUASRYVALPHELEUGLYVAL 195
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DB 678 GCG---GCAAGCTGCGCGCTGCTCGCGGAGATGTCGCGCGCTTCGACGAGAGACTG 734
QY 196 ALAPHETRYGLYLEUGLY----- 201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 735 CTGTACTGGGGCATCGCGGAGAGACACCTGAGCGCTGTCAAGCGCGCTACCTGACG 794
QY 202 -----ALAIALALALEUALARGLEUARGGLYASPROGLIUGLYCYS----- 214
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 795 AAGATTGAGAGTTCCGCGAGATGCTGAGCGGAGGAAAGAGACGAGCGCTGAGACG 854
QY 215 -----PROVALPROGLIARGPROLEUPROALARGALAPHE 227
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 855 GAGGCGCGCGACAGCGAGGCGCGCGGAGGCGAGGCGCGCGCTGGCGCGC-----TGC 908
QY 228 ALAARGIINLEUTRPLEUARGPHEGLUPHETROGLIUSERSERGLAIALAARGVALLEU 247
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DB 909 ATGCGGCGACTGCGCGCATGCTGAGAGCGCGCATGCGGCGCTGCGCGCAAGTGTTC 968
QY 248 ALAVALSERVALLEUVALILEUVALSERILEVALVALPHECYSLEUGLYTHYLEU 267
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DB 969 GCTGCTGTGCTGCTTCTGTCGACCGCTGACCGCGCTCAACCTTCGTCAGACACTTG 1028
QY 268 PROASPHETARGASPASPARGASGLYTHRGILEUVALAIALAIALAIALAGLYPRO 287
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1029 CCCAGCCTGAGGAGGAGAGAGAG----- 1052
QY 288 VALPHEPROALAPROLEUASNGLYSERSEGLIMETPROGLIASNPROALARGLEUPRO 307
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1053 -----CAGGCGCACCTGTTCACATGTGCCACAC----- 1082
QY 308 PHEASNAPROPHETPHEVALIAGLYTHYLEUCYSILECYSRTPHESERPHLEGLILEU 327
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1083 -----GTCTTCATCTGTGAGTGTGCTGCTGAGCTGTCTCTGAGTTC 1130
QY 328 LEUVALARGLEUVALIYSPROSERLYSALAILPHEPHELYASNVALMETASNLEU 347
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1131 CTCTGTGGGCTCATTCAGGCGCGCCAGCAATGTGCGCTTCGCGGAGCGCGCTGAGCTG 1190
QY 348 ILEASPHVALAIALILEUPROTRYRPHENVALALEUGLYTHRGILEUALA----- 365
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1191 ATGACCTGTGCGCATCTGCTTACATCATGACGCTGCTGTGAGCGCGCGCGCGCA 1250
QY 366 -----ARGLINARGGLYVALIYGLINGLINALMETSERILEUALA-----ILEUARG 381
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DB 1251 GCGCGTGCAGCGCGCGCGCGCGCAACGCTTACCTGAGCAAGGTGGGCTGTGTGCGC 1310
QY 382 VALILEARGLEUVALARGVALPHEARGILEPHELYSLEUSERARGHISERTLYSGLYLEU 401
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1311 GTCTGTGGGCGCTGCGCATCTGTACGTGATGCTGCGCGCGCATCTCCGCGGCTG 1370
QY 402 GLNILEUGLYINLTHREUARGALASERMETARGILEUGLYLEULEUILEPHEPHE 421
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1371 CAGACGCTGGGCTCACGCGCGCGCGCTGCACCGCGAGCTTCGCGGCTGCTGCTTTC 1430
QY 422 LEUPHEILEGLYVALIILEUPHESERSERIALVALIYTRPHEALAGLYVALASPARGLYAL 441
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1431 CTCTGTGCTGCGCATGCGCGCTTCCGCGCTTCTTACCTCATCAAGAGATGAGCGC 1490
QY 442 ASPSER---HISPHETSERILEPROGLIUSERPHETRPRPALAVALIYTHMETRTH 460
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1491 GACAGCGCGAGTTCACAGCATCTCTGCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1550
QY 461 THRVALGLYTRGLIYASPMETALAPROVALIYHVALGLYGLYSILEVALIYGLYSERLEU 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1551 ACGGTGACATATGCGCAGCATGTCCCGCAGAGACCGCGCGAGAGTGGCGCTGAGC 1610
QY 481 CYSALAILAIALAGLYVALLEUTHRIIESERLEUPROVALIYVALIILEVALISERASPH 500
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1611 ACGATCTGTGAGCGCATCTGCTCATGCGCTTCCAGTCACTTCATCTTCACACCTTC 1670

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QY 501 SerTyrPheTyrHisArgGluThrGluGlyGluAlaGlyMetPhe 516  
 DB 1671 TCCCCCTCTTACCTGAGCTCAACAGAGCAAGAGAGGATGTTTC 1718

## RESULT 15

PCT-US94-08449A-1

Sequence 1, Application PC/TUS9408449A

GENERAL INFORMATION:

APPLICANT: LI, ET AL.

TITLE OF INVENTION: Potassium Channel Protein 1 and 2

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/08449A

FILING DATE: SUBMITTED HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-105

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1740

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2127 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

PCT-US94-08449A-1

Alignment Scores:

Pred. No.: 3,75e-36 Length: 2127

Score: 611.50 Matches: 174

Percent Similarity: 44.60% Conservative: 74

Best Local Similarity: 31.29% Mismatches: 204

Query Match: 20.96% Indels: 105

DB: 5 Gaps: 14

US-09-804-014A-8 (1-559) x PCT-US94-08449A-1 (1-2127)

QY 17 GlysAspProGlyThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArg 36  
 DB 196 GGGGACGGAAGCCGGCGGGCCAACTCCGAGGGGACGCCGCGAGCGAAGCTTGAG 255  
 QY 37 AlaGlyArgAlaSerArgGlnArgAlaArgGly----- 47  
 DB 256 GGC-----CGAGAGGAGTGTGAAGCCCAAAATGACCTTACCGGGAGACA 303  
 QY 48 -----ArgProValAlaLeuArgProAlaGlyAlaThrValProProSerArgPro 65  
 DB 304 ATTGTGACTAGACTACAGCGCGCTGAGCTGCACCTCGGAGCGCTTCCTCCACCGGCGCT 363  
 QY 66 SerArgProAlaGlyLeuPheTyrAlaArgThrProAspThrGlyHisArgAlaGlyAla 85  
 DB 364 TCC-----TCCCGCAGCGCC 378

QY 86 AlaValGlyAlaThrArgArgPheAlaGlyArgGlyCysAlaArgHis---GlyAla 104  
 DB 379 AGGCCATCAAGGGCGGCTTCTACCGCGGCGAGCGGCGCCGAGATGAGACCC 438  
 QY 105 AlaValProAlaAlaProCysGlyCysGluArgLeuValLeuAsnValAlaGlyLeu 124  
 DB 439 GCGAGGCTGTGAGCCCGGAGACCGCGCG--CGTCGATCATCATCAACCTAGCGGCGATC 497  
 QY 125 ArgPheGluThrArgAlaArgThrLeuGlyArgPheProAspThrLeuGluysPro 144  
 DB 498 AAGTACTCCCTCCCTGAGACACGCGTGCAGAGTTCCCTGACGCGCGCTGGCGCAGCTC 557  
 QY 145 AlaArgArgGlyArgPhe-----TyrAspAlaArg 155  
 DB 558 AAGCGCTGCACCAACTTCGACGACATCTCAACGCTGCGATGACTACGACGTCACCTGC 617  
 QY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175  
 DB 618 AAGAGTTCTTCTTGCACCGCAACCGCGGCGCTTGGCAGTATCTGACCTTCCGCGCG 677  
 QY 176 SerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGlyVal 195  
 DB 678 GCG--GGCAAGCTGCGCTGCTGCGCGAGATGCGCGCTGCTCTCCAGAGAGAGCTG 734  
 QY 196 AlaPheTyrGlyLeuGly----- 201  
 DB 735 CTGTACTGGGGCATCGCGAGGACCACTGACGCGCTGCGAAGCGCGCTTACCTGCAG 794  
 QY 202 -----AlaAlaAlaLeuAlaArgLeuArgLysProLys----- 214  
 DB 795 AAGATTGAGAGAGTTCGCGGAGATGTTGAGCGGAGGAGAGAGAGACGCGCTGAGCAGC 854  
 QY 215 -----ProValProProGluArgProLeuProArgArgAlaPhe 227  
 DB 855 GAGGCGCGGACAGCGAGGCGCGCGCGAGGCGAGGCGCGCTGCGGCGC-----TGC 908  
 QY 228 AlaArgGlnLeuTyrLeuLeuPheGluPheProGluSerGlnAlaAlaArgValLeu 247  
 DB 909 ATCGCGGACGTGCGGACATGTGTGGAGAGCGCGACCTCGGGGCTGCTGCGCAAGTGTTC 968  
 QY 248 AlaValAlaSerValLeuValIleLeuValSerIleValValPheCysLeuGluThrLeu 267  
 DB 969 GCCTGCTGCTGATGCTTTCGACCGTCCACCGCGCTCAACCTGCTCCGTCAGACCTTG 1028  
 QY 268 ProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaGlyPro 287  
 DB 1029 CCCAGCTGAGGAGAGAGAG----- 1052  
 QY 288 ValPheProAlaProLeuAsnGlySerGlnMetProGlyAsnProProArgLeuPro 307  
 DB 1053 -----CAGGCGCACTGTTCCAGATGTGCCACAC----- 1082  
 QY 308 PheAsnAspProPhePheValAlaGluThrLeuCysIleCysTrpPheSerPheGluLeu 327  
 DB 1083 -----GTCCTTACGTGAGGTGCGGTGGTGGCTGTTCTCCCTGGAGTTTC 1130  
 QY 328 LeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeu 347  
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 QY 348 IleAspPheValAlaIleLeuProTyrPhePheAlaIleGlyThrGluLeuAla----- 365  
 DB 1191 ATCGACCTGTGTGCGCTTCTGCTTCACTACACAGCTGCTGTGTGACGCGCGCGCGCA 1250  
 QY 366 -----ArgLnaArgGlyValGlyGlnAlaMetSerLeuAla-----IleLeuArg 381  
 DB 1251 GCGCGCGCAAGCCGCGCGGCAACAGCTACCTGAGACAGGTGGGCTGTGTGCTGCGCGC 1310  
 QY 382 ValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeu 401  
 DB 1311 GTGCTGCGGCGCTGCGATCTCTAGCGATGATGCGCTGCGCGCACCTCCTGGGCGCTG 1370



GenCore version 5.1.3  
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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: February 20, 2003, 11:49:51 : Search time 2234 Seconds  
(without alignments)  
4052.496 Million cell updates/sec

Title: US-09-804-014A-8  
Perfect score: 2918  
Sequence: 1 MERRRTRSRKDKGKDGDPG.....VPELPPLMAPPREHLVTEV 559

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-O=/cgn2.1/USPTO\_spool/US09804014/runat\_10022003.161449.27221/app.query.fasta.1.711  
-DB=IST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -DOPC=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09804014.qcgn.1.1.813 &runat\_10022003.161449.27221 -NCRU=6 -ICPU=3  
-NO\_XLPRX -NO\_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	1107	37.9	1085	17	CNS035KP
2	986.5	33.8	1058	14	BM924998
3	983.5	33.7	900	17	CNS02RD3
4	896	30.7	839	17	CNS03DKC
5	892	30.6	876	13	BM117089
6	853	29.2	745	14	BM963332
7	815	27.9	636	17	AZ339279
8	794	27.2	954	14	BQ714749
9	765	26.2	2146	11	BC023222
10	760.5	26.1	1060	17	CNS058RO
11	744	25.5	559	12	BC812963
12	743	25.5	629	17	AG163977
13	736	25.2	575	13	BM128683
14	732	25.1	593	13	BM128211
15	729	25.0	963	17	CNS02ISY
16	719.5	24.7	1109	17	CNS045OM
17	700	24.0	697	10	BS541281
18	693.5	23.8	640	13	BG973314
19	693	23.7	772	13	B1764377
20	690	23.6	628	14	BQ807519
21	676	23.2	443	17	AQ939702
22	649.5	22.3	468	9	A1324179
23	638	21.9	522	9	A1322534
24	634	21.7	900	14	BQ938497
25	633.5	21.7	2265	11	BC019010
26	625	21.4	1054	17	CNS05DBK
27	616.5	21.1	927	14	BQ930283
28	613	21.0	506	13	B1467889
29	606	20.8	434	10	BE654741
30	589.5	20.2	434	9	BE654741
31	574	19.7	687	13	B1295790
32	567	19.4	457	9	A1694783
33	566.5	19.4	457	11	A1694783
34	564.5	19.3	631	10	BB622001
35	559	19.2	990	17	CNS04EVP
36	557.5	19.1	990	17	CNS04EVP
37	554.5	19.0	770	12	BS530500
38	553.5	19.0	1087	17	CNS02H90
39	549	18.8	526	13	B1339926
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43	517	17.7	668	14	BQ187015
44	515	17.6	400	12	BF108522
45	510	17.5	437	12	BE865003

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CNS035KP/c	CNS035KP	Tetradon nigroviridis genome survey sequence PUC-Orl end of clone 214T01 of library G from Tetradon nigroviridis, genomic survey sequence.	AL228850.1	GI:7887843	GSS: genome survey sequence.	Tetradon nigroviridis.	Tetradon nigroviridis
CNS035KP	CNS035KP	1085 bp DNA linear GSS 15-MAY-2000	AL228850				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1085)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Benoit,A., Fizames,C., Wincker,P., Brotier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
TITLE Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1085)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Weissenbach,J.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Benoit,A. and  
Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1085)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-Apr-2000)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES  
source  
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/db\_xref="taxon:99883"  
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/clone\_lib="g"  
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PDC-071"

BASE COUNT 201 a 308 c 372 g 198 t 6 others

ORIGIN

Alignment Scores:  
Pred. No.: 1 29e-75 Length: 1085  
Score: 1107.00 Matches: 222  
Percent Similarity: 75.71% Conservative: 43  
Best Local Similarity: 63.43% Mismatches: 64  
Query Match: 37.94% Indels: 22  
DB: 17 Gaps: 3

US-09-804-014A-8 (1-559) x CNS035KP (1-1085)

QY 113 CysCysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThr 132  
|||||  
Db 1012 TGGCTGGAGGGCGKTTTCATCAATCTTCAGGCTGGCTTGAACCCAGCGAGAGACC 953  
QY 133 LeuGly-ArgPheProAspThrLeuLeuGlyAspProAlaArgGlyArgPheTras 152  
|||  
Db 952 CTGGCCCCAGTTCCCGAGACCTCTCGGAGAACCCAGAGAGAGATGGCTACTTCA 893  
QY 152 PAspAlaArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyr 172  
|||  
Db 892 CCCGCTGGCGAGAGAGTACTTTCACCGGACCGGCCAGCTTGCAGCCACTCTCTA 833  
QY 172 rTyrTyrGlnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLe 192  
|||||  
Db 832 CTACTACAGTGGCGGCGGCTGAGGCGGCTCAACGTCCTCCCTGACATGTTCTCT 773  
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Db 712 GGGCTTCATCCGGAGAGAGAGCGCGCTCCCGGAGAACAGATTCACAGCGGACGCTCTG 653  
QY 232 PleuLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerVa 252  
|||  
Db 652 GCT-CTCTTCGAGACCGGAGAGCTCGGGTCCGGCGGCGGATCGCCATCGTCTCTGT 594  
QY 252 lLeuValllleuValSerllleValValPheCysLeuGluThrLeuProAspPheArgas 272  
|||||

Db 593 GATGTCATCTCATCTCCATCTGTCATCTTTCGCTGGAGAGCTCCGAGACTGAGGA 514  
QY 272 PAspArgAspGlyThrGlyLeuAlaAlaAlaAlaGlyProValPheProAlaPr 292  
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Db 533 GGGACCTG---AGCGAGCGGCTGCGAGGTGCCGGGCAACACCATCTTCTCAACAGCC 477  
QY 292 oLeuAsnGlySerSerGlnMetProGlyAsnProProAlaGluProPheAsnAspProp 312  
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Db 476 C-----TACATCTGACGAGACCCCTT 456  
QY 312 ePheValValGluThrLeuCysllleCysTrpPheSerPheGluLeuValArgLeuLe 332  
|||||  
Db 455 CTTCATCTGAGACACCTCTGATCTGCTGCTCTCTTCGAGCTCATATGCTGCGCTTCTT 396  
QY 332 uValCysProSerGlyAlaAlaPhePheGlyAsnValMetAsnLeuIlleAspPheValAl 352  
|||||  
Db 395 CGCCTGCCCCAGCAGAGCGGCTTCTTCAAGAACATGATCAACACCATGACATCGTGGC 336  
QY 352 alleuProTyrPheValAlaLeuGlyThrGluAlaArgGln----- 367  
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Db 335 CATCATCCCTCTACTCATCAGCTGGGAGAGCTGGCCGAGAGGCAACAGAGAGG 276  
QY 368 ----ArgGlyValGlyGlnGlnAlaMetSerLeuAlaIlleLeuArgValIlleArgLeuVa 386  
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Db 275 CAAGGCGCGGCTGGGAGAGCCACCTCGCTGCACTCTAGGATCATCCGCTGGT 216  
QY 386 lArgValPheArglllePheLysLeuSerArgHisSerGlyGlyLeuGlnIlleLeuGlyG 406  
|||||  
Db 215 CCCGCTTCCGATCTTCAAGCTGTCCCGCCACCTCAAGAGGGCTCAAGATCTCTGGGCCA 156  
QY 406 nThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIllePhePheLeuPheIlleGlyVa 426  
|||||  
Db 155 GACCTGAAGAGCCAGCATGCGCAGCTGCGCTCATCTCTCTCTCATCCGGGT 96  
QY 426 lValleuPheSerSerAlaValTyrPheAlaGluValAlaAspArgValAspSerHisPheTh 446  
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QY 446 rSerllleProGluSerPheTrpPAla 455  
|||||  
Db 35 CAGCATCCCGGAGCGCTTCTGGTGGGGG 8

RESULT 2  
BM924998 1058 bp mRNA linear EST 12-MAR-2002  
LOCUS AGENCOURT.6627466 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5762269  
DEFINITION 5', mRNA sequence.  
ACCESSION BM924998  
VERSION BM924998.1 GI:19375377  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1058)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12812 row: d column: 14  
High quality sequence start: 8  
High quality sequence stop: 689.  
Location/Qualifiers  
1..1058  
/organism="Homo sapiens"





## Alignment Scores:

Pred. No.: 3,58e-66 Length: 900  
 Score: 983.50 Matches: 199  
 Percent Similarity: 80.77% Conservative: 32  
 Best Local Similarity: 69.58% Mismatches: 40  
 Query Match: 33.70% Indels: 17  
 DB: 17 Gaps: 2

US-09-804-014a-8 (1-559) x CNS02RD3 (1-900)

```

QY 227 PheAlaArgGlnLeuThrPheLeuPheGluPheProGluSerGlnAlaAlaArgVal 246
DB 895 TTCAAGGGGAGATCGCTGCTTTCAGATACCGGAGACCTCCACCCCGCCAGGGC 836
QY 247 LeuAlaValValSerValLeuValIleLeuValSerIleValValPheCysLeuGluThr 266
DB 835 ATCCGGGTGGTCTCCCTCGTGTATGTATCTTCATCTGTCATCTTCTGCTGGAGAGC 776
QY 267 LeuProAspPheArgAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaGly 286
DB 775 CTGCGGAGATTACGAGGAGAGAGAG----- 749
QY 287 ProValPheProAlaProLeuAlaGlySerSerGlnMetProGlyAsnProProArgLeu 306
DB 748 -----TACCTGACGCGCGGGGCACTCCAGCGA-----GCCGACACGAGTTTACG 701
QY 307 ProPheAsnAspProPhePheValAlaGluThrLeuCysIleCysTrpPheSerPheGlu 326
DB 700 CCTTCAACGACGCCCTTTTCATCTGTGAGAGCGGTCTGCATCATCTGTTCTCTTTGAG 641
QY 327 LeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsn 346
DB 640 ATTATATGTCGCTCTTCGCCAGCCCAAGACCGGCTTCTTTAAACATCATGATGAC 581
QY 347 LeuIleAspPheValAlaIleLeuProThrPheValAlaLeuGlyThrGluLeuAlaArg 366
DB 580 TCCATTAACATCGTGTCTATTTCTCTTATTTCATCACTCGCGCAGGAGCTTGAGCCAG 521
QY 367 GlnArgGlyValGlyGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuVal 386
DB 520 CACGAGGGGCAAGGGGAGCAAGCATGAS-TTGGCCATTCCTGAGAAATATATCGGCTGTC 462
QY 387 ArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGln 406
DB 461 CGCGTGTCCGATCTTCATCTGTCCAGACACTCAAGGGGCTGACAGATCTGGGCAAT 402
QY 407 ThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyVal 426
DB 401 ACCCTGGCGCCAGCATGAGGAGCTGCGCTCTCATTTCTTCTGTGTGATCGGCGTC 342
QY 427 ValLeuPheSerSerAlaValIlePheAlaGluValAspArgValAspSerHisPheThr 446
DB 341 ATCTCTTCTTCACGCGGGGTACTTTCGCGGAGGGGAGGCCACCTCCAGTTGACC 282
QY 447 SerIleProGluSerPheTrpTrpAlaValAlaIleThrMetThrThrValGlyTyrGlyAsp 466
DB 281 AGCATCCCGGCGGCTGTGTGTGGCTGTGTACCATGACGAGCGTGGGCGCAT 222
QY 467 MetAlaProValIleThrAlaGlyLysIleValGlySerLeuCysAlaIleAlaGlyVal 486
DB 221 ATGAGGCTATACGAGTGGTGGGAGATCGTGGCTCCCTGCGGCAATGGCGGGCTG 162
QY 487 LeuThrIleSerLeuProValIleValSerAsnPheSerTyrPheTyrHisArg 506
DB 161 TTAAAGATCGGGCTGCCGTG-CCGGTCACTGCTGTCAACTTAATTACTTTTACCACCGG 103
QY 507 GluThrGluGluGlu 512
DB 102 GAGACGATACGAAGAC 85

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RESULT 4  
 CNS03DKC/c  
 Locus CNS03DKC 839 bp DNA linear GSS 15-MAY-2000

```

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
ACCESSION 017A20 of library G from Tetraodon nigroviridis, genomic survey
VERSION AL239205
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
REFERENCE 1 (bases 1 to 839)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
HUMAN gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
TITLE Unpublished
JOURNAL 2 (bases 1 to 839)
REFERENCE Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
AUTHORS Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 839)
AUTHORS Genoscope.
JOURNAL Direct Submission
COMMENT Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..839
location/Qualifiers
1..839
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99863"
/db_xref="017A20"
/clone_1fb="G"
/note="Genoscope sequence ID : COB017BA10PL1-end : T7"
BASE COUNT 157 a 246 c 281 g 155 t
ORIGIN
Alignment Scores:
Pred. No.: 1.87e-59 Length: 839
Score: 896.00 Matches: 176
Percent Similarity: 73.63% Conservative: 39
Best Local Similarity: 60.27% Mismatches: 57
Query Match: 30.71% Indels: 20
DB: 17 Gaps: 3
US-09-804-014a-8 (1-559) x CNS03DKC (1-839)
QY 118 ValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPhePro 137
DB 118 ValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPhePro 137
QY 838 GTCATCAACATCTCAGGCTCGCTCGTCAACCCAGCTGAGAGACCTGGCCAGTTCCG 779
DB 838 GTCATCAACATCTCAGGCTCGCTCGTCAACCCAGCTGAGAGACCTGGCCAGTTCCG 779
QY 138 AspThrLeuLeuGlyAspProAlaArgGlyLysThrPheTyrAspAlaArgGlu 157
DB 138 AspThrLeuLeuGlyAspProAlaArgGlyLysThrPheTyrAspAlaArgGlu 157
QY 778 GAGACCCCTCGGGGAAACCCAGGAAAGAGATGCGCTACTTTCGACCCGCTGGAGACAG 719
DB 778 GAGACCCCTCGGGGAAACCCAGGAAAGAGATGCGCTACTTTCGACCCGCTGGAGACAG 719
QY 158 TyrPhePheAspArgAlaArgProSerPheAspAlaValLeuTyrTyrGlnSerGly 177
DB 158 TyrPhePheAspArgAlaArgProSerPheAspAlaValLeuTyrTyrGlnSerGly 177
QY 718 TACTTCTTCGACCGGAAACCGGCCAGCTGACGCCATCTCTACTACAGTCGGGC 659
DB 718 TACTTCTTCGACCGGAAACCGGCCAGCTGACGCCATCTCTACTACAGTCGGGC 659
QY 178 GlnArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluValAlaPhe 197
DB 178 GlnArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluValAlaPhe 197
QY 658 GGCCGGCTGAGGCGGCGGTCACAGCTCCCGCTGACATGTTCTGGAGAGATCAATTC 599
DB 658 GGCCGGCTGAGGCGGCGGTCACAGCTCCCGCTGACATGTTCTGGAGAGATCAATTC 599
QY 198 TyrGlyLeuGlyAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysProValPro 217
DB 198 TACGAGCTGGCATGAGAGCCATGAGAAATTCCGCGAAGACGAGGCTTCATCCGGGAG 539

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```

QY 218 ProgluArgProleuProArgArgAlaPheAlaArgGlnLeuTrpLeuPheGluPhe 237
    |||||
Db 538 GAGGAGCGCGCGCTCGGAGACAGAGTTCACGCGGACGCTGCTCTTCAGACAC 479
QY 238 ProgluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuValIleLeuVal 257
    |||||
Db 478 CCGGAGAGCTCGGCTCGGAGGAGCATCGCATCTCTGTGTGTGTGTGTGTGTGTGTGT 419
QY 258 SerIleValValPheCysLeuGlnIleuTrpProAspPheArgAspAspArgspgIyTrp 277
    |||||
Db 418 TCCATCGTCATCTCTCTCGGAGAGCGCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 362
QY 278 GlysAlaAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSer 297
    |||||
Db 361 CCGGTCGAGGTCCTCGCGCGGACACACCATCTCTTCTACAGAGCC----- 317
QY 298 GlnMetProGlyAsnProProArgLeuProPheAsnAspProPhePheValAlaGluTrp 317
    |||||
Db 316 -----TACATCTGAGCGAGACCCCTTCTCTCATCTGTGTGTGTGTGTGTGTGTGT 281
QY 318 IleCysIleCysTrpPheSerPheGluLeuLeuValArgLeuLeuValCysProSerLys 337
    |||||
Db 280 CTCTGCATCATCTCTCTCTCTCGAGCTCATCTGCTGCTCTGCTGCTGCTGCTGCTGCTG 221
QY 338 AlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPhe 357
    |||||
Db 220 GCGGCGCTTCTCAAGACATGATGACACCATCATGATGATGATGATGATGATGATGATGAT 161
QY 358 ValAlaLeuGlyThrGluLeuAlaArgGln-----ArgGlyAlaGly 371
    |||||
Db 160 ATCAGCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 101
QY 372 GlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIle 391
    |||||
Db 100 GAGCAGGCGCCATCGCTGCGCATCTCAGGATCATCGGCTGCTGCTGCTGCTGCTGCTG 41
QY 392 PheLysLeuSerArgHisSerLysGlyLeuGlnIle 403
    |||||
Db 40 TTCAAGCTGTCCGCGCATCTCAAGGAGGCTCCAGAGCTT 5

```

**RESULT 5**  
**LOCUS** B1117089 876 bp mRNA linear EST 26-JUN-2001  
**DEFINITION** 602867882P1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:5016164 5',  
**ACCESSION** B1117089  
**VERSION** B1117089.1 GI:14567990  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
**REFERENCE** 1 (bases 1 to 876)  
**AUTHORS** NIH-MGC http://mgi.nci.nih.gov/  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: DCTD/DRP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: L10CM1826 row: d column: 21  
 High quality sequence stop: 830.  
**FEATURES**  
 location/Qualifiers  
 1..876  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5016164"  
 /clone\_lib="NIH\_MGC\_7"

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/tissue_type="small cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

**BASE COUNT** 179 a 264 c 233 g 200 t  
**ORIGIN**

**Alignment Scores:**  
 Pred. No.: 3,99e-59 Length: 876  
 Score: 892.00 Matches: 191  
 Percent Similarity: 72.73% Conservative: 33  
 Best Local Similarity: 62.01% Mismatches: 62  
 Query Match: 30.57% Indels: 22  
 DB: 13 Gaps: 4

US-09-804-014a-8 (1-559) x B1117089 (1-876)

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QY 159 PhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGlnSerGly 178
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Db 4 TTCTTGACCGCAGACCGCGCCAGCTTCGACGCCATCTTACTACACAGTCCGCGGC 63
QY 179 ArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluValAlaPheTyr 198
    |||||
Db 64 CCGCTCGAGGCGCGGTCAACGTCGCCCTGACATGTCTCCGAGAGATCAAGTTTAC 123
QY 199 GlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlySerProValProPro 218
    |||||
Db 124 GAGTTGGGCGAGAGCGCGGTGAGAGTTCGGGAGAGAGAGGCTTCATCAAGAGAG 183
QY 219 GluArgProLeuProArgArgAlaPheAlaArgGlnLeuTrpLeuPheGluPhePro 238
    |||||
Db 184 GAGCGCTCTGCGCGAGAGAGAGATCCAGCGCAGAGTGTGCTCTTCAGATGCC 243
QY 239 GluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuValIleLeuValSer 258
    |||||
Db 244 GAGAGCTCGGGCGCCGAGGATCATCGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
QY 259 IleValValPheCysLeuGlnIleuTrpProAspPheArgAspAspArgspgIyTrp 278
    |||||
Db 304 ATCGTCATCTTTGCTGAGAGCGTCCCGAGCTGAGAGATGACAGAGATTCACAGGCG 363
QY 279 LeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGln 298
    |||||
Db 364 ACCGTCACCGCATCGACACACAGCGCTCATC-----TACATTCCAACATC--- 411
QY 299 MetProGlyAsnProProArgLeuProPheAsnAspProPhePheValAlaGluTrpLeu 318
    |||||
Db 412 -----TTACAGACACCCCTTCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 444
QY 319 CysIleCysTrpPheSerPheGluLeuLeuValArgLeuLeuValCysProSerLysAla 338
    |||||
Db 445 TGTATATCTGTGTCTCTCTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
QY 339 IlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheVal 358
    |||||
Db 505 GACTTCTTCAAAAACATCATGAATCTCATGACATTTGTGCTCATCTTCTTTCATC 564
QY 359 AlaLeuGlyThrGluLeuAlaArgGln-ArgGly-----ValGlyGlnGlnAlaMetSer 376
    |||||
Db 565 ACCGTGCGACGAGATAGCTGAGCAGCAGAGAAACAGAGAGGAGAGAGAGAGAGAGAGAG 624
QY 376 IleAlaIleLeuArgValIleArgLeuValArgValPheArgIle-PheLysLeuSerA 396
    |||||
Db 625 CCGGCGCATCTCTCAAGCTCATCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 684
QY 396 rgtHisSerLysGlyLeuGlnIleLeuGlyGlnTrpLeuArgAlaSerMetArgGluLeu- 415

```

```

Db      685 GCCACTTAAGGGCTCAATCTCTGGGCCAAGACCTCAAGCTAGTAATGACAGAGCT 744
Qy      416 - -glyleuLeuIlePhePheLeuPhe--IleGlyValIleuPheSerSerAlaVal-T 434
Db      745 AGGGCTGCCATCTTTCTCTCTCAATGCGGGTCATCTGTCTTCTGAGTGTG 804
Qy      434 yPheAlaGlyValAspArgValAspSerHis-PheThrSerIleProGlySerPheTrp 453
Db      805 ACCTTGGCGAGGCGGAGCAAGCTAGTCGCGACATCTCATCTATCCCGCATGTTCTCG 864
Qy      454 TrpAlaValVal 457
Db      865 TGGCGCGTGTGTG 876

RESULT 6
BM963332      745 bp      mRNA      linear      EST 18-MAR-2002
LOCUS      BM963332
DEFINITION      UI-M-EOO-bwm-1-05-0-UI.r1 NIH_BMAP_EOO Mus musculus cDNA clone
ACCESSION      BM963332
VERSION      BM963332.1
KEYWORDS      GI:19546752
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      NIH-MGC http://mgi.nci.nih.gov/
JOURNAL      1 (bases 1 to 745)
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
      Unpublished (1999)
      Contact: Robert Strausberg, Ph.D.
      Email: cga@bbs-remail.nih.gov
      Tissue Procurement: Dr. James Lin, University of Iowa
      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/BLNT at:
      http://image.llnl.gov
      This clone was contributed by the Brain Molecular Anatomy Project
      (BMAP)
FEATURES
      source
      Location/Qualifiers
          1..745
              /organism="Mus musculus"
              /strain="C57BL/6"
              /db_xref="taxon:10090"
              /clone="IMAGE:5697484"
              /clone_1db="NIH_BMAP_EOO"
              /tissue_type="whole brain"
              /dev_stage="embryo 15.5 dpc"
              /lab_host="DH10B (T1 phage resistant)"
              /note="Organ: brain; Vector: pYX-Asc; Site:1: EcoR I;
              Site:2: Not I; The library was constructed according to
              Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
              1996. Denatured mRNA was size fractionated on a 1% agarose
              gel. First strand cDNA synthesis was primed with an
              oligo-dT primer containing a Not I site. Double stranded
              cDNA was size selected according to mRNA size fraction,
              ligated with EcoR I adaptor, digested with Not I, and then
              sequenced directionally into pYX-Asc vector. The library tag
              sequence located between the Not I site and the polyA tail
              is CAGCCAGCAGC. This library was created for the
              University of Iowa Mouse Brain Molecular Anatomy Project
              (BMAP). 'Gene discovery in the Developing Mouse Nervous
              System', supported by National Institutes of Mental Health
              (NIMH), Hemlin Chin, Ph.D., program coordinator."
BASE COUNT      139 a      216 c      202 g      188 t
ORIGIN
Alignment Scores:      3,43e-56      Length:      745
Pred. No.:

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Score:      853.00      Matches:      176
Percent Similarity:      77.91%      Conservative:      18
Best Local Similarity:      70.68%      Mismatches:      29
Query Match:      29.23%      Indels:      26
DB:      14      Gaps:      5

US-09-804-014a-8 (1-559) x BM963332 (1-745)
Qy      319 CysIleCysTrpPheSerPheGlyLeuValArgLeuValCysProSerLysAla 338
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3 TGTATCGTGTGTTACAGCTTTGAGCTCTGCTGGGCTTCTCGCTGTCCACAGAGCG 62
Qy      339 IlePhePheLysAsnValMetAsnLeuIleAspPheAlaIleLeuProTyrPheVal 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      63 GCGTCTTTTGGCAATATCATGAAATCATGACTTGTGTGGCATTTTCCCTTACTTATC 122
Qy      359 AlaLeuGlyThrGlyLeuAlaArg-----GlnArgGlyVal----- 370
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      123 ACCTTGGGCGACCGAGCTAGTGCACAGCTACAGCAGCAGCAGTGTGAGTGGCAGTGT 182
Qy      371 -----GlyGlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgVal 388
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      183 CAGATGGGCGACGAGCGCATGTCCTTACCATCCTCAGGCGTGTATCCGCGTGTCCGGGTG 242
Qy      389 PheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeu 408
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      243 TTCCGATCTTCAAGCTCTCCGCCCATTTCCAGAGGGCGTGCAGATCTCGGTAGACCTTA 302
Qy      409 ArgAlaSerLeuArgGlyLeuGlyLeuIleIlePhePheLeuHelIleGlyValIleLeu 428
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      303 CAGCGCTCATGGCGGGGAGCTCGGGCTCTCATCTTCTCTTTCATCGGAGTATCTC 362
Qy      429 PheSerSerAlaValTyrPheAlaGlyValAspArgValAspSerHisPheThrIle 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      363 TTTTTCAGCGCTGTCTACTCTCGCAGAGCGTGAAGATGTGATCGTCTTCCCTAGATC 422
Qy      449 ProGlySerPheTrpIleAlaValIleThrMetThrValIleTyrGlyAspMetAla 468
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      423 CCAGATCCCTCTTGTGTGGGCTGTGTGTTCAATACACACGCTAGGTATGGGGCATGTAC 482
Qy      469 ProValThrValGlyGlyLysIleValGlySerLeuCysAlaIleAlaGlyValIleThr 488
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      483 CCCATGACGATGAGGGGCAAGATGTGGGCTCACTGGCCCATGCTGGGGCTCTAC 542
Qy      489 IleSerLeuProValProValIleValIleAsnPheSerPheThrPheTrpHisArgIleThr 508
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      543 ATTGCATTACGGGTACCGGTCATTTCTCCATTTTCAACTTTCATCCACGAGAGAG 602
Qy      509 GluGlyGluGlyAlaGlyMetPheSerHisValAspMet---GlnProCysGlyProLeu 527
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      603 GAGCAGAGAGGAGGAGCAGCCAGTATACCCACGTCATTTGTGGCAGCCACTCCGAGACTTG 662
Qy      528 GluGlyLysAlaGlnGlyGlyLeuValAspGlyGluValProLeuLeuProProLeu 547
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      663 AAGGCAACGAGCAATGGG-----CTT 683
Qy      548 Trp-----AlaProProArgGluHis 554
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      684 TGGCACTGACTTGGCGAGAGCTTTCAC 710

RESULT 7
LOCUS      A2339279      636 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION      IM0070M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION      A2339279
VERSION      A2339279.1
KEYWORDS      GI:10413383
SOURCE      house mouse.
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 636)

```

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: M column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 636.

## FEATURES

## source

1..636  
Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUCG1M0070M07"

/clone\_lib="Mouse 10kb plasmid UUCG1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, P1-resistant, F-"

/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (q147321419b/AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## BASE COUNT

181 a 163 c 161 g 131 t

## ORIGIN

## Alignment Scores:

Pred. No.: 2,48e-53 Length: 636

Score: 815.00 Matches: 165

Percent Similarity: 85.65% Conservative: 14

Best Local Similarity: 78.95% Mismatches: 27

Query Match: 27.93% Indels: 3

DB: 17 Gaps: 0

US-09-804-014a-8 (1-559) x AZ339279 (1-636)

QY 314 ValValGluThrLeuGlyTyrPheSerPheGluLeuValArgLeuLeuVal 333

DB 636 GTGGTGGAGACCTTGTCATCATCTGCTCTTGAGCTTCTGGCGGTTATTTGCT 577

QY 334 CysProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIle 353

DB 576 TGGCCAGTAAGACCACTTCTCCAGAAATATCATGACTTGATAGCATTTGGCCATC 517

QY 354 LeuProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnGln 373

DB 516 ATTCTTATTTATTTATTCACCTGTGGCGACTGAGCTGACGACAGATGATGGGACAG 457

QY 374 AlaMetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLys 393

DB 456 GCCATGTCGCTGGCCATCTCGAGATCATCCGCTTAAAGGTTTCCGATCTTCAG 397

QY 394 LeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArg 413

DB 396 CTCCTCCCGCATTCCTAAGGGGCTGACAGATCTCGAGACAGACGCTGAAGGCTTCATGCGG 337

QY 414 GluLeuGlyLeuLeuIlePhePheLeuPheIleGlyValAlaLeuPheSerSerAlaVal 433

DB 336 GACCTGGGCTGTTCATATTTCTTCATTTGAGGGTATCCTTTCTTCACGTGAGTC 277

QY 434 TyrPheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTyr 453

DB 276 TACTTTGCTGAGCAGACGCCCTTCTTCGGGTTTAAACAGTATCCCGATGGCTTCGG 217

QY 454 TrpAlaValAlaThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGly 473

DB 216 TGGGAGTAGTAAACATTACACAGTGGTTATGGATATGACACCGACGACGATAGGA 157

QY 474 GlyLysIleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProVal 493

DB 156 GGCAGAGTTGGGCTCTTTTGTGTCATGCGAGGTGTCCTTGACCATTCATTACCACT 97

QY 493 LProValIleValSerAsnProSerTyrPheTyrHisArgGluThrGluGlyGluGlu 512

DB 96 TCTGTGATTTGATTCACCTTAAGACTTCTTACACCGGAGACAGAGGTAAGAG 37

QY 513 AlaGlyMetPheSerHisVal 519

DB 36 CTAGCCAGTACATGACGCTG 16

RESULT 8

BO714749 954 bp mRNA linear EST 16-JUL-2002

LOCUS BO714749

DEFINITION AGENCOURT\_8480590 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6310048

5', mRNA sequence.

ACCESSION BO714749

VERSION BO714749

KEYWORDS BO714749.1 GI:21853648

SOURCE EST.

ORGANISM house mouse.

Mus musculus.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 954)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13731 row: 1 column: 17

High quality sequence stop: 576.

Location/Qualifiers

1..954

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:6310048"

/clone\_lib="NIH\_MGC\_129"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: olfactory epithelium; Vector:

pcmv-SPORT6.1.ccdB; Site\_1: EcoRV; Site\_2: NotI; Cloned

unidirectionally. Primer: Oligo dT. Average insert size

2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this

is a NIH-MGC Library."

BASE COUNT 179 a 284 c 254 g 237 t

ORIGIN

Alignment Scores:			
Pred. No.:	1,59e-51	Length:	954
Score:	794.00	Matches:	176
Percent Similarity:	69.74%	Conservative:	36
Best Local Similarity:	57.89%	Mismatches:	68
Query Match:	27.21%	Indels:	24
DB:	14	Gaps:	7
US-09-804-014a-8 (1-559) x B0714749 (1-954)			
QY	123	GlyLeuAArgHegluThrArgAlaArgThleuGlyArgPheProAspThrLeuLeuGly	142
DB	2	GGTTGGCTTTGAGACGACGCTGGCACCCTGGCGAGTTTCCCAACACCCTCTGGGG	61
QY	143	AspProAlaArgArgGlyArgPheTyArgAspAlaArgArgGluArgGlyArgPhePheAspArg	162
DB	62	GACCCAGTCAACGCCCGCTACTTGATCCCTTGAGAAATGAGTCTTCTTGACCCG	121
QY	163	HisArgProSerPheAspAlaValLeuTyArgGlnSerGlyArgLeuArgArg	182
DB	122	AACGGCGCTGATTCGATGACATTTTCTACTACAGTCTGGGGCGCGCTCGCAGG	181
QY	183	ProAlaHisValProLeuAspValPheLeuGluGluValAlaPheTyArgGlyArgGlyAla	202
DB	182	CCGGTCATGTCCTCCCTGAGTGTGTGACAGATGAGATCCGCTTTACAGCTGGGGAC	241
QY	203	AlaAlaLeuAlaArgLeuArgGluAspGluGlyCysProValProProGluArgProLeu	222
DB	242	GAGGCCATGAGACGCCCTCCGGGAGATGAAGGCTTCATCAAGGAAGAGAGACCCCTG	301
QY	223	ProArgArgAlaPheAlaArgGlnLeuTrpLeuLeuPheGluPheProGluSerSerGln	242
DB	302	CCCCGCAATGATCCAGCCAGGCTGGCTTATCTTCATATCCCAAGAGCTCTGGG	361
QY	243	AlaAlaArgValLeuAlaValSerValLeuValIleLeuValSerIleValValPhe	262
DB	362	TCAGCAAGACCCATGCGCATGCTGCTGTGTCATCTCATCTATCATCACTTC	421
QY	263	CysLeuGluThrLeuProAspPheArgAspAspArgGlyThrGlyLeuAlaAla	282
DB	422	TGCTTGAGACTGCTGCTGAGTTCAGGATGAACGGAG-----CTGTTACGCCAC	472
QY	283	AlaAlaAlaGlyProValPheProAlaPro-----LeuAsnGlySer-----	296
DB	473	CCCCAGTGGCGCGCCAGCCCGCCAGCCCGCCAGGCAATGAGAGGCTGTGT	532
QY	297	-----SerGlnMetProGlyAsnProProArgLeuPro-----PheAsnAspProPhe	312
DB	533	GTCCTTTCCTGCGCCACAGTGGCTCGCTCTGCTAGGACACTGGCTGACCAATTC	592
QY	313	PheValValGluThrLeuCysIleCysTrpPheSerPheGluLeuLeuValArgLeuLeu	332
DB	593	TTTCATCGTGGAGAACACATGTGATGTGATGCTTTGAGCTGCTGGCGCTTCTTT	652
QY	333	ValCysProSerIleValIlePhePheLysAsnValIleCysLeuIleAspPheValAla	352
DB	653	GCTTGCCCGCAGCAAGCGAATTCCTCTCGGAATATTATGAACATCATGATATTGTGGCC	712
QY	353	IleLeuProTyArgPheValAlaLeuGlyThrGluLeuAlaArg-----GlnArgGly---	369
DB	713	ATCTTCCCTACTTTATCACCTGGGCGCCAGAGCTGGCGAGAGCAAAAGGGGGTGG	772
QY	370	-----ValGlyGlnGlnAlaMetSerLeuAla-IleLeuArgValIleArg-LeuV	386
DB	773	GGGGTCAAAATGGGCAACAGGCAATTCCTGACCAATCTCTGAGGTGATCCGCCCTGG	832
QY	386	AlaArgValPheArgIle-Phe-LysLeuSerArgHisSerIleGly---LeuGlnIleLe	404
DB	833	CCCGGGGTGTCCCAATCTTCCCAAGGTTTCCCGCTTTCAAGGAACATTGCAAAATCT	892
QY	404	ugly 405	

DB	893	CGGG 896	
RESULT 9			
LOCUS	BC023222/c	954 bp	RNA
DEFINITION	AGENCOURT_8480590 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6310048		
ACCESSION	B0714749		
VERSION	B0714749.1	GI:21853648	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 954)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@rs-femail.nih.gov		
	Tissue Procurement: Susan L. Sullivan, PhD.		
	cDNA Library Preparation: Resgen, Invitrogen Corp		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Plate: LLAM13731 row: 1 column: 17		
	High quality sequence stop: 576.		
FEATURES	Location/Qualifiers		
Source	1..954		
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	/db_xref="taxon:10090"		
	/clone="IMAGE:6310048"		
	/clone_lib="NIH_MGC_129"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: Olfactory epithelium; Vector: pcwv-SPOK6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH_MGC Library."		
BASE COUNT	179 a 284 c 254 g 237 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	6.51e-49	Length:	2146
Score:	765.00	Matches:	18
Percent Similarity:	56.25%	Conservative:	9
Best Local Similarity:	37.50%	Mismatches:	19
Query Match:	26.22%	Indels:	2
DB:	11	Gaps:	1
US-09-804-014a-8 (1-559) x BC023222 (1-2146)			
QY	3	ArgArgArgThrGlySerArgArgGlnLys-----AspGlyGluysGlyAspProGly	20
DB	1702	AAGAAAGCGACAGAAAGAAAGAAAGCGAGGAGGAGCGAGAAAGACGAGAGA	1643
QY	21	ThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgGlaGlaGlyArgAla	40
DB	1642	AAAGGAGAAACGAGAAACGAGAAAGAGACGAGAAACGAGAAAGAAAGAGCGAGAGA	1583
QY	41	SerArgGlnArgAlaArgGlyArg	48
DB	1582	AACAGACAGAGAAAGAAACGAGAGA	1559
RESULT 10			
LOCUS	CNS058RO	1060 bp	DNA
DEFINITION	Tetrisodon nigroviridis genome survey sequence T7 end of clone 02019 of library A from Tetradon nigroviridis, genomic survey		
ACCESSION	AL326301		

KEYWORDS	ALJ26301.1	GI:8219890
GENES	GSS: genome survey sequence.	
SOURCE	Tetradodon nigroviridis.	
ORGANISM	Tetradodon nigroviridis	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradodon.	
AUTHORS	1 (bases 1 to 1060) Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.	
TITLE	Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1060) Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis	
TITLE	Unpublished	
JOURNAL	3 (bases 1 to 1060) Genoscope.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (12-APR-2000)	
TITLE	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/tetradodon">http://www.genoscope.cns.fr/tetradodon</a> .	
COMMENT	Location/Qualifiers	
FEATURES	1..1060 /organism="Tetradodon nigroviridis" /db_xref="taxon:99883" /clone="020L19" /clone_lib="A" /note="Genoscope sequence ID : CONA020CF10C1-end : T7"	
SOURCE	BASE COUNT 238 a 239 c 231 g 309 t 43 others	
ORIGIN		
Alignment Scores:		
Pred. NO.:	6.84e-49	Length: 1060
Score:	760.50	Matches: 151
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Best Local Similarity:	71.23%	Mismatches: 34
Query Match:	26.06%	Indels: 4
DB:	17	Gaps: 2
US-09-804-014A-8 (1-559) x CNS058RO (1-1060)		
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DB	15	CCATCTCCNNGAAGCATCTCCNATCCCTTCTTCATCTCGAGACCGCTTGATTCCTGG 74
OY	323	PheSerPheGluLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLys 342
DB	75	TTCTTTTGTGAGCTGTGTGCAGATTGTGGGTCTCTCTACGACAGAAAGATTTCCTCAC 134
OY	343	AsnValMetAnLeuIleAspPheValAlaIleLeuProTyrrPheValAlaLeuGlyThr 362
DB	135	AACCTCATGACATATTGATATCTCATTCACATCATCTTATTATTGTACCGGTGACA 194
OY	363	GluLeu-----AlaArgGlnArgGlyAlaGlyGlnGlnAlaMetSerLeuAlaIleLeu 380
DB	195	GAAATCTTCACAAACCGGAGAGAGCGTCAGAGACAGAAC---ATGTCTTTGGCCATTCTG 251
OY	381	ArgValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGly 400
DB	252	CGCATCATTCGGCTGGTAGAGTATTCGCTATTTTCAACACTCTCCAGCATTTCCAAAGGT 311
OY	401	LeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhe 420
DB	312	CTGCAGATCTCTGGACAGACCCCTGAAGGAAAGCATAGCGCTGA-NTTGATTGGCTCATTTT 370

Oy	421	PheunPheileigLValleuPheserSeraLaValTyPheAlagLValAsparg	440
Dd	371	TTCCTTCAATCGGGGATCATCTCTTCCAGAGCTACTACTTTGCCGAGGTGCAGCAG	430
Oy	441	ValasSerHisPheThrSerIleProgluSerPheTrpIPalaValaValThmetThr	460
Dd	431	CCAACACGAGATTGTAGCATACCAGTGAGCTCTGTGGGCGCGCTTAACCATGACT	490
Oy	461	ThraValglyTYRGLYASpmetalAProvalThraValglylysisIlevalIGlyserIleu	480
Dd	491	ACTGTCGGTTATGGGACATGTGTCCTCACCTGAGGAGCAAATAGTGGGACAGCTG	550
Oy	481	CysAlaIlealagLValleuThrIleSerIeuProValIProvalIleValSerAnpHe	500
Dd	551	TGCGCATCGCTGAGAGTCTAACCTTGTCTGTGCTGCCGTGCCCGCATTTTCCACTTT	610
Oy	501	SerTYrPheTYrHisArgGLuThrgluIlglygluIu	512
Dd	611	AACCTACTCTACACAGAGACAGAACTGAGC	646
RESULT 11			
B6812963			
LOCUS	B6812963	559 bp	mRNA linear EST 22-MAY-2001
DEFINITION	da33c603.y1 NICHD XGC Brn1 Xenopus laevis cDNA IMAGE:4740197		
KEYWORDS	5' similar to TR:070259 070259 VOLTAGE-GATED POTASSIUM CHANNEL		
ACCESSION	B6812963		
VERSION	B6812963.1	GI:14183943	
ORGANISM	Xenopus laevis		
SOURCE	African clawed frog.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
JOURNAL	Xenopodinae; Xenopus.		
COMMENT	1 (bases 1 to 559)		
	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.D.,		
	'Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,		
	'B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,		
	Waterson,R. and Wilson,R.		
	WashU Xenopus EST project, 1999		
	Unpublished (1999)		
	Contact: Sandy Clifton, Ph.D.		
	WashU Xenopus EST project, 1999		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	cDNA Library Preparation: Life Technologies, Inc.		
	cnla library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	clone distribution: Xenopus clones from this library are available		
	through the I.M.A.G.E. Consortium/LNLN at: info@image.lnl.gov		
	High quality sequence stop: 420.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..559		
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	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.5 kb. Constructed by Life		
	Technologies. Note: This is a Xenopus Gene Collection (XGC		
	) library."		
BASE COUNT	135 a 120 c 133 g 171 t		
ALIGNMENT SCORES:	6.5e-48	Length:	559
Pred. No.:			

Score:	74.00	Matches:	140
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Query Match:	25.50%	Indels:	0
DB:	12	Gaps:	0

US-09-804-014A-8 (1-559) x BG812963 (1-559)

QY	307	Prophenase	AspProPhePheValValIuPheLeuCysIleCysTrpPheSerPheGlu	326
Db	53	CCCCGCGAGGACCCCTTTTATTTGTTGGAGACCATCTGATCTGCTGGTTTCTTTGAG	112	
QY	327	LeuLeuValArgLeuLeuValCysProSerIysAlaIlePhePheLysAsnValMetAsn	346	
Db	113	CTTTCAGAGAGGATTATTTGCGCTGACCAAGGACGAGCTTTCTTCAGAGACATATATGAAAC	172	
QY	347	LeuIleAspPheValAlaIleLeuProIyrPheValAlaLeuGlyThnGluLeuAlaArg	366	
Db	173	ATGATTGATTTTGTGGCCATCATACCAATATTTGTTGGCTGGGACATGAACTTCTCTGCC	232	
QY	367	GlnArgGlyValGlyGlnGlnAlaMetSerLeuAlaIleLeuArgValIleArgLeuVal	386	
Db	233	AACAAGAGAGGGGCAACCTGCATGTCTTTGGCCATCTCAGGGTTATCCGTTTGGTC	292	
QY	387	ArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGln	406	
Db	293	AGAGCTTCCTCGATCTTAAACTCTCACGTCACCTTAAGAGGCTTTCAGACTCTTGGGACAG	352	
QY	407	ThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyVal	426	
Db	353	ACATTGAAAGCCAGTATAGGGAATTGGGGCTGCTGATATTTTCTTTCAATGGGGTT	412	
QY	427	ValLeuPheSerSerAlaValTyrPheAlaGluValAspArgValAspSerHisPheThr	446	
Db	413	ATACCTCTCTCAGCTCAGTCTACTTTCTGCTGAGGCTGATCATGGATACAAAGTTTACA	472	
QY	447	SerIleProGluSerPheTrpTrpAlaValValThrMetThrThrValGlyTyrGlyAsp	466	
Db	473	AGTATCCCTGGAAGCTTTTGGTGGGCTGTGTGCACCATGACAAAGTAGGGTATGTGAT	532	
QY	467	MetAlaProValThrValGlyGly 474		
Db	533	ATGTACTCTGAAACAGTAGGGGGA 556		
RESULT 12				
LOCUS	AG163977			
DEFINITION	Ag163977	629 bp DNA linear GSS 09-JAN-2002		
ACCESSION	AG163977	Pan troglodytes DNA, clone: RP43-031A01.T7, genomic survey		
VERSION	AG163977.1	sequence.		
KEYWORDS	GSS.			
SOURCE		Pan troglodytes male lymphocytes DNA, clone_1lb:RP43-031A01.T7.		
ORGANISM		Male BAC Library clone:RP43-031A01.T7.		
REFERENCE		Pan troglodytes		
AUTHORS		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				







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Db      705  GCTGACCATGAGTGTTCGAGAGAGGGTGCATCAACATCTCAGACTGGCTTGAGACT 646
Qy      129  ArgAlaArgThrLeuGlyArgPheProAspThrLeuLeuGlyAspPro-AlaArgArg1 148
Db      645  CAACCTAAACCTCTCCAGAGAGCTATTCGGGGACCTAAAAAAAGGAT 586
Qy      148  YArgPheTyraAspAspAlaArgArg1uTyPhePheAspArgHisArgProSerPheAs 168
Db      585  GCGGATTTTCGATCCGCTGAGAGAAATGATTTTTCGATAGGAACAGACCGAGTTTCA 526
Qy      168  pAlaValLeuTyTyTyTyGlnSerGlyGlyArgLeuArgArgProAlaHisValProLe 188
Db      525  TGCCATATTTGATNACTACCACTCAGGGGGGCGACTACGAAGCCAGTCACGTCACCT 466
Qy      188  uAspValPheLeuGluGluValAlaPheTyGlyLeuGlyAlaAlaAlaLeuAlaArgLe 208
Db      465  CGATATTTCTCAGAGAGAGATTCGCTCTATGAGTTGGTGAGAGGCCATTGAGATGTT 406
Qy      208  uArgGluAspGluGlyCysProValProGluArgProGluArgArgAlaPheAl 228
Db      405  CAGAGAAAGATGAGGGGCTTCATTAGAGAGAGAGCGCTCTCTCCAGATTAAGAGTTTCA 346
Qy      228  aArgGlnLeuTrpLeuLeuPheGluPheProGlnSerSerGlnAlaAlaArgValLeuAl 248
Db      345  GAGACAGGTGTGGCTCTTGTGAGTACCAGAGAGCTCAGGCTCCCGTAGAGATTATCCG 286
Qy      248  aValValSerValLeuValIleLeuValSerIleValValPheCysLeuGluThrLeuPr 268
Db      285  CATATTTCTGTGATGATCTGATATCTATAGTCAGTTCTGTGAGAGCGCTTCC 226
Qy      268  oAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProVa 288
Db      225  CAATTTCCGCAACGACGAAGATGAATGCACAGTCACATGCAAAAGTCTTCACCT-- 168
Qy      288  lPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnProProArgLeuPro-- 307
Db      167  -----GAAACCAACACAMMAAAATAAGCTA 142
Qy      308  -----PheAsnAspProPhePheValValGluThrLeuGlyIleCysTrpPh 323
Db      141  TACAGCCACATACCTTACCAGCCACTCTTATTCCTAGAGACACTCTGCATCATATAGGTT 82
Qy      323  eSerPheGluLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAs 343
Db      81  CTCCTTTGAGTTTCGTGGAGGTTTTTTTGGCCGCCAACAGACGAGGTTTTTTGTATA 22
Qy      343  nValMetAsnLeuIleAsp 349
Db      21  CATATGAACATTTATTGAC 3
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Search completed: February 20, 2003, 14:28:49  
Job time : 2250 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 04:22:08 ; Search time 682.436 Seconds  
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10661.374 Million cell updates/sec

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Scoring table: IDENTITY\_NUC

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_inv:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	250	100.0	1341	6	AX352535	AX352535 Sequence
2	250	100.0	1447	9	AF315818	AF315818 Homo sapi
3	250	100.0	1747	6	AX268121	AX268121 Sequence
4	250	100.0	4372	9	HS310479	HS310479 Homo sapi
c	250	100.0	157633	9	AC008687	AC008687 Homo sapi
5	216.4	86.6	91668	2	AC095540	AC095540 Rattus no
6	216.4	86.6	172671	2	AC128792	AC128792 Rattus no
c	216.4	86.6	208632	2	AC073711	AC073711 Mus muscu
7	213.2	85.3	1075	10	MMKNCN1	AF032100 Mus muscu
8	213.2	85.3	1599	6	I26643	I26643 Sequence 9
9	213.2	85.3	1599	6	I26643	AF032099 Mus muscu
10	162.2	64.9	445	10	MMU409348	AF032099 Mus muscu
11	157.2	62.9	4234	9	HSBK2	X17622 Human HBK2
12	157.2	62.9	122903	9	AC005833	AC005833 Homo sapi
13	157.2	62.9	122903	9	AC005833	AC005833 Homo sapi
14	157.2	62.9	122903	9	AC005833	AC005833 Homo sapi
15	155	62.0	780	9	HS337055	HS337055 Homo sapi
16	153.4	61.4	444	9	HS336845	HS336845 Homo sapi
17	150.2	60.1	609	9	HS337128	HS337128 Homo sapi
18	146	58.4	1780	4	CFU08596	U08596 Canis fami
19	145	58.0	2098	10	RATKV2AA	M27159 Rat potassi
20	145	58.0	2743	10	RRCK2	X17621 Rat RCK2 mR
21	145	58.0	191664	2	AC125751	AC125751 Rattus no
c	145	58.0	198849	2	AC129061	AC129061 Rattus no
22	142.8	57.1	1820	9	HUMPCD	M55515 Human potas
23	142.8	57.1	2883	4	MPU45979	U45979 Mustela put
24	142.8	57.1	2883	4	MPU45979	U45979 Mustela put
25	140.8	56.3	690	9	HS337061	HS337061 Homo sapi
26	140.2	56.1	3219	10	MUSMURINE	M95688 Mus musculu
27	140.2	56.1	259159	2	AC124756	AC124756 Mus muscu
28	139.8	55.9	2755	9	HUMPOUCH	M83254 Human cardi
c	139.8	55.9	185952	9	AC005906	AC005906 Homo sapi
29	139.8	55.9	185952	9	AC005906	AC005906 Homo sapi
30	139.6	55.8	1488	9	HUMKCHA	L02750 Human potas
31	139.6	55.8	1836	9	HUMPOCH	L23499 Homo sapien
32	139.6	55.8	2397	9	HUMKCHN	M38217 Homo sapien
33	139.6	55.8	90458	2	AL513469	AL513469 Homo sapi
c	139.6	55.8	150001	9	AC006063	AC006063 Homo sapi
34	139.6	55.8	155343	9	AL365361	AL365361 Human DNA
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35	138	55.2	1551	4	OCU38240	U38240 Oryctolagus
36	138	55.2	1551	4	OCU38240	U38240 Oryctolagus
37	138	55.2	1883	10	RATRGK5	M30312 Rat voltage
38	136.4	54.6	1994	6	AR050270	AR050270 Sequence
39	136.4	54.6	1994	6	AR050270	AR050270 Sequence
40	136.4	54.6	2264	10	MUSMK3A	M30441 Mouse intro
41	136.4	54.6	2264	10	RATKV3AA	M31744 Rat potassi
42	136.4	54.6	2956	10	RNRCK3	X16001 Rat mRNA fo
43	136.4	54.6	3004	9	HUMKCHAN	M85217 H.sapiens K
c	134.8	53.9	227736	2	AC121825	AC121825 Mus muscu
44	134.2	53.7	752	9	HS332766	HS332766 Homo sapi
45	133.4	53.4	2867	6	AX333745	AX333745 Sequence

ALIGNMENTS

RESULT 1  
AX352535  
LOCUS AX352535  
DEFINITION Sequence 7 from Patent WO0194390.  
ACCESSION AX352535  
VERSION AX352535.1 GI:18617765  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS 1  
TITLE Curtis, R.A.  
52906, 33408, and 12189, potassium channel family members and uses  
thereof

AX352535  
Sequence 7 from Patent WO0194390.  
AX352535  
AX352535.1  
GI:18617765

1341 bp  
DNA  
linear

PAT 06-FEB-2002

JOURNAL Patent: WO 0194390-A 7 13-DEC-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
CDS <1. .1341  
/note="unnamed protein product"  
/codon\_start=1  
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/db\_xref="GI:18617766"  
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DRDGTGLAAAAGPPAPLNGSSQMPGNPRLPFNDPFCWFSPELLVRL  
LVCPSKAIFKFNVMNLIDFVAILPYFVALGTALARQGVQQQAMSAAILRLVLRVVF  
RFLKLSHSGKGLQILGOTLRASMRGLLIFELFVGLVSSAYFAEYDVRDVSHTS  
IPBSFWAVVTMTVGYGDMAPVTGGKIVGSLCAITAGVLTISLPVPVIVSNFSYFIH  
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BASE COUNT 190 a 443 c 411 g 297 t  
ORIGIN

Query Match 100.0%; Score 250; DB 6; Length 1341;  
Best Local Similarity 100.0%; Pred. No. 2.1e-31;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACGGCGCGCGCTGGGCGG 60  
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QY 61 CTTCCCGGACACTCTGCTAGGGACACCGACGGCGCGCGCTTCACGACGCGCGG 120  
|||||  
DB 69 CTTCCCGGACACTCTGCTAGGGACACCGACGGCGCGCGCTTCACGACGCGCGG 128  
|||||  
QY 121 CCGGAGTATTCTTCGACCGGACCGCCAGCTTCGAGCGCGCTCTACTACTACCA 180  
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DB 129 CCGGAGTATTCTTCGACCGGACCGCCAGCTTCGAGCGCGCTCTACTACTACCA 188  
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QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCTTCGAGCTCTCCCTGGAAGAGGT 240  
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DB 189 GTCGGTGGCGGCTGGCGGCGCGCGCGCTTCGAGCTCTCCCTGGAAGAGGT 248  
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QY 241 GGCCTTCTAC 250  
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DB 249 GGCCTTCTAC 258  
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RESULT 2  
AF315818 1447 bp mRNA linear PRI 19-JUN-2001  
LOCUS Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete  
cds.  
ACCESSION AF315818  
VERSION AF315818.1 GI:14485554  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1447)  
AUTHORS Bardenkruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.  
TITLE Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 1447)  
Bardenkruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7535, South Africa  
FEATURES Location/Qualifiers

JOURNAL Patent: WO 0194390-A 7 13-DEC-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .1447  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="19"  
/map="19q13.3"  
CDS 38. .1408  
/note="hkvl.7"  
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DRDGTGLAAAAGPPAPLNGSSQMPGNPRLPFNDPFCWFSPELLVRL  
LVCPSKAIFKFNVMNLIDFVAILPYFVALGTALARQGVQQQAMSAAILRLVLRVVF  
RFLKLSHSGKGLQILGOTLRASMRGLLIFELFVGLVSSAYFAEYDVRDVSHTS  
IPBSFWAVVTMTVGYGDMAPVTGGKIVGSLCAITAGVLTISLPVPVIVSNFSYFIH  
RTEGEAGMFSHVDMQPCPLGKANGLVGDEVPPELPPPLWAPPKHLVTEV"  
BASE COUNT 204 a 480 c 451 g 312 t  
ORIGIN

Query Match 100.0%; Score 250; DB 9; Length 1447;  
Best Local Similarity 100.0%; Pred. No. 2.1e-31;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACGGCGCGCGCTGGGCGG 60  
|||||  
DB 76 GCGGCTGGTCTCAACGTGGCGCGGCTTCGAGACGGCGCGCGCTGGGCGG 135  
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QY 61 CTTCCCGGACACTCTGCTAGGGACACCGACGGCGCGCGCTTCACGACGCGCGG 120  
|||||  
DB 136 CTTCCCGGACACTCTGCTAGGGACACCGACGGCGCGCGCTTCACGACGCGCGG 195  
|||||  
QY 121 CCGGAGTATTCTTCGACCGGACCGCCAGCTTCGAGCGCGCTCTACTACTACCA 180  
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DB 196 CCGGAGTATTCTTCGACCGGACCGCCAGCTTCGAGCGCGCTCTACTACTACCA 255  
|||||  
QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCTTCGAGCTCTCCCTGGAAGAGGT 240  
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DB 256 GTCGGTGGCGGCTGGCGGCGCGCGCGCTTCGAGCTCTCCCTGGAAGAGGT 315  
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QY 241 GGCCTTCTAC 250  
|||||  
DB 316 GGCCTTCTAC 325  
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RESULT 3  
AX268121 1747 bp DNA linear PAT 26-OCT-2001  
LOCUS Sequence 7 from Patent WO0168851.  
DEFINITION AX268121  
ACCESSION AX268121  
VERSION AX268121.1 GI:16516622  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Padigar,M., Vernet,C.A., Fernandes,E., Shinkets,R.A., Spaderna,S.K., Majumder,K. and Li,L.  
TITLE Polypeptides and nucleic acids encoding same  
JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1. .1747  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 255 a 582 c 575 g 335 t  
ORIGIN

Query Match 100.0%; Score 250; DB 6; Length 1747;

Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTGGTCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGCGCACGCTGGCGG 60  
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Db 382 GCGGCTGGTCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGCGCACGCTGGCGG 441  
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QY 61 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGG 120  
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Db 442 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTAGCAGACGCGG 501  
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QY 121 CCGCGAGTATTTCTCGACCGGACCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 180  
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Db 502 CCGCGAGTATTTCTCGACCGGACCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 561  
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QY 181 GTCCGGTGGCGGCTGCGCGCGCGCGCACGCTGGCGCTTCGAGCGCGCTCTACTACTACCA 240  
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Db 562 GTCCGGTGGCGGCTGCGCGCGCGCGCACGCTGGCGCTTCGAGCGCGCTCTACTACTACCA 621  
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QY 241 GGCGTCTCTAC 250  
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Db 622 GGCGTCTCTAC 631  
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RESULT 4  
HSA310479  
LOCUS HSA310479 4372 bp mRNA linear PRI 30-MAY-2001  
DEFINITION Homo sapiens mRNA for potassium voltage-gated channel,  
shaker-related subfamily, member 7 (KCNA7 gene).  
ACCESSION AJ310479  
VERSION AJ310479.1 GI:12830376  
KEYWORDS KCNA7 gene; Kv1.7 gene; potassium voltage-gated channel,  
shaker-related subfamily, member\*.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 4372)  
Kashuba,V.I., Kvasha,S.M., Protopopov,A.I., Gizatullin,R.2.,  
Rynditch,A.V., Wahlestedt,C., Wasserman,W.W. and Zabarovsky,E.R.  
Initial isolation and analysis of the human Kv1.7 (KCNA7) gene, a  
member of the voltage-gated potassium channel gene family  
Gene 268 (1-2), 115-122 (2001)  
21261947  
11368907  
2 (bases 1 to 4372)  
Kashuba,V.  
Direct Submission  
Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumorbiology  
Center, Karolinska Institute, Box 280, 171 77, SWEDEN  
Location/Qualifiers  
1. 4372  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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357..1727  
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subfamily, member 7"  
/protein\_id="CAC29065.1"  
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CLETLPDFRDRDGTGLAAAGAPFPAPLNGSSQMPNPNPNDPFFVETLIC  
WFSPELLVRLVCPKSAIFFKNMNLDFVAILPYFVALGTALARQGVGQAMSLAI  
LRVIRLVRFRIKLSRHSKGLIQLGQTLRASMRELGLLIFFLFTGVVLFSSAVYFAE

BASE COUNT 930 a 1117 c 1408 g 917 t  
ORIGIN  
Query Match 100.0%; Score 250; DB 9; Length 4372;  
Best Local Similarity 100.0%; Pred. No. 1.7e-31;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTGGTCTCAAGCTGGCGGGCTGGCTTCGAGACGGCGCGCACGCTGGCGG 60  
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Db 455 CTTCCGGGACACTCTGCTAGGAGACCCAGCGCGCGCGCTTCTAGCAGACGCGG 514  
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QY 121 CCGCGAGTATTTCTCGACCGGACCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 180  
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Db 515 CCGCGAGTATTTCTCGACCGGACCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 574  
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QY 181 GTCCGGTGGCGGCTGCGCGCGCGCGCACGCTGGCGCTTCGAGCGCGCTCTACTACTACCA 240  
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Db 575 GTCCGGTGGCGGCTGCGCGCGCGCGCACGCTGGCGCTTCGAGCGCGCTCTACTACTACCA 634  
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QY 241 GGCGTCTCTAC 250  
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Db 635 GGCGTCTCTAC 644  
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RESULT 5  
AC008687/c  
LOCUS AC008687 157633 bp DNA linear PRI 03-OCT-2001  
DEFINITION Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.  
ACCESSION AC008687  
VERSION AC008687.5 GI:15887249  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 157633)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Unpublished  
2 (bases 1 to 157633)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 157633)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 157633)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Oct 3, 2001 this sequence version replaced gi:10312243.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www-shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.2.  
STS Content:  
SHGC-15869 G15229  
SHGC-15864 G15225  
SHGC-5822 G14090  
SHGC-58615 G42524.

FEATURES source Location/Qualifiers

1. .157633  
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BASE COUNT 33926 a 43885 c 42816 g 37006 t  
ORIGIN

Query Match 100.0%; Score 250; DB 9; Length 157633;  
Best Local Similarity 100.0%; Pred. No. 8e-32;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCAACGTGGCGGCGTTCGAGACGCGGCGCGACGTGGGCGG 60  
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Db 83795 CTTCCCGGACACCTGTAGGGGACCGACGCGCGCGCGTCTTACGACGCGCG 83736

QY 121 CCGGAGTATTCTTCGACCGGACCGCGCGCGCGTTCGAGCGCGTCTTACTACTACCA 180  
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Db 83735 CCGGAGTATTCTTCGACCGGACCGCGCGCGCGTTCGAGCGCGTCTTACTACTACCA 83676

QY 181 GTCGGTGGCGGCGTGGCGGCGCGCGCGTTCGAGCGCGTCTTCTGGAAGAGGT 240  
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Db 83675 GTCGGTGGCGGCGTGGCGGCGCGCGCGTTCGAGCGCGTCTTCTGGAAGAGGT 83616

QY 241 GGCCTTCTAC 250  
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Db 83615 GGCCTTCTAC 83606

RESULT 6

AC095540  
LOCUS Rattus norvegicus clone CH230-8F24, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
DEFINITION 46 unordered pieces.

AC095540

AC095540.3 GI:21717912

HTG: HTGS\_PHASE1.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 91668)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amaralungu,H.C., Are,J.R., Ayale,M., Banks,T.,  
Barbieri,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,  
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Delavie,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Falls,I., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,  
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,  
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,F., Johnson,R., Jollivet,S., Joudah,S.,  
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulsegad,H.,  
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,

Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,  
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,  
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,  
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,  
Scherer,S., Scott,G., Shen,H., Shookhariani,N., Sisson,I.,  
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,  
Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 91668)

Worley,K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 91668)

Worley,K.C.

Direct Submission

Submitted (11-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Jul 10, 2002 this sequence version replaced gi:17942061.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GCQP

Center clone name: CH230-8F24

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 49207 bases at least Q40

Consensus quality: 54398 bases at least Q30

Consensus quality: 57691 bases at least Q20

-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 46 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 1515: contig of 1515 bp in length  
\* 1516 1615: gap of unknown length  
\* 1616 2954: contig of 1339 bp in length  
\* 2955 3054: gap of unknown length  
\* 3055 4473: contig of 1419 bp in length  
\* 4474 4573: gap of unknown length  
\* 4574 5901: contig of 1328 bp in length  
\* 5902 6001: gap of unknown length  
\* 6001 7092: contig of 1091 bp in length  
\* 7093 7192: gap of unknown length  
\* 7193 8420: contig of 1228 bp in length  
\* 8421 9954: gap of unknown length  
\* 9955 10054: contig of 1434 bp in length  
\* 10055 11083: contig of 1029 bp in length  
\* 11084 12807: contig of 1624 bp in length



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* 12808 12907: gap of unknown length
* 12908 14313: contig of 1406 bp in length
* 14314 14413: gap of unknown length
* 14414 16062: contig of 1649 bp in length
* 16063 16162: gap of unknown length
* 16163 17546: contig of 1384 bp in length
* 17547 17646: gap of unknown length
* 17647 18847: contig of 1201 bp in length
* 18848 18947: gap of unknown length
* 18948 20144: contig of 1197 bp in length
* 20145 20244: gap of unknown length
* 20245 22036: contig of 1792 bp in length
* 22037 22136: gap of unknown length
* 22137 23484: contig of 1348 bp in length
* 23485 23584: gap of unknown length
* 23585 24923: contig of 1339 bp in length
* 24924 25023: gap of unknown length
* 25024 27127: contig of 2104 bp in length
* 27128 27227: gap of unknown length
* 27228 29339: contig of 2112 bp in length
* 29340 29439: gap of unknown length
* 29440 30983: contig of 1544 bp in length
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* 31084 32945: contig of 1862 bp in length
* 32946 33045: gap of unknown length
* 33046 34553: contig of 1508 bp in length
* 34554 34653: gap of unknown length
* 34654 36212: contig of 1559 bp in length
* 36213 36312: gap of unknown length
* 36313 38343: contig of 2031 bp in length
* 38344 38443: gap of unknown length
* 38444 39956: contig of 1513 bp in length
* 39957 40056: gap of unknown length
* 40057 41680: contig of 1624 bp in length
* 41681 41780: gap of unknown length
* 41781 43601: contig of 1821 bp in length
* 43602 43701: gap of unknown length
* 43702 45106: contig of 1405 bp in length
* 45107 45206: gap of unknown length
* 45207 47277: contig of 2071 bp in length
* 47278 47377: gap of unknown length
* 47378 49203: contig of 1826 bp in length
* 49204 49303: gap of unknown length
* 49304 51119: contig of 1816 bp in length
* 51120 51219: gap of unknown length
* 51220 53672: contig of 2453 bp in length
* 53673 53772: gap of unknown length
* 53773 55859: contig of 2087 bp in length
* 55860 55959: gap of unknown length
* 55960 57754: contig of 1795 bp in length
* 57755 57854: gap of unknown length
* 57855 60067: contig of 2213 bp in length
* 60068 60167: gap of unknown length
* 60168 62032: contig of 1865 bp in length
* 62033 62132: gap of unknown length
* 62133 64766: contig of 2634 bp in length
* 64767 64866: gap of unknown length
* 64867 67617: contig of 2751 bp in length
* 67618 67717: gap of unknown length
* 67718 70695: contig of 2978 bp in length
* 70696 70795: gap of unknown length
* 70796 73832: contig of 3037 bp in length
* 73833 73932: gap of unknown length
* 73933 75932: contig of 2000 bp in length
* 75933 76032: gap of unknown length
* 76033 78610: contig of 2578 bp in length
* 78611 78710: gap of unknown length
* 78711 82812: contig of 4102 bp in length
* 82813 82912: gap of unknown length
* 82913 85429: contig of 2517 bp in length
* 85430 85529: gap of unknown length
* 85530 88068: contig of 2539 bp in length
* 88069 88168: gap of unknown length

FEATURES             * 88169      91668: contig of 3500 bp in length.
Source
1..91668
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-8F24"

BASE COUNT   20713 a 21006 c 21177 g 21287 t 7485 others
ORIGIN

Query Match      86.6%; Score 216.4; DB 2; Length 91668;
Best Local Similarity 91.6%; Pred. No. 2.3e-26;
Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GGGGCTGGTGCACACGTGGCGGGCTGGCTTCGAGACGCGGCGCGCACGCTGGGCGG 60
      |||||
Db 75282 GCGGCTGGTGCACACGTGGCGGGTGGCTTCGAGACCCGCGCGCACGCTCGGCGG 75341
      |||||

QY 61 CTTCCCGGACACTCTGTAGGGACCCAGCGCGCGCGCTTACGACGACGCGG 120
      |||||
Db 75342 CTTCCCGGACACGCTGCTGGGGACCCGGTGGCGCGCGCTTACGACGCGCGG 75401
      |||||

QY 121 CCGCGAGTATTCTTCGACCGCGCGCGCGCGCTTCGACGCGCGCTCTACTACTACCA 180
      |||||
Db 75402 CCGCGAGTATTCTTCGACCGCGCGCGCGCGCTTCGATCGGCTCTACTACTACCA 75461
      |||||

QY 181 GTCCGCTGGCGGCTGCGCGCGCGCGCGCTGCGCTCGAGCTCTTCTTGAAGAGGT 240
      |||||
Db 75462 GTACGGCGCGCGCTGAGACGCGCGCGCGCTGCGCTCGAGCTTCTTGGAGAGGT 75521
      |||||

QY 241 GGCCTTCTAC 250
      |||||
Db 75522 GTCTTCTAC 75531

RESULT 7
AC128792
LOCUS
DEFINITION
Rattus norvegicus clone CH230-262A9, *** SEQUENCING IN PROGRESS
***, 55 unordered pieces.
ACCESSION AC128792.1 GI:21952595
VERSION AC128792.1
KEYWORDS HTG; HTGS-PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 172671)
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhaq,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinsh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorelli,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsy,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoen,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
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Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 172671)  
 Worley, K.C.  
 Direct Submission  
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 ----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information -----  
 Center project name: KAJM  
 Center clone name: CH230-262A9  
 ----- Summary Statistics -----  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 108496 bases at least Q40  
 Consensus quality: 114733 bases at least Q30  
 Consensus quality: 119570 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 55 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1740: contig of 1740 bp in length  
 \* 1741: 1840: gap of unknown length  
 \* 1841: 3040: contig of 1200 bp in length  
 \* 3041: 3140: gap of unknown length  
 \* 3141: 4347: contig of 1207 bp in length  
 \* 4348: 4447: gap of unknown length  
 \* 4448: 5658: contig of 1211 bp in length  
 \* 5659: 5758: gap of unknown length  
 \* 5759: 7065: contig of 1307 bp in length  
 \* 7066: 7165: gap of unknown length  
 \* 7166: 8912: contig of 1747 bp in length  
 \* 8913: 9012: gap of unknown length  
 \* 9013: 10121: contig of 1109 bp in length  
 \* 10122: 10221: gap of unknown length  
 \* 10222: 11495: contig of 1274 bp in length  
 \* 11496: 11595: gap of unknown length  
 \* 11596: 12895: contig of 1300 bp in length  
 \* 12896: 12995: gap of unknown length  
 \* 12996: 14936: contig of 1940 bp in length  
 \* 14936: 15035: gap of unknown length  
 \* 15036: 16336: contig of 1301 bp in length  
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 \* 16437: 18286: contig of 1850 bp in length  
 \* 18287: 18386: gap of unknown length  
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 \* 10381: contig of 1995 bp in length  
 \* 20481: gap of unknown length  
 \* 21823: contig of 1342 bp in length  
 \* 21923: gap of unknown length  
 \* 23103: contig of 1180 bp in length  
 \* 23203: gap of unknown length  
 \* 24338: contig of 1035 bp in length  
 \* 24338: gap of unknown length  
 \* 26341: contig of 1903 bp in length  
 \* 26341: gap of unknown length  
 \* 28299: contig of 1958 bp in length  
 \* 28399: gap of unknown length  
 \* 29886: contig of 1487 bp in length  
 \* 29886: gap of unknown length  
 \* 31191: contig of 1205 bp in length  
 \* 31191: gap of unknown length  
 \* 33131: contig of 1840 bp in length  
 \* 33131: gap of unknown length  
 \* 35206: contig of 1975 bp in length  
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 \* 38150: contig of 2844 bp in length  
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 \* 39779: contig of 1429 bp in length  
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 \* 45028: contig of 1817 bp in length  
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 \* 46530: contig of 1402 bp in length  
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 \* 49509: contig of 2879 bp in length  
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 \* 53815: gap of unknown length  
 \* 57135: contig of 3320 bp in length  
 \* 57235: gap of unknown length  
 \* 59889: contig of 2654 bp in length  
 \* 59889: gap of unknown length  
 \* 62234: contig of 2245 bp in length  
 \* 62334: gap of unknown length  
 \* 66086: contig of 3752 bp in length  
 \* 66186: gap of unknown length  
 \* 70673: contig of 4487 bp in length  
 \* 70773: gap of unknown length  
 \* 73088: contig of 2315 bp in length  
 \* 73188: gap of unknown length  
 \* 75049: contig of 1861 bp in length  
 \* 75149: gap of unknown length  
 \* 78164: contig of 3015 bp in length  
 \* 78264: gap of unknown length  
 \* 81938: contig of 3674 bp in length  
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 \* 85018: contig of 2980 bp in length  
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 \* 89432: contig of 4314 bp in length  
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 \* 93510: contig of 3978 bp in length  
 \* 93610: gap of unknown length  
 \* 97571: contig of 3961 bp in length  
 \* 97671: gap of unknown length  
 \* 102274: contig of 4603 bp in length  
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 \* 108265: contig of 2646 bp in length  
 \* 108265: gap of unknown length  
 \* 113533: contig of 5168 bp in length  
 \* 113533: gap of unknown length  
 \* 117825: contig of 4192 bp in length  
 \* 117825: gap of unknown length  
 \* 124230: contig of 6305 bp in length

\* 124231 124330: gap of unknown length  
 \* 124331 129365: contig of 5035 bp in length  
 \* 129366 129465: gap of unknown length  
 \* 129466 136317: contig of 6852 bp in length  
 \* 136318 136417: gap of unknown length  
 \* 136418 144084: contig of 7667 bp in length  
 \* 144085 144184: gap of unknown length  
 \* 144185 151956: contig of 7772 bp in length  
 \* 151957 152056: gap of unknown length  
 \* 152057 159994: contig of 7938 bp in length  
 \* 159995 160094: gap of unknown length  
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## FEATURES

source

1. 172671  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone="CH230-262A9"

Query Match 86.6%; Score 216.4; DB 2; Length 172671;  
 Best Local Similarity 91.6%; Pred. No. 2.1e-26;  
 Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 GGGCTGGTCTCAAGTCGGCGGCTGCGCTTCGAGACGGCGCGCACGCTGGCGG 60  
 |||||  
 Db 86020 GCGCTGGTGTCAAGTCGGCGGTTGCGCTTCGAGACCGCGCGCACGCTCGCGG 86079  
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 QY 61 CTTCGGGACACTCTCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGCGG 120  
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 Db 86080 CTTCGGGACAGCTGCTGGGACCGCGTGGCGCGCACGCTTCTACGACGCGCGG 86139  
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 QY 121 CGCGAGTATTTCTTCGACCGGACCGGCCAGCTTCGAGCGCGTCTCTACTACTACCA 180  
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 Db 86140 CGCGAGTATTTCTTCGACCGACCGGCCAGCTTCGATGCGGTCTCTACTACTACCA 86199  
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 QY 181 GTCGGTGGCGCTGCGCGCGCGCGCGCTTCGAGCTTCGCTTCTTGAAGAGT 240  
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 Db 86200 GTCAGCGCGCGCTGAGACGGCGCGCGCGCTTCGAGCTTCGCTTCTTGAAGAGT 86259  
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 QY 241 GGCCTTCTAC 250  
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 Db 86260 GTCCTTCTAC 86269

RESULT 8  
 AC073711/c 208632 bp DNA linear HTG 18-JUL-2000  
 LOCUS Mus musculus clone RP23-193A10, WORKING DRAFT SEQUENCE, 7 ordered  
 DEFINITION pieces.

ACCESSION AC073711  
 VERSION AC073711.2 GI:9256763  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
 SOURCE Mus musculus.

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS DOE Joint Genome Institute.  
 TITLE Sequencing of Mouse  
 JOURNAL unpublished

REFERENCE 2 (bases 1 to 208632)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission

JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Jul 18, 2000 this sequence version replaced gi:8810328.

-----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>

Project Information  
 Center Project Name: 1810994  
 Center clone name: RPCI-23\_193A10

-----  
 Summary Statistics  
 Consensus quality: 204234 bases at least Q40  
 Consensus quality: 207322 bases at least Q30  
 Consensus quality: 207805 bases at least Q20  
 Estimated insert size: 221930; agarose-fp estimation  
 Estimated insert size: 208382; sum-of-contrigs estimation  
 Quality coverage: 8.77 in Q20 bases; agarose-fp estimation  
 Quality coverage: 9.34 in Q20 bases; sum-of-contrigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 7 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

\* 1 93558: contig of 93558 bp in length  
 \* 93559 93658: gap of unknown length  
 \* 93659 94751: contig of 1093 bp in length  
 \* 94752 94851: gap of unknown length  
 \* 94852 118285: contig of 23434 bp in length  
 \* 118286 118385: gap of unknown length  
 \* 118386 157043: contig of 38658 bp in length  
 \* 157044 157143: gap of unknown length  
 \* 157144 164561: contig of 7418 bp in length  
 \* 164562 164661: gap of unknown length  
 \* 164662 176791: contig of 12130 bp in length  
 \* 176792 176891: gap of unknown length  
 \* 176892 208632: contig of 31741 bp in length.

## FEATURES

source

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 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="RP23-193A10"  
 /clone\_lib="RPCI mouse BAC library 23"

BASE COUNT 48823 a 51932 c 52697 g 54580 t 600 others

Query Match 86.6%; Score 216.4; DB 2; Length 208632;  
 Best Local Similarity 91.6%; Pred. No. 2e-26;  
 Matches 229; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAAGTCGGCGGCTGCGCTTCGAGACGGCGCGCACGCTGGCGG 60  
 |||||  
 Db 74588 GCGGCTGGTCTCAAGTCGGCGGTTGCGCTTCGAGACCGCGCGCACGCTGGCGG 74529  
 |||||  
 QY 61 CTTCGGGACACTCTCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGCGG 120  
 |||||  
 Db 74528 CTTCGGGACAGCTGCTGGGGACCCGCTGCGCGCGCACGCTTCTACGACGCGCGG 74469  
 |||||  
 QY 121 CGCGAGTATTTCTTCGACCGGACCGGCCAGCTTCGAGCGCGTCTCTACTACTACCA 180  
 |||||  
 Db 74468 CGCGAGTATTTCTTCGACCGACACCGGCCAGCTTCGATGCGGTGCTCTACTACTACCA 74409  
 |||||  
 QY 181 GTCGGTGGCGCTGCGCGCGCGCGCGCACGCTTCGAGCTTCCTCTTGAAGAGT 240  
 |||||  
 Db 74408 GTCGGCGCGCGCTGAGACGGCGCGCGCACGCTTCGAGCTTCCTCTTGAAGAGT 74349  
 |||||

QY 241 GGCCTTCTAC 250  
 |||||  
 Db 74348 GTCCTTCTAC 74339

## RESULT 9

MMKNCN1

LOCUS

DEFINITION

exon 1.

ACCESSION

AF032100

VERSION

AF032100.1

KEYWORDS

1075 bp DNA linear ROD 21-MAR-2001  
 Mus musculus voltage-gated potassium channel Kv1.7 (Kcna7) gene,

1 of 2	Unclassified.	1 (bases 1 to 1599)
Mus musculus.	Chandy, K.G., Kalman, K., Chandy, G. and Gutman, G.A.	
Mus musculus	Voltage-gated potassium channel gene, Kv1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Patent: US 5559009-A 9 24-SEP-1996;	
1 (bases 1 to 1075)	Location/Qualifiers	
Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.	1..1599	
Genomic organization, chromosomal localization, tissue distribution, and biophysical characterization of a novel mammalian Shaker-related voltage-gated potassium channel, Kv1.7	/organism="unknown"	
J. Biol. Chem. 273 (10), 5851-5857 (1998)		
98157988	BASE COUNT	233 a 521 c 502 g 343 t
9488722	ORIGIN	
2 (bases 1 to 1075)	Query Match	85.3%; Score 213.2; DB 6; Length 1599;
Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.	Best Local Similarity	90.8%; Pred. No. 1.9e-25;
Direct Submission	Matches	227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Submitted (30-OCT-1997) Physiology and Biophysics, University of California, Irvine, CA 92697, USA		
Location/Qualifiers		
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BASE COUNT	190 a 343 c 351 g 191 t	
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Best Local Similarity	90.8%; Pred. No. 1.9e-25;	
Matches	227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;	
1 CGCGGTGGTCTCAACGTGGCGGGCTGCGCTTCGAGACGCGGGCGCACGCTGGGGCG 60		
Db 534 CGCGGTGGTCTCAACGTGGCGGGTGGCTTCGAGACCGCGCGCGCGCGCTCGGGCG 593		
61 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCGCTTCTACTACTACCA 120		
Db 594 CTTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCGCTTCTACTACTACCA 653		
121 CGCGGAGTATTTCTGACGGCGCACCGCGCGCGCGCTTCTACTACTACCA 180		
Db 654 CGCGGAGTATTTCTGACGGCGCACCGCGCGCGCGCTTCTACTACTACCA 713		
181 GTCGGTGGCGGCTGCGGGCGCGCGCGCGCTGCGCTTCGAGCTTCTTCTGGAAGGTT 240		
Db 714 GTCGGCGCGCGCTGAGAGCGCGCGCGCGCGCTGCGCTTCTTCTGGAGAGGT 773		
241 GGCTTCTTAC 250		
Db 774 GTCTTCTTAC 783		
RESULT 10		
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LOCUS	Sequence 9 from patent US 5559009.	
DEFINITION	126643	
ACCESSION	126643	
VERSION	126643.1	
KEYWORDS	GI:1606513	
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Unknown.		
Unknown.		

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HVPDLVLEEVSVYGLRRLARLREDECAVAERPLPPFARQLWLLFEFPESQAAR
VLPVNSVLIVSVYVFCLELTPFRDRDDPGLAPVAATGSELRARLNGSPMPGAP
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Best Local Similarity 90.8%; Pred. No. 1.8e-25;
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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QY 61 CTTCCGGGACACTCTAGGAGGACCGCGCGCGCGCGCGCTTCTAGCAGACGCGCG 120
DB 333 CTTCCGGGACACTCTAGGAGGACCGCGCGCGCGCGCGCTTCTAGCAGACGCGCG 392
QY 121 CCGCGAGTATTCTTCGACCGGACCGCGCGCGCGCGCGCTTCTACTACTACCA 180
DB 393 CCGCGAGTATTCTTCGACCGGACCGCGCGCGCGCGCGCTTCTACTACTACCA 452
QY 181 GTCCGGTGGCGGCTGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGGT 240
DB 453 GTCCGGTGGCGGCTGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGGT 512
QY 241 GGCCTTCTAC 250
DB 513 GTCCTTCTAC 522
RESULT 12
MMU409348
LOCUS
DEFINITION
Mus musculus partial Kcna7 gene for voltage-gated potassium channel
Kv1.7, exon 1.
ACCESSION
AJ409348
VERSION
AJ409348.1 GI:13508802
KEYWORDS
KCN7 gene; voltage-gated potassium channel Kv1.7.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 445)
REFERENCE
Kashuba,V.I., Kvasha,S.M., Protodopov,A.I., Gizatullin,R.Z.,
Rynditch,A.V., Wahlstedt,C., Wasserman,W.W. and Zabarovsky,E.R.
Initial isolation and analysis of the human Kv1.7 (KCN7) gene, a
member of the voltage-gated potassium channel gene family
Gene 268 (1-2), 115-122 (2001)
JOURNAL
21261947
MEDLINE
11368907
PUBMED
11368907
REFERENCE
Kashuba,V.
2 (bases 1 to 445)
Direct Submission
AUTHORS
Submitted (23-MAR-2001) Kashuba V., Microbiology and Tumor Biology
Center, Karolinska Institute, Box 280, 171 77, SWEDEN
JOURNAL
Location/Qualifiers
1..445
/organism="Mus musculus"
FEATURES
source
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Matches 170; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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DB 262 GCGGCTGTGCTCAACGTGGCGGCTGCGCTTCGAGACCGCGCGCGCGCGCTTCTAGCAGACGCGCG 321
QY 61 CTTCCGGGACACTCTCTAGGAGGACCGCGCGCGCGCGCGCTTCTAGCAGACGCGCG 120
DB 322 CTTCCGGGACACTCTCTAGGAGGACCGCGCGCGCGCGCGCTTCTAGCAGACGCGCG 381
QY 121 CCGCGAGTATTCTTCGACCGGACCGCGCGCGCGCGCGCTTCTACTACTACCA 180
DB 382 CCGCGAGTATTCTTCGACCGGACCGCGCGCGCGCGCGCTTCTACTACTACCA 441
QY 181 GTC 183
DB 442 GTC 444
RESULT 13
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LOCUS
DEFINITION
Human HBK2 mRNA for potassium channel protein.
ACCESSION
X17622
VERSION
X17622.1 GI:32032
KEYWORDS
membrane protein; potassium channel protein.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4234)
Direct Submission
AUTHORS
Submitted (23-NOV-1989) Pongs O., Ruhr Universitaet, Lehrstuhl fuer
Biochemie, Universitaetstr 150, D-4630 Bochum
2 (bases 1 to 4234)
REFERENCE
Grupe,A., Schroter,K.H., Ruppertsberg,J.P., Stocker,M., Drewes,T.,
Beckh,S. and Pongs,O.
Cloning and expression of a human voltage-gated potassium channel.
A novel member of the RCK potassium channel family
EMBO J. 9 (6), 1749-1756 (1990)
JOURNAL
90269208
MEDLINE
2347305
PUBMED
2347305
FEATURES
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RQSEEDDEDSDYTFHGCITPGEHGTGSSSLTLGGSFFDPLFLVETLCIVWTFE  
ELLVRSAPSKPAFRNIMLIDIVAIFPIITGLTVELVQQEQOQPSAGGGGQNGQ  
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AYFAEADDDSLFSPIDAFWAVTWTVTGVDMPMTVGKIVGSLCAITAGVITI  
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BASE COUNT 851 a 1174 c 1227 g 982 t  
ORIGIN

Query Match 62.9%; Score 157.2; DB 9; Length 4234;  
Best Local Similarity 76.8%; Pred. No. 1.5e-16;  
Matches 192; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GCGCGTGGTCTCAAGCTGGCGGGCTGCGCTTCGAGACGGCGCGGCGTGGCGG 60  
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QY 61 CTTCCGGGACACTCTCTAGGGGACCGACGCGCGCGCGCTTCTACGACGACGCGG 120  
Db 1045 GTTTCGGGACACCTGCTCGGAGACCTTGGCGGCGAGTCCGCTTCTCGACCCCTGAG 1104  
QY 121 CCGCGAGTATTTCTCGACGGCAGCGGCCAGCTTCGACGGCGTCTCTACTACTACCA 180  
Db 1105 GAACGAGTACTTCTCGACCGCAACCGGCCAGCTTCGACGGCATCTCTACTACTACCA 1164  
QY 181 GTCCGTTGGCGGCTGGCGGCGCGGCGGACGCTGCGCTTCTCTGGAAGAGT 240  
Db 1165 GTTGGGGGCGGCTGGGAGGCGGCTCAACGTGCCCTGGACATTTTCTTGGAGAGAT 1224  
QY 241 GGCTTCTAC 250  
Db 1225 CCGCTTCTAC 1234

RESULT 14  
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LOCUS  
DEFINITION Homo sapiens 12p13.3 BAC RCI11-234B24 (Roswell Park Cancer  
Institute Human BAC Library) complete sequence.  
ACCESSION AC005833  
VERSION AC005833.1 GI:4165003  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 122903)  
Muzny,D., Aronson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,  
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,  
Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,  
Kondejowski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W.,  
Logan,O., Lu,J., Marondei,I., Martinez,C., Merscher,S., Miller,A.,  
Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,  
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,  
Vo,O., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W.,  
Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 122903)  
Worley,K.C.  
Direct Submission  
Submitted (20-OCT-1998) Molecular and Human Genetics, Baylor  
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 122903)

AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Worley,K.C.

Direct Submission  
Submitted (29-DEC-1998) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

Worley,K.C.

Direct Submission  
Submitted (20-JAN-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

Worley,K.C.

Direct Submission  
Submitted (30-JAN-1999) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

Worley,K.C.

Direct Submission  
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Jan 20, 1999 this sequence version replaced gi:4071009.  
INFORMATION: <http://gc.bcm.tmc.edu:8088/home.html> or email  
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the  
entire insert of this clone. Overlapping regions of clones are only  
sequenced and submitted once, so the sequence for the remainder of  
the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the  
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches  
of a local database that includes entries from dbSTS, GDB, and  
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
unpublished,) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST  
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
EST and cDNA sequences. Genes demonstrate at least two exons  
flanked by consensus splice sites that maintained sequence  
continuity across the splice junctions. Sequences that are not  
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
standard of double strand coverage with a minimum of 2 clones and 2  
reads with no ambiguities or 2 chemistries with a minimum of 2  
clones and 3 reads with no ambiguities. If the sequence quality for  
a region does not meet this standard, it will be indicated in the  
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
standards - estimated error rate less than 1 per 10,000 bases.  
Reports of lowest quality individual bases and measures of base  
quality are listed below. Description of the metrics can be found  
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----

Contig length: 122912  
Phrap values in estimate: 121736  
Average error rate (BCM-Phrap estimate): 9.84188e-05  
Fraction of Phrap values less than 40 : 0.0170533  
Number of consensus changing edits: 8  
Number of N's in consensus : 0

Consensus changing edits			Edited+Context	
Position	Original+Context			
13624	gagaaataaa(c)ttgtctttgc		gagaaataaa(a)ttgtctttgc	
13769	ggagggggg(n)cgatagacat		ggagggggg(a)cgatagacat	
28984	cgagcgggg(n)gctcaacgct		cgagcgggg(g)gctcaacgct	
44274	gatgctctcg(n)aagacatc		gatgctctcg(g)aagacatc	
64600	gtgcaatgat(n)naaccagaat		gtgcaatgat(g)naaccagaat	
64601	tgcaatgat(n)aaccagaat		tgcaatgat(g)aaccagaat	
106923	gcctggggga(n)ccatggttct		gcctggggg(a)ccatggttct	
107127	caatggacat(n)actgocctgt		caatggacat(g)actgocctgt	

  

Bases with BCM-Phrap value < 20			Surrounding Sequence	
Quality	Position			
46			ttaaaggag(t)ggatgggtg	
6	13718		ttatacagtc(t)gggacgtgt	
7	37709		gatagctact(a)gctacacatg	
7	37711		tagctactag(t)caacatcggc	
7	37712		agctactagt(c)acacatggct	
7	37728		tggtactta(a)atgtaaatta	
7	37729		ggctactta(a)tgtaaatata	
8	47		ttaacggagt(g)ggatgggtg	
8	48		taacggagt(g)gatgggtgga	
8	49		aacggagt(g)atgggtggat	
8	13716		gattatacag(t)ctgggactgt	
8	13717		attatacagt(c)tgggactgt	
8	13720		atacagtctg(g)ggactgtgt	
8	13773		gggggacg(a)tagcattagg	
8	13774		gggggacg(a)tagcattagg	
8	37701		ttcaataga(t)agctactagt	
8	37702		tcaatagt(a)gctactatgc	
8	37708		tgatagctac(t)gctacacat	
8	37723		acttaaatgt(a)aaattaata	
9	13733		cagctcggg(a)cgcttgggg	
9	13775		gggggacg(a)gctataggag	
9	37381		atagaacta(c)ctcatgtcct	
9	37692		tgctgcactg(t)tcaatgatgt	
9	37693		gctgcactg(t)caatgatata	
9	37693		ctgcactgt(c)aatatgatag	
9	37710		atagctacta(g)tcacacatgg	
9	37731		ctactaaat(g)taaatattat	
9	37732		tacttaaat(g)aaattaatta	
9	37736		taaatgtaa(t)taattaaat	
10	14252		taagttaa(t)gatagggaaga	
10	37370		agctgtagca(c)atagaactta	
10	37379		acatagaact(t)acctatgtc	
10	37685		atctctgct(g)cactgttcaa	
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10	37735		ttaaatgtaa(a)ttaaattaaa	
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10	53115		ccatttgtat(g)ttctcttttg	
10	53176		attataaat(t)tttacctata	
11	14250		ttttaagtta(a)tggaataggaa	
11	14253		taagttaatg(g)ataggaaagt	
11	14274		tcagttactg(c)aaagtattgca	
11	14275		cagttactgt(c)agattttgca	
11	14277		gtactgtcaa(g)attgttcatt	
11	37687		cttctgctgc(a)ctgttcaata	
11	37696		cactgttcaa(t)atgatagcta	
11	37719		agtcacacat(g)gctacttaaa	
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12	37684		tatctctgct(t)gcactgttca	
12	37688		ttctgtgca(c)tggttcaatat	
12	37697		actgttcaat(a)tgatagctac	

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12	tgttcaatat(g)atagctacta	37699	
12	caatatgata(g)ctactagtca	37703	
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12	ggctcagggc(a)tggtgctctct	65742	
13	ttttttttt(t)caagcaggcc	136	
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13	aactcttat(t)aaatatagg	35224	
13	actcttatt(a)aatatatgtt	35225	
13	cagctgtagc(a)catagaactt	37369	
13	gcacatagaa(c)ttactctatg	37377	
13	catagaactt(a)cttatgtccc	37380	
13	tcacacatgg(c)acttaaatg	37721	
13	acatggtac(t)taaatgtaaa	37725	
13	ggattattaa(a)tttttacct	53174	
14	acggattggg(a)tggttgatt	50	
14	caaagaagct(t)ccataaccg	73	
14	aggcaaaatg(g)ggaacaagg	164	
14	acagctcggg(g)actgtgtgg	13722	
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14	ataataata(a)aaaagtcaca	13912	
14	taaaaaaagt(c)aaacaaaaa	13919	

  

Query Match			
Best Local Similarity 62.9%; Score 157.2; DB 9; Length 122903;			
Matches 192; Conservative 0; Mismatches 58; Indels 0; Gaps 0;			
QY	1	CGCGCTGGTGCACAGCTGGCGGGCTCGAGACGCGGCGCGCACGCTGGCGCG	60
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QY	61	CTTCCCGGACACTGCTAGGGGACCCAGCGCGCGCGCGCTTACGACGACGCGCG	120
Db	115326	GTTTCGGACACGCTGCTCGGAGACCCCTGGCGGCGAGTCCGCTTCTCGACCCCTGAG	115385
QY	121	CCGCGAGTATTCTTCGACGCGGCGCGCGCGCTTCGAGCGCGTCTACTACTACCA	180
Db	115386	GAACGAGTACTTTCGACCGCAACCGGCGCGCTTCGAGCGCATCTCTACTACTACCA	115445
QY	181	GTCCGGTGGCGGCTCGGCGCGCGCGCGCGCTCGCGCTTCGAGCGCTTCTCTGGAAGAGGT	240
Db	115446	GTCTGGGCGCGCTCGGAGGCGCGTCAACGTGCCCTTGGACATTTCTCTGGAGGAGAT	115505
QY	241	GGCCTTCTAC 250	
Db	115506	CGGCTTCTAC 115515	

  

RESULT 15	
HSA337055	780 bp DNA linear PRI 18-JUL-2002
LOCUS	Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION	NLI-YE2R.
ACCESSION	AJ337055
VERSION	AJ337055.1 GI:15881473
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	1 (bases 1 to 780)
	Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
	Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
	Levitsky, V.G., Kolchanov, N.A., Protodanov, A.I., Kashuba, V.I.,
	Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
TITLE	NotI flanking sequences: a tool for gene discovery and verification
JOURNAL	of the human genome
MEDLINE	Nucleic Acids Res. 30 (14), 3163-3170 (2002)
	22131767

PUBMED 12136098  
REFERENCE 2 (bases 1 to 780)  
AUTHORS Zabarovsky,E.R.  
TITLE Direct Submission  
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,  
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,  
Sweden

FEATURES  
source Location/Qualifiers  
1..780  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NL1-YE2R"

BASE COUNT 121 a 241 c 280 g 134 t 4 others  
ORIGIN

Query Match 62.0%; Score 155; DB 9; Length 780;  
Best Local Similarity 100.0%; Pred. No. 4.9e-16;  
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GCGGCGCTTCTACGACGACGCGCGCGAGTATTTCGACCGCGCACCGGCCAGCT 155  
|||||  
Db 1 GCGGCGCTTCTACGACGACGCGCGCGAGTATTTCGACCGCGCACCGGCCAGCT 60  
|||||

QY 156 TCGACGCGCTGCTCTACTACTACCACTCCGGTGGCGGCTGCGGCGCGCGCACGTC 215  
|||||

Db 61 TCGACGCGCTGCTCTACTACTACCACTCCGGTGGCGGCTGCGGCGCGCGCACGTC 120  
|||||

QY 216 CGCTCGACGCTTCTCTGGAAGAGTGCGCTTCTAC 250  
|||||

Db 121 CGCTCGACGCTTCTCTGGAAGAGTGCGCTTCTAC 155  
|||||

Search completed: February 20, 2003, 10:11:48  
Job time : 1055.44 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 05:50:07 ; Search time 413.95 seconds  
(without alignments)  
9781.067 Million cell updates/sec

Title: US-09-804-014A-7\_COPY\_382\_631  
Perfect score: 250  
Sequence: 1 gcgctgtgtcgaactgg.....tggagaggtgcctcttac 250

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	214.8	85.9	468	9 AI324179	AI324179 mh83g06.x
2	192.8	77.1	687	13 BI295790	BI295790 UI-R-DK0-
3	191.6	76.6	522	9 AI322534	AI322534 mh83g06.y
4	177.8	71.1	477	9 AA021711	AA021711 mh83g06.r
5	157.2	62.9	770	12 BF530500	BF530500 602071745
6	155	62.0	443	17 AQ939702	AQ939702 NRS-028R

7	140.2	56.1	900	14	BQ938497	BQ938497	AGENCOURT
8	140.2	56.1	927	14	BQ930283	BQ930283	AGENCOURT
9	135.4	54.2	704	10	BB612634	BB612634	BB612634
c	135.2	54.1	839	17	CNS03DKC	CNS03DKC	Tetraodon
11	134.4	53.8	414	9	AL843701	AL843701	AL843701
12	125	50.0	316	9	AL844004	AL844004	AL844004
13	123.6	49.4	537	17	FR0032804	FR0032804	AL015668 F.rubripe
c	121.8	48.7	1085	17	CNS03SKO	CNS03SKO	Tetraodon
c	120.6	48.2	1023	17	CNS02A6D	CNS02A6D	AL228850 Tetraodon
c	116.2	46.5	433	17	DR17024S	DR17024S	AL188158 Tetraodon
17	112	44.8	665	13	BM492036	BM492036	AL732913 Danio rer
18	109.6	43.8	954	14	BQ714749	BQ714749	BQ714749
c	108.8	43.5	954	10	BQ714749	BQ714749	AGENCOURT
c	106.6	42.6	1109	17	CNS045OM	CNS045OM	AL275647 Tetraodon
21	103.2	41.3	1109	10	CNS045OM	CNS045OM	AL275647 Tetraodon
c	98.6	39.4	1109	13	CNS045OM	CNS045OM	AL275647 Tetraodon
c	98.2	39.3	1058	14	BM924998	BM924998	BM924998
c	96.6	38.6	1058	17	BM924998	BM924998	AGENCOURT
c	92.8	37.1	1058	12	BM924998	BM924998	AGENCOURT
c	90.6	36.2	1054	17	CNS05DBK	CNS05DBK	AL332201 Tetraodon
c	87.2	34.9	1054	9	CNS05DBK	CNS05DBK	AL332201 Tetraodon
28	84	33.6	640	13	BC973314	BC973314	602841921
c	83.4	33.4	963	17	CNS02F5Y	CNS02F5Y	AL198511 Tetraodon
30	83	33.2	557	10	BE666693	BE666693	150296 MA
31	82.4	33.0	557	9	BE666693	BE666693	150296 MA
32	80.4	32.2	876	13	BI117089	BI117089	602867882
33	78.2	31.3	876	13	BI117089	BI117089	602867882
34	70	28.0	876	17	BI117089	BI117089	602867882
c	69.4	27.8	876	10	BI117089	BI117089	602867882
c	69.2	27.7	876	9	BI117089	BI117089	602867882
c	69.2	27.7	876	9	BI117089	BI117089	602867882
38	68.6	27.4	628	14	BQ807519	BQ807519	NISC_kk05
39	67.8	27.1	628	9	BQ807519	BQ807519	NISC_kk05
40	64.4	25.8	628	17	BQ807519	BQ807519	NISC_kk05
41	62.6	25.0	628	9	BQ807519	BQ807519	NISC_kk05
42	62.6	25.0	628	9	BQ807519	BQ807519	NISC_kk05
43	62.4	25.0	628	9	BQ807519	BQ807519	NISC_kk05
44	62.4	25.0	628	9	BQ807519	BQ807519	NISC_kk05
45	62.4	25.0	628	12	BQ807519	BQ807519	NISC_kk05

ALIGNMENTS

RESULT 1  
AI324179/c  
LOCUS  
DEFINITION  
AI324179.1 Soares mouse placenta 4NBMP13.5 14.5 Mus musculus cDNA  
clone IMAGE:457594 3' similar to gb:X17622-cds1 POTASSIUM CHANNEL  
PROTEIN KVL6 (HUMAN); gb:Y00305 Mouse MBK1 mRNA for mouse brain  
potassium channel (MOUSE);, mRNA sequence.  
ACCESSION  
AI324179  
VERSION  
AI324179.1  
KEYWORDS  
GI:4058608  
SOURCE  
house mouse  
ORGANISM  
Mus musculus  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 468)  
AUTHORS  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and  
Waterston, R.  
TITLE  
The WashU-RHMI Mouse EST Project  
JOURNAL  
Unpublished (1996)  
COMMENT  
Contact: Marra M/Mouse EST Project  
WashU-RHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:274482  
This clone was previously sequenced on the 5' end only, this new data is from the 3' end  
High quality sequence stop: 453.

## FEATURES

source  
1. .468  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:457594"  
/sex="unknown"  
/tissue\_type="placenta"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 75 a 166 c 176 g 51 t

Query Match 85.9%; Score 214.8; DB 9; Length 468;  
Best Local Similarity 91.2%; Pred. No. 2.3e-36;  
Matches 228; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 1 GCGCGTGGTCTCAAGCTGGCGGGTGGCTTCGAGACGCGCGCGCGCGCGCG 60  
Db 288 GCGCGTGGTCTCAAGCTGGCGGGTGGCTTCGAGACGCGCGCGCGCGCGCG 229  
QY 61 CTTCCGGGACACCTCTAGGGACCGACGCGCGCGCGCGCGCTTCTACGACGCGCG 120  
Db 228 CTTCCGGGACACCTCTGGGGACCGCGGTGGCGCGCGCGCTTCTACGCGCGCG 169  
QY 121 CCGCGAGTATTTCTGACGGGACCGCGCGCGCGCGCGCGCGCTCTACTACTACCA 180  
Db 168 CCGCGAGTATTTCTGACGGGACCGCGCGCGCGCGCGCGCTCTACTACTACCA 109  
QY 181 GTCGCGTGGCGGCTCGGGGCGCGCGCGCGCGCGCGCTCTCTGGAAGAGGT 240  
Db 108 GTCGCGGCGCGGCTGAGACGCGCGCGCGCGCGCGCTCTCTGGAAGAGGT 49  
QY 241 GGCCTTCTAC 250  
Db 48 GTCCTTCTAC 39

RESULT 2  
BI295790  
LOCUS  
DEFINITION BI295790 687 bp mRNA linear EST 19-JUL-2001  
UI-R-DK0-cfa-f-09-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone  
ACCESSION UI-R-DK0-cfa-f-09-0-UI 3', mRNA sequence.  
VERSION BI295790  
KEYWORDS BI295790.1 GI:14959590  
SOURCE EST.  
Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 687)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)

## MEDLINE COMMENT

97044477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41.  
>AT-rich#Low\_complexity 45-170, >BI\_MM#SINE/Alu 264-317,  
>GC-rich#Low\_complexity  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

Source  
1. .687  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-DK0-cfa-f-09-0-UI"  
/dev\_stage="ADULT"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-DK0 library is a subtracted library derived from a mixture of five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%), aorta-nRAP (20%), and placenta-nRPP (20%). Each original RNA from seven different developmental time-points: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, and adult day 200. (Exception: the aorta pool does not contain embryonic day 17 RNA and the placenta pool contains only the three embryonic stages). Each library was normalized individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DK0 subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CT0s), heart (CS0s), kidney (CU0s), aorta (CW0s), and placenta (CX0s). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CT0), heart (CS0), kidney (CU0), aorta (CW0), and placenta (CX0). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.  
TAG\_LIB=UI-R-DK0  
TAG\_TISSUE=rat placenta pool  
TAG\_SEQ=TCAGCAGT

BASE COUNT 140 a 217 c 203 g 126 t 1 others  
ORIGIN  
Query Match 77.1%; Score 192.8; DB 13; Length 687;  
Best Local Similarity 90.0%; Pred. No. 1.1e-31;  
Matches 206; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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QY 1 GCGGCTGGTCTCAACGTGGCCGGGCTGGCTTCGAGACGCGCGCGCACGCTGGCGCG 60
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Db 459 GCGGCTGGTCTCAACGTGGCCGGGTTGGCTTCGAGACCGCGCGCACGCTGGCGCG 518
|||||

QY 61 CTTCGCGGACACTCTGCTAGGAGACCCAGCGCGCGCGCGCTTCTACGACACGCGCG 120
|||||
Db 519 CTTCGCGGACACTCTGCTAGGAGACCCAGCGCGCGCGCTTCTACGACACGCGCGCG 578
|||||

QY 121 CCAGGAGTATTTCTTCGACCGGACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 180
|||||
Db 579 CCAGGAGTATTTCTTCGACCGGACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 638
|||||

QY 181 GTCCGCTGGGCGGCTCGCGCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACTTTC 229
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Db 639 ATCAGCGCGCGGCTGAACGCGCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACTTTC 687
|||||

RESULT 3
AI322534 522 bp mRNA linear EST 23-DEC-1998
LOCUS mh83g06.y1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus CDNA
DEFINITION clone IMAGE:457594 5' similar to gb:XI7622_cds1 POTASSIUM CHANNEL
PROTEIN KVI.6 (HUMAN);, mRNA sequence.
ACCESSION AI322534
VERSION AI322534.1 GI:4056963
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilsson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
This read has been verified (found to hit its original self in the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
This read has been verified (found to hit its original self in the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
1..522
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457594"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TCTTACCAATCTGAAGTGGGAGCGCGCGCGGAATTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library

```

```

went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 58 a 192 c 188 g 84 t
ORIGIN
Query Match 76.6%; Score 191.6; DB 9; Length 522;
Best Local Similarity 87.7%; Pred. No. 2e-31;
Matches 221; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

QY 1 GCGGCTGGTCTCAACGTGGCCGGGCTGGCTTCGAGACGCGCGCGCACGCTGGCGCG 60
|||||
Db 223 GCGGCTGGTCTCAACGTGGCCGGGTTGGCTTCGAGACCGCGCGCACGCTGGCGCG 282
|||||

QY 61 CTTCGCGGACACTCTGCTAGGAGACCCAGCGCGCGCGCTTCTACGACACGCGCG 120
|||||
Db 283 CTTCGCGGACACTCTGCTAGGAGACCCAGCGCGCGCGCTTCTACGACACGCGCG 342
|||||

QY 121 CCAGGAGTATTTCTTCGACCGGACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 180
|||||
Db 343 CCAGGAGTATTTCTTCGACCGGACCGCGCGCGCTTCGAGCGCGCTCTACTACTACCA 402
|||||

QY 181 GTCCGCTGGGCGGCTCGCGCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACTTTC 238
|||||
Db 403 GTCCGCGCGCGGCTCGAGACCGCGCGCGCGCTTCGAGCGCGCTCTACTACTACTTTC 462
|||||

QY 239 GTGGCCTTCTTAC 250
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Db 463 GTGTCCTTCTTAC 474
|||||

RESULT 4
AA021711 477 bp mRNA linear EST 21-JAN-1997
LOCUS mh83g06.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus CDNA
DEFINITION clone IMAGE:457594 5' similar to gb:XI7622_cds1 POTASSIUM CHANNEL
PROTEIN KVI.6 (HUMAN);, mRNA sequence.
ACCESSION AA021711
VERSION AA021711.1 GI:1485501
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 477)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilsson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:274482
Seq primer: -28MI3 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
1..477
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"

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/lab_host="DH10B"
/notes="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'
TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Patima Bonaldo."
```

BASE COUNT 55 a 177 c 161 g 84 t

ORIGIN

Query Match 71.1%; Score 177.8; DB 9; Length 477;  
Best Local Similarity 88.2%; Pred. No. 1.7e-28;  
Matches 216; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

QY 1 GCGGCTGGTCTCAACGTGGCGGGGTGCGCTTCGAGACGGCGCGCGACGCTGGGCGG 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 223 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACCGCGCGCGCACGCTCGGCGG 282  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 CTTCCCGGACACACTCTGTAGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 283 CTTCCCGGACACACTCTGTAGGGACCCAGCGCGCGCGCGCTTCTACGACGCGCGG 342  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 121 CCGCGAGTATTTCTTGACCGGACCGCGCGCGCGCGCTTCGACGCGCGTCTCTACTACTACCA 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 343 -CGCGAGTATTTCTTGACCGGACCGCGCGCGCGCTTCGATTCGATTCGCTCTACTACTACCA 401  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 CTCGGTGGCGGCTGGCGGCGCGCGCGCGCGCTTCGCGCTGCGCTCTTCCTGGAAGAGGT 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 402 GTCGGGCGCGCGCTGAGAGCGGCGCTC-TACCTGCCCTCGACGCTCTCTCTGGAGGAGGT 460  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 241 GGCCT 245  
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Db 461 GTCTT 465

RESULT 5  
BF530500

LOCUS BF530500 770 bp mRNA linear EST 11-DEC-2000  
DEFINITION 602071745F1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4214506  
5', mRNA sequence.

ACCESSION BF530500  
VERSION BF530500.1 GI:11617863  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 770)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>,  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
AUTHORS Contact: Robert Strausberg, Ph.D.  
TITLE Tissue Procurement: David N. Louis, M.D.  
JOURNAL CDNA Library Preparation: Life Technologies, Inc.  
COMMENT DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9788 row: j column: 11  
High quality sequence stop: 671.  
Location/Qualifiers  
1. .770  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4214506"  
/tissue\_type="anaplastic oligodendroglioma with lp/19q"

loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/notes="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 135 a 231 c 228 g 176 t

ORIGIN

Query Match 62.9%; Score 157.2; DB 12; Length 770;  
Best Local Similarity 76.8%; Pred. No. 4.2e-24;  
Matches 192; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGGGTTCGCTTCGAGACGGCGCGCGACGCTGGGCGG 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 GCGGCTGGTCAATATCTCCGGGCTGCGCTTGGAGACACAAATGGCGACCCCTGTGCT 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 CTTCCCGGACACACTCTGTAGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGG 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 GTTCCGGACACACTCTGTAGGGACCCCTGCGCGCGGAGTCCGCTTCTTCGACCCCTGAG 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 121 CCGCGAGTATTTCTTGACCGGACCGCGCGCGCGCTTCGACGCGCTCTCTACTACTACCA 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 GACGAGTACTTCTTGACCGGACCGCGCGCGCTTCGACGCGCATCTCTACTACTACCA 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 GTCGGTGGCGGCTGGCGGCGCGCGCGCTTCGCGCTCGACGCTCTCTCTGGAAGAGGT 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 181 GTCTGGGCGCGCTGCGGAGCGGTCACGCTGCCCTTGACATTTTCTCTGGAGGAGAT 240  
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QY 241 GGCCTTCTAC 250  
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Db 241 CCGCTTCTAC 250

RESULT 6  
AQ939702

LOCUS AQ939702 443 bp DNA linear GSS 23-AUG-2000  
DEFINITION NR5-028R Human NotI clones Homo sapiens genomic, DNA sequence.  
ACCESSION AQ939702  
VERSION AQ939702.1 GI:7216080  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 443)  
REFERENCE Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie  
L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J.,  
Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.  
NotI clones in the analysis of the human genome  
Nucleic Acids Res. 28 (7), 1635-1639 (2000)  
20175728  
Contact: Podowski RM  
Center for Genomics Research  
Karolinska Institute  
17177 Stockholm, Sweden  
Tel: +46-8-728-6372  
Fax: +46-8-337983  
Email: Raf.Podowski@cgr.ki.se  
Class: NotI site.  
Location/Qualifiers  
1. .443  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human NotI clones"  
/note="Organ: Lung; DNA was isolated from A549 cells after  
sodium arsenite exposure for 4 weeks. This fragment was  
differentially methylated relative to untreated controls  
and was identified using methylation sensitive AP-PCR and  
sequenced."

BASE COUNT 43 a 167 c 152 g 80 t 1 others  
ORIGIN

Query Match	62.0%	Score 155:	DB 17:	Length 443;
Best Local Similarity	100.0%;	Pred. No. 1.2e-23;		
Matches 155;	Conservative	0;	Mismatches 0;	Indels 0;
QY	96	CGGCGCGCTTCTACGACGACGCGCGCGAGTATTTCCTCGACCGCGCACCGT 155		
Db	1	CGGCGCGCTTCTACGACGACGCGCGCGAGTATTTCCTCGACCGCGCACCGT 60		
QY	156	TCGACGCGGCTCTACTACTACAGTCCGGTGGCGGCTGCGGCGCGCGCACGTGC 215		
Db	61	TCGACGCGGCTCTACTACTACAGTCCGGTGGCGGCTGCGGCGCGCGCACGTGC 120		
QY	216	CGCTCGACGCTTCTCTCGAAGAGGTGGCCTTCTAC 250		
Db	121	CGCTCGACGCTTCTCTCGAAGAGGTGGCCTTCTAC 155		
RESULT 7				
BQ338497				
LOCUS				
DEFINITION	B0938497	900 bp	mRNA	linear EST 21-AUG-2002
	5', mRNA sequence.			IMAGE:6466414
ACCESSION	B0938497			
VERSION	B0938497.1	GI:22353975		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 900)			
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAMI3990 row: k column: 23 High quality sequence stop: 663.			
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	Location/Qualifiers			
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	/db_xref="taxon:10090"			
	/clone="IMAGE:6466414"			
	/clone_lib="NIH_MGC_94"			
	/tissue_type="retina"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."			
BASE COUNT	162 a	267 c	294 g	177 t
ORIGIN				
Query Match	56.1%	Score 140.2;	DB 14:	Length 900;
Best Local Similarity	72.7%;	Pred. No. 1.7e-20;		
Matches 181;	Conservative	0;	Mismatches 68;	Indels 0;
QY	1	CGGCGTGGTCTCAACGTGGCGGGCTTTCGACGCGGCGCGCAGCTGGGCCG 60		
Db	354	GAGGTTGGTGATCAACATCTCCGGGGCTTCGACGCGGCGCGCAGCTGGCT 413		
QY	61	CTTCCCGGACACTCTGCTAGGGAGCCAGCGCGCGGGCGGCTTCTACGACGACGGCG 120		
Db	414	GTTCCTCTGACACGCTGCTAGGAGACCTTGGCCGCGAGAGTCGGTTCTTTGACCCCTT 473		
QY	121	CCGCGAGTATTTCCTGACCGCGCACCGCGCCAGCTTCGACGCGCGTGTCTACTACCA 180		

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Db 534 ATCTGGAGGTGGCTGGCGCAGGCGCTGTTAATGTGCCCCCTCGACATTTTATGGAAGAGAT 593
QY 241 GGCGTTCTTA 249
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Db 594 CCGCTTCTTA 602

RESULT 9
BB612634 704 bp mRNA linear EST 26-OCT-2001
BB612634 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732440K03 5', mRNA sequence.
BB612634
BB612634.1 GI:16453519
EST.
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 704)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Osada
Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
source
1. Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4732440K03"
/clone_lib="RIKEN full-length enriched, 10 day neonate
skin"
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/dev_stage="10 days neonate"
/lab_host="DH10B"
/note="Site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATAATTAATCCCCCCTCCCC
3']. cDNA was cloned into the XhoI and BamHI sites
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"
BASE COUNT 122 a 264 c 113 g 205 t
ORIGIN
Query Match 54.2%; Score 135.4; DB 10; Length 704;
Best Local Similarity 71.5%; Pred. NO. 1.8e-19;
Matches 178; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
... QY 2 CGGCTGTGCTCAACGTGGCGGCTGCGCTTCGAGACGGCGGCGCGCTGGCGCGC 61
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Db 78 CGTGTGTGCTCAACTGGCGCGCTTGCCTTCTTTACCCCGCGCCACTCTGGGCTA 137
QY 62 TTCGCGGACTCTGTAGGGACCCAGCGCGCGCGCGCTTCTACGACGAGCGCGC 121
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Db 138 TTTCGCGGACTCTGCTGGGGACCCCAACGCACCTCATCCACTTTTACCACCGCCCTCGC 197
QY 122 CGCGAGTATTTCTTCGACCGCGCCCGCCAGCTTCGACCGCTGCTCTACTACAG 181
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Db 198 CCAAAATTTTATTTTATTTACCTCCACCTTCCCAACTTCAATGCGGTGCTCTACTACAC 257
QY 182 TCGCGTGGCGGCTGCGCGCGCGCGCGCGCTCGCGCTCGACGCTTCTTCCTGGAGAGGTG 241
Db 258 TCTGTACGCGTTTGAACAGCGCGCCACATACCCCTACACTTCTTCTCTTAAGAAGTA 317
QY 242 GCCTTCTAC 250
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Db 318 TCCTCTAC 326

RESULT 10
CNS03DKC/c
LOCUS
DEFINITION
CNS03DKC 839 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
017A20 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL239205
VERSION
AL239205.1 GI:7898340
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis.
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 839)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 839)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	Unpublished	3 (bases 1 to 839)	Genoscope.	Direct Submission	Submitted (12-APR-2000)	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .

<b>FEATURES</b>	<b>SOURCE</b>
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/chr10_111100000
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157 a 246 c 281 q 155 t
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RESULT 11	
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LOCUS	
DEFINITION	AL843701 F000M Takifugu rubripes cDNA clone F000M10ae12, mRNA linear EST 30-JUL-2002
ACCESSION	AL843701
VERSION	AL843701.1 GI:22021529
KEYWORDS	sequence.
SOURCE	EST.
ORGANISM	Takifugu rubripes.
	Takifugu rubripes.

REFERENCE	tetraodon.tdr, tdr.tdr.
AUTHORS	1 (bases 1 to 414)
TITLE	Clark, M.S.
JOURNAL	Takifugu rubripes ESTs
COMMENT	Unpublished (2002)
	Contact: Clark MS
	MRC Human Genome Mapping Project Resource Centre
	Hinxton, Cambridge, CB10 1SB, UK
	Email: biohelp@hgmrc.ac.uk
	Vector: pME18S-FL3
	V_type: phagemid
	PRIMER: ME-735FW
	Library created by Koichi Kawakami, Masahide Sasaki, Yutaka Suzuki,
	Sumio Sugano

The Institute of Medical Science, The University of Tokyo,  
Shirokanedai, Minato-ku, Tokyo 108-8639, Japan  
and  
Kiyoshi Kikuchi, Shugo Watabe  
Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate  
School of Agricultural and Life Sciences, The University of Tokyo,  
Bunkyo-ku, Tokyo 108-8639, Japan  
Library sequenced by Melody S. Clark and Amanda Thompson MRC Human  
Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10  
1SB. UK.

FEATURES	SOURCE
1. <b>Feature 1</b>	Source 1
2. <b>Feature 2</b>	Source 2
3. <b>Feature 3</b>	Source 3
4. <b>Feature 4</b>	Source 4
5. <b>Feature 5</b>	Source 5
6. <b>Feature 6</b>	Source 6
7. <b>Feature 7</b>	Source 7
8. <b>Feature 8</b>	Source 8
9. <b>Feature 9</b>	Source 9
10. <b>Feature 10</b>	Source 10
11. <b>Feature 11</b>	Source 11
12. <b>Feature 12</b>	Source 12
13. <b>Feature 13</b>	Source 13
14. <b>Feature 14</b>	Source 14
15. <b>Feature 15</b>	Source 15
16. <b>Feature 16</b>	Source 16
17. <b>Feature 17</b>	Source 17
18. <b>Feature 18</b>	Source 18
19. <b>Feature 19</b>	Source 19
20. <b>Feature 20</b>	Source 20
21. <b>Feature 21</b>	Source 21
22. <b>Feature 22</b>	Source 22
23. <b>Feature 23</b>	Source 23
24. <b>Feature 24</b>	Source 24
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26. <b>Feature 26</b>	Source 26
27. <b>Feature 27</b>	Source 27
28. <b>Feature 28</b>	Source 28
29. <b>Feature 29</b>	Source 29
30. <b>Feature 30</b>	Source 30
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34. <b>Feature 34</b>	Source 34
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39. <b>Feature 39</b>	Source 39
40. <b>Feature 40</b>	Source 40
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96. <b>Feature 96</b>	Source 96
97. <b>Feature 97</b>	Source 97
98. <b>Feature 98</b>	Source 98
99. <b>Feature 99</b>	Source 99
100. <b>Feature 100</b>	Source 100

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BASE COUNT      81 a 125 c 139 g 68 t
ORIGIN
/note= vector: pMEROS-FLS
1 others

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RESULT	12
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LOCUS	316 bp mRNA linear EST 30-JUL-2002
DEFINITION	F00M Takifugu rubripes cDNA clone F00M15aE10, mRNA sequence.
ACCESSION	AL844004
VERSION	AL844004.1 GI:22021832
KEYWORDS	EST.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 316)	Clark, M.S.	Clarkifugu rubripes ESTs	
		Unpublished (2002)		
	Contact: Clark MS			
	MRC Human Genome Mapping Project Resource Centre			
	Hinxton, Cambridge, CB10 1SB, UK			
	Email: biohelp@hgmp.mrc.ac.uk			
	Vector: pME185-FL3			
	V_type: phagemid			
	PRIMER: ME-735FW			





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FEATURES
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      /note="Genoscope sequence ID : C0AG214AE01SP1-end :
      PUC-Ori"
BASE COUNT      201 a   308 c   372 g   198 t   6 others
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Query Match      48.7%; Score 121.8; DB 17; Length 1085;
Best Local Similarity 70.1%; Pred. No. 1.4e-16;
Matches 176; Conservative 1; Mismatches 73; Indels 1; Gaps 1;
QY 1 GGGGCTGGTCTCAACGTCGCGGGCTGCGCTTCGAGACGCGGGCGCACGCTGG-GCC 59
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Db 1004 GCGCGKGTTCATCAACATTCAGGCTGCGCTTCGAAACCCAGCTGAACACCTGCCCC 945
QY 60 GTTCCCGGACACTCTGTAGGGGACCCAGCGCGCGCGCTTCTACGACGACGCGC 119
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Db 944 AGTTCCCGGAGACCTCTCTGGGAACCCCGAGGAAGGATGCGCTACTTCGACCCGCTGC 885
QY 120 GCGGCGAGTATTTCTCGACGGCGACGCCCGAGCTTCGACGCGGTCTCTACTATACC 179
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Db 884 GGAACGAGTACTTCTTCGACCGGAACCGCGCCAGCTTCGACGCCATCTCTACTATACC 825
QY 180 AGTCCGGTGGGCGGTGCGGGCGCGCGCACGTCGCGCTCGACGCTCTTCCTGGAAGAGG 239
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Db 824 AGTCGGCGCGCGGTGAGCGCGCGGTCAACGTCGCCGCTGGACATGTTCTCGGAGAGA 765
QY 240 TGGCCTCTTAC 250
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Db 764 TCAATTTCTAC 754

RESULT 15
CNS02A6D/c
LOCUS
DEFINITION
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  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
  251113 of library G from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  AL188158
VERSION
  AL188158.1 GI:7826262
KEYWORDS
  GSS: genome survey sequence.
SOURCE
  Tetraodon nigroviridis.
  Tetraodon nigroviridis.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
  Tetraodontidae; Tetraodon.
REFERENCE
  1 (bases 1 to 1023)
  Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
  Saurin,W. and Weissenbach,J.
  Human gene number estimate provided by genome wide analysis using
  Tetraodon nigroviridis DNA sequence
  Unpublished
JOURNAL
  Unpublished
REFERENCE
  2 (bases 1 to 1023)
  Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
  Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
  Weissenbach,J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Unpublished
JOURNAL
  Unpublished
REFERENCE
  3 (bases 1 to 1023)
  Genoscope.
  Direct Submission
  Submitted (12-APR-2000)
  This sequence is a single read and was generated as part of a large
  scale clone-end sequencing project of the Tetraodon nigroviridis
  genome. For more information, please take a look at
  http://www.genoscope.cns.fr/Tetraodon.
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      PUC-Ori"
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Best Local Similarity 68.5%; Pred. No. 2.6e-16;
Matches 165; Conservative 1; Mismatches 75; Indels 0; Gaps 0;
QY 1 GCGGCTGGTCTCAACGTCGCGGGCTGCGCTTCGAGACGCGGGCGCACGCTGGGCCG 60
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Db 319 GCGGGTGGTCTCAACGTCGCGGGCTGAAGTTTGAACCCAGCTGAAGACCCCTCAGCCA 260
QY 61 CTTCCCGGACACTCTCTAGGGGACCCAGCGCGCGCGCTTCTTACGACGACGCGCG 120
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Db 259 GTTCCCGGACACGCTCTTGGGAGACCCCGACAAACGATWAGTACTTCGACCCGCTGAG 200
QY 121 CCGCGAGTATTCTTCGACCGGACCCCGCCAGCTTCGAGCGCGTCTCTACTACTACCA 180
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QY 241 G 241
Db 79 G 79
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Job time : 662.95 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2003, 04:22:08 ; Search time 1517.74 Seconds  
(without alignments)  
10661.374 Million cell updates/sec

Title: US-09-804-014a-7\_COPY\_970\_1525

Perfect score: 556

Sequence: 1 gttcttggtgagagacgc.....ccctgccagtgccgcgtcatt 556

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_htg.\*
- 3: gb\_in.\*
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- 8: gb\_pl.\*
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- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
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- 18: em\_in.\*
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- 33: em\_htg\_mus.\*
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- 35: em\_htg\_rdd.\*
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- 37: em\_htg\_vrt.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	556	100.0	1341	6	AX352535	AX352535 Sequence
2	556	100.0	1447	9	AF315818	AF315818 Homo sapi
3	556	100.0	1747	6	AX268121	AX268121 Sequence
c	556	100.0	157633	9	AC008687	AC008687 Homo sapi
5	554.4	99.7	4372	9	HS310479	AJ310479 Homo sapi
6	532	95.7	691	6	AX354900	AX354900 Sequence
c	439.8	79.1	208632	2	AC073711	AC073711 Mus muscu
8	438.2	78.8	1599	10	AF032099	AF032099 Mus muscu
9	438.2	78.8	2459	10	MMKNC2	AF032101 Mus muscu
10	436.6	78.5	1599	6	I26643	I26643 Sequence 9
11	430.8	77.5	172671	2	AC128792	AC128792 Rattus no
12	416.6	74.9	770	9	HS340320	AJ340320 Homo sapi
13	357	64.2	664	9	HS338833	AJ338833 Homo sapi
14	351	63.1	420	6	AX268139	AX268139 Sequence
15	351	63.1	420	6	AX268140	AX268140 Sequence
16	350.2	63.0	1551	4	OC038240	U38240 Oryctolagus
17	340.4	61.2	2178	4	OC038182	U38182 Oryctolagus
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c	339	61.0	155343	9	AL365361	AL365361 Human DNA
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34	327.8	59.0	1872	4	AF056943	AF056943 Oryctolag
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38	325.6	58.6	1780	4	CFU08596	U08596 Canis famli
39	324.8	58.4	760	9	HS329753	AJ329753 Homo sapi
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41	324.6	58.4	2264	10	RATKV3AA	M31744 Rat potassi
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ALIGNMENTS

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LOCUS AX352535  
DEFINITION Sequence 7 from Patent WO0194390.  
ACCESSION AX352535  
VERSION AX352535.1 GI:18617765  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Curtis,R.A.  
TITLE 52906, 33408, and 12189, potassium channel family members and uses thereof

AX352535. 1341 bp DNA linear PAT 06-FEB-2002

JOURNAL	Patent: WO 0194390-A 7 13-DEC-2001;
FEATURES	Millennium Pharmaceuticals, Inc. (US)
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QY	894 CATCGGTGAGCTGGGCTCTCTCTTTTCTTCTTCTCATCGGTGCTGCTCTTTCCAG 953
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QY	361 CGCCGTCTACTTTGCCGAAGTTGACCGGGTGGACTCCCATTTCACTAGCATCCCTGAGTC 420
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QY	1134 GCAGTGCCTGCTATT 1149
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LOCUS	Homo sapiens voltage-gated potassium channel KCNA7 mRNA, complete
DEFINITION	cds.
ACCESSION	AF315818
VERSION	AF315818.1 GI:14485554
KEYWORDS	Homo sapiens.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1447)
AUTHORS	Bardien-Kruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE	Characterization of the human voltage-gated potassium channel gene, KCNA7, a candidate gene for inherited cardiac disorders, and its exclusion as cause of progressive familial heart block I (PFHBI)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1447)
AUTHORS	Bardien-Kruger,S., Wulff,H., Arleff,H., Brink,P., Chandy,K.G. and Corfield,V.
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-2000) SANBI, University of Western Cape, Modderdam Road, Cape Town 7535, South Africa
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QY	181 CCAGCAGGCCATGTCACTGGCCATCTCTGAGAGTCACTCCGATTGGTGGTCTCTTCCGCAT 240
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QY	301 CATCGGTGAGCTGGGCTCTCTCTTTTCTTCTTCTCATCGGTGCTGCTCTTTTCCAG 360
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QY	961 CATCGGTGAGCTGGGCTCTCTCTTTTCTTCTTCTCATCGGTGCTGCTCTTTTCCAG 1020
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QY	361 CGCCGTCTACTTTGCCGAAGTTGACCGGGTGGACTCCCATTTCACTAGCATCCCTGAGTC 420
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QY 541 GCCAGTGGCCGTCATT 556

Db 1201 GCCAGTGGCCGTCATT 1216

RESULT 3

LOCUS AX268121 1747 bp DNA linear PAT 26-OCT-2001

DEFINITION Sequence 7 from Patent WO0168851.

ACCESSION AX268121

VERSION AX268121.1 GI:16516622

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Padigaru,M., Vernet,C.A., Fernandes,E., Shinkets,R.A.,

TITLE Spaderna,S.K., Majumder,K. and Li,L.

JOURNAL Polypeptides and nucleic acids encoding same

REFERENCE Patent: WO 0168851-A 7 20-SEP-2001;

Curagen Corporation (US)

FEATURES

source

1. 1747

Location/Qualifiers

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BASE COUNT 255 a 582 c 575 g 335 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e-122;

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Db 1030 CTTGTCTGTCCAAGCAGGCTATCTTCTTCAAGAACGTGATGAACCTCATCGATTTTGT 1089

QY 121 GGCTATCTCTTCCCTACTTTGTGGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGG 180

Db 1090 GGCTATCTCTTCCCTACTTTGTGGCACTGGGCACCGAGCTGGCCCGCAGCGAGGGGTGG 1149

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QY 421 CTTCTGGTGGCGGTAGTCACCATGACTACAGTTGGCTATGAGACATGGCACCGCTCAC 480

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QY 541 GCCAGTGGCCGTCATT 556

Db 1510 GCCAGTGGCCGTCATT 1525

RESULT 4

LOCUS AC008687/c

DEFINITION Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.

ACCESSION AC008687

VERSION AC008687.5 GI:15887249

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL 1 (bases 1 to 157633)

REFERENCE DOE Joint Genome Institute and Stanford Human Genome Center.

AUTHORS Direct Submission

TITLE Unpublished

JOURNAL 2 (bases 1 to 157633)

REFERENCE DOE Joint Genome Institute.

AUTHORS Direct Submission

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint

REFERENCE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

AUTHORS 3 (bases 1 to 157633)

TITLE DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Direct Submission

REFERENCE Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell

AUTHORS Drive, Walnut Creek, CA 94598, USA

TITLE DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Direct Submission

REFERENCE Submitted (03-OCT-2001)/DOE Joint Genome Institute, 2800 Mitchell

AUTHORS Drive, Walnut Creek, CA 94598, USA

TITLE DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Submitted (03-OCT-2001)/DOE Joint Genome Institute, 2800 Mitchell

COMMENT On Oct 3, 2001 this sequence version replaced gi:10312243.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.2.

STS Content:

SHGC-15869 G15229

SHGC-15864 G15225

SHGC-5822 G14090

SHGC-58615 G42524.

Location/Qualifiers

1. 157633

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BASE COUNT 33926 a 43885 c 42816 g 37006 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-122;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTGTGTCTCCAAGCAGGCTATCTTCTTCAAGAACGTGATGAACCTCATCGATTTTGT 120

Db 82058 CTTGTGTCTCCAAGCAGGCTATCTTCTTCAAGAACGTGATGAACCTCATCGATTTTGT 81999

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HSA310479 4372 bp mRNA linear PRI 30-MAY-2001
LOCUS Homo sapiens mRNA for potassium voltage-gated channel,
DEFINITION shaker-related subfamily, member 7 (KCNA7 gene).
ACCESSION AJ310479
VERSION AJ310479.1 GI:12830376
KEYWORDS KCNA7 gene; Kv1.7 gene; potassium voltage-gated channel,
SOURCE shaker-related subfamily, member*.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4372)
Kashuba,V.I., Kvasha,S.M., Protodopov,A.I., Gizatullin,R.Z.,
Rynditch,A.V., Wahlestedt,C., Wasserman,W.W. and Zabarovsky,E.R.
Initial isolation and analysis of the human Kv1.7 (KCNA7) gene, a
member of the voltage-gated potassium channel gene family
TITLE Gene 268 (1-2), 115-122 (2001)
JOURNAL member of the voltage-gated potassium channel gene family
MEDLINE 21261947
PUBMED 11368907
REFERENCE 2 (bases 1 to 4372)
AUTHORS Kashuba,V.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumorbiology
Center, Karolinska Institute, Box 280, 171 77, SWEDEN
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Best Local Similarity 99.8%; Pred. No. 3.1e-122;
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RESULT 6
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LOCUS Sequence 10 from Patent WO0192303.
DEFINITION AX354900
ACCESSION AX354900
VERSION AX354900.1 GI:18619603
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
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AUTHORS Benjamin,C.W., Roberds,S.L., Karnovsky,A.M., Ruble,C.L. and Gotow,L.F.  
TITLE Human ion channels  
JOURNAL Patent: WO 0192303-A 10 06-DEC-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
FEATURES Location/Qualifiers  
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ACCESSION AC073711  
VERSION AC073711.2 GI:9256763  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 208632)  
REFERENCE  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Mouse  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 208632)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint

COMMENT

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 18, 2000 this sequence version replaced gi:8810328.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 1810994  
Center clone name: RPI-23\_193A10  
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Summary Statistics  
Consensus quality: 204234 bases at least Q40  
Consensus quality: 207322 bases at least Q30  
Consensus quality: 207805 bases at least Q20  
Estimated insert size: 221930; agarose-fp estimation  
Estimated insert size: 208382; sum-of-contigs-estimation  
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation  
Quality coverage: 9.34 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
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\* 93559 93658: gap of unknown length  
\* 93659 94751: contig of 1093 bp in length  
\* 94752 94851: gap of unknown length  
\* 94852 118285: contig of 23434 bp in length  
\* 118286 118385: gap of unknown length  
\* 118386 157043: contig of 38658 bp in length  
\* 157044 157143: gap of unknown length  
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\* 164562 164661: gap of unknown length  
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AUTHORS Kalman,K., Nguyen,A., Tseng-Crank,J., Dukes,I.D., Chandy,G.,  
Hustad,C.M., Copeland,N.G., Jenkins,N.A., Mohrenweiser,H.M.,  
Brandriff,B., Cahalan,M.D., Gutman,G.A. and Chandy,K.G.  
TITLE Direct Submission  
JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of  
California, Irvine, CA 92697, USA  
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DEFINITION Sequence 9 from patent US 5559009.  
ACCESSION I26643  
VERSION I26643.1 GI:1606513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1599)  
AUTHORS Chandy,K.G., Kalman,K., Chandy,G. and Gutman,G.A.  
TITLE Voltage-gated potassium channel gene, Kvl.7, vectors and host cells  
comprising the same, and recombinant methods of making potassium  
channel proteins  
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;  
FEATURES  
Location/Qualifiers  
source 1..1599  
BASE COUNT 233 a 521 c 502 g 343 t  
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RESULT 11
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DEFINITION Rattus norvegicus clone CH230-262a9, *** SEQUENCING IN PROGRESS
AC128792
VERSION AC128792.1 GI:21952595
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
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Rattus.
1 (bases 1 to 172671)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayelle,M., Banks,T.,
Barberia,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davalila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Haves,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homi,F., Howard,S., Huber,J., Hulyk,S., Hune,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
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Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
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Rives,M., Rojas,A., Rojibokan,I., Roife,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vaquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 172671)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAJM
Center clone name: CH230-262a9
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 108496 bases at least Q40
Consensus quality: 114733 bases at least Q30
Consensus quality: 119570 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1740: contig of 1740 bp in length
* 1741 1840: gap of unknown length
* 1841 3040: contig of 1200 bp in length
* 3041 3140: gap of unknown length
* 3141 4347: contig of 1207 bp in length
* 4348 4447: gap of unknown length
* 4448 5658: contig of 1211 bp in length
* 5659 5759: gap of unknown length
* 5759 7066: contig of 1307 bp in length
* 7066 7166: gap of unknown length
* 7166 8912: contig of 1747 bp in length
* 8913 9012: gap of unknown length
* 9012 10121: contig of 1109 bp in length
* 10122 10221: gap of unknown length
* 10222 11495: contig of 1274 bp in length
* 11496 11595: gap of unknown length
* 11596 12895: contig of 1300 bp in length
* 12896 12995: gap of unknown length
* 12996 14935: contig of 1940 bp in length
* 14936 15035: gap of unknown length
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* 18387 20381: contig of 1995 bp in length
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Best Local Similarity 94.0%; Pred. No. 2.7e-89;
Matches 453; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

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QY 61 CTTGGTCTGTCCCAAGCAAGCTATCTTCTTCAAGAAGCTGATGAACCTCATCGATTTGT 120
DB 350 CTTGGTCTGTCCCAAGCAAGCTATCTTCTTCAAGAAGCTGATGAACCTCATCGATTTGT 409

QY 121 GGCTATCTTCCCTACTTTTGTGGCACTGGGACCGAGCTGGCCGGGAGGGGTGGG 180
DB 410 GGCTATCTTCCCTACTTTTGTGGCACTGGGACCGAGCTGGCCGGGAGGGGTGGG 469

QY 181 CCAGCAGCCATGTCACCTGCGCATCTCGAGATCATCCGATTTGGTGGTGTCTTCCGCAT 240
DB 470 CCAGCAGCCATGTCACCTGCGCATCTCGAGATCATCCGATTTGGTGGTGTCTTCCGCAT 529

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QY 301 CATGCGTGAGCTGGGCCCTCTCATCTTTTCTCTTCTCATCGGTGTGGTCTCTTTCCAG 360
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DB 768 TG 769

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LOCUS
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NRL-S18R.
ACCESSION AJ338833
VERSION AJ338833.1 GI:15883251
KEYWORDS
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ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 664)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 664)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
Source Location/Qualifiers
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Matches 363; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 650 CGCGGTCTACTTTG 663

RESULT 14
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LOCUS
DEFINITION Sequence 25 from Patent WO0168851.
ACCESSION AX268139
VERSION AX268139.1 GI:16516630
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Padigaru,M., Vernet,C.A., Fernandes,E., Shimkets,R.A.,
Spaderna,S.K., Majumder,K. and Li,L.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0168851-A 25 20-SEP-2001;
Curagen Corporation (US)
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Source Location/Qualifiers
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/db_xref="taxon:9606"
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LOCUS AX268140 420 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 26 from Patent WO0168851.
ACCESSION AX268140
VERSION AX268140.1 GI:16516631
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Padigaru, M., Vernet, C.A., Fernandes, E., Shinkets, R.A.,
TITLE Spaderna, S.K., Majumder, K. and Li, L.
JOURNAL Polypeptides and nucleic acids encoding same
Patent: WO 0168851-A 26 20-SEP-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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Query Match 63.1%; Score 351; DB 6; Length 420;  
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Search completed: February 20, 2003, 10:18:24



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Listing first 45 summaries

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8: gb\_pl:\*  
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13: gb\_un:\*  
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41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2918	100.0	1747	6	AX268121	Sequence
2	2801.5	96.0	4372	9	HS310479	Homo sapi
c 3	2620.5	89.8	157633	9	AC008687	Homo sapi
4	2402	82.3	1447	9	AF315818	Homo sapi
5	2288.5	78.4	1341	6	AX352535	Sequence
6	2210.5	75.8	1599	10	AF032099	Mus muscu
7	2203	75.5	1599	6	I26643	Sequence 9
c 8	1992.5	68.3	208632	2	AC073711	Mus muscu
9	1962.5	67.3	172671	2	AC128792	Rattus no
10	1584	54.3	2264	10	RATKV3AA	
11	1577.5	54.1	90458	2	AL513469	Homo sapi
c 12	1577.5	54.1	153543	9	AL365361	Human DNA
13	1568.5	53.8	1994	6	AR050270	Sequence
14	1568.5	53.8	1994	10	MUSMK3A	Mouse intro
15	1545	52.9	1836	5	HUMPOCH	L23499 Homo sapien
16	1544.5	52.9	1836	5	HUMPOCH	L23499 Homo sapien
17	1543.5	52.9	1883	10	RATRGK5	M30312 Rat voltage
18	1543.5	52.9	3004	9	HUMKCHAN	M85217 H.sapiens K
19	1541	52.8	4234	9	HSHBK2	X17622 Human HBK2
20	1538	52.7	1820	9	HUMPCD	M55515 Human potas
21	1537	52.7	1551	4	OCU38240	U38240 Oryctolagus
22	1536	52.6	2956	10	RNRCK3	X16001 Rat mRNA fo
23	1533.5	52.6	122903	9	AC005833	Homo sapi
24	1531.5	52.5	122903	5	AC005833	Homo sapi
25	1530	52.4	2397	9	HUMKCHN	M38217 Homo sapien
c 26	1524	52.2	22736	2	AC121825	Mus muscu
27	1523	52.2	191664	2	AC125751	Rattus no
c 28	1523	52.2	198849	2	AC129061	Rattus no
c 29	1521.5	52.1	150001	9	AC006063	Homo sapi
30	1520	52.1	2743	10	RNRCK2	X17621 Rat RCK2 mR
31	1519.5	52.1	3219	10	MUSMURINE	M96688 Mus musculu
c 32	1519.5	52.1	259159	2	AC124756	Mus muscu
33	1519.5	52.1	304681	2	AC016483	
c 34	1511	51.8	3065	4	BTPTCHA	
35	1508.5	51.7	4384	4	AF286022	Bos taurus
c 36	1498.5	51.4	191664	2	AC125751	Rattus no
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38	1496.5	51.3	3822	10	RNCKIA	X12589 Rat mRNA fo
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ALIGNMENTS

RESULT 1

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LOCUS Sequence 7 from Patent WO0168851.  
DEFINITION  
ACCESSION AX268121  
VERSION AX268121.1 GI:16516622  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Padigaru, M., Vernet, C.A., Fernandes, E., Shimkets, R.A.,  
Spaderna, S.K., Majumder, K. and Li, L.  
TITLE Polypeptides and nucleic acids encoding same  
JOURNAL Patent: WO 0168851-A 7 20-SEP-2001;  
Curagen Corporation (US)  
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HSA310479 4372 bp mRNA linear PRI 30-MAY-2001  
LOCUS Homo sapiens mRNA for potassium voltage-gated channel,  
DEFINITION shaker-related subfamily, member 7 (KCNA7 gene).  
ACCESSION AJ310479  
VERSION 1 GI:12830376  
KEYWORDS KCNA7 gene; Kv1.7 gene; potassium voltage-gated channel,  
shaker-related subfamily, member\*;  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 4372)  
Kashuba, V.I., Kvashina, S.M., Protodopov, A.I., Gizatullin, R.Z.,  
AUTHORS Rynditch, A.V., Wahlestedt, C., Wasserman, W.W. and Zabarovsky, E.R.  
TITLE Initial isolation and analysis of the human Kv1.7 (KCNA7) gene, a  
member of the voltage-gated potassium channel gene family  
JOURNAL Gene 268 (1-2), 115-122 (2001)  
MEDLINE 21261947  
PUBMED 11368907  
REFERENCE 2 (bases 1 to 4372)  
AUTHORS Kashuba, V.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumoriobiology  
Center, Karolinska Institute, Box 280, 171 77, SWEDEN  
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QY	444	sPheThrSerIleProGluSerPheTrpAlaValValThrMetThrValGlyTyr	464
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DEFINITION	Homo sapiens chromosome 19 clone CTB-60B18, complete sequence.		
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VERSION	AC008687.5	GI:15887249	
KEYWORDS	HTG.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 157633)		
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 157633)		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint		
AUTHORS	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
TITLE	3 (bases 1 to 157633)		
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.		
REFERENCE	Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell		
AUTHORS	Drive, Walnut Creek, CA 94598, USA		
TITLE	4 (bases 1 to 157633)		
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.		
REFERENCE	Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell		
AUTHORS	Drive, Walnut Creek, CA 94598, USA		
TITLE	On Oct 3, 2001 this sequence version replaced gi:10312243.		
JOURNAL	Draft Sequence Produced by DOE Joint Genome Institute		
COMMENT	www.jgi.doe.gov		
	Finishing Completed at Stanford Human Genome Center		
	www-shgc.stanford.edu		
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	Estimated Total Number of Errors is 0.2.		
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Qy	381	gValIleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLe	401
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Qy	461	rValGlyTyrGlyAspMetAlaProValThrValGlyGlyLysIleValGlySerLeuCy	481
Db	81668	AGTTGGCTATGGAGACATGGCACCCGTCACCTGTGGTGGCAAGATAGTGGGCTCTCTGTG	81609
Qy	481	sAlaIleAlaGlyValLeuThrIleSerSerLeuProValProValIleValSerAsnPhSe	501
Db	81608	TGCCATTGCGGGCGTGTGACTATTTCCTGCCAGTGGCCGCTCATTTGCTCCAAATTTCCAG	81549
Qy	501	rTyrPheTyrHisArgGluThrGluGlyGluAlaGlyMetPheSerHisValAspMe	521
Db	81548	CTACTTTTATCACCGGGAGACAGAGGGCGAAGAGCTGGATGTTTCAACCATGTGGACAT	81489
Qy	521	tGlnProCysGlyProLeuGluGlyLysAlaAsnGlyGlyLeuValAspGlyGluValPr	541
Db	81488	GCAGCCTTGTGGCCCACTGGAGGGCAAGCCAAATGGGGGCTGGTGGACGGGAGGTACC	81429
Qy	541	oGluLeuProProProLeuTrpAlaProProArgGluHisLeuValThrGluVal	559
Db	81428	TGAGTACCACTTCACCTGCGGACCCCAAGGAACACCTGTGTCCACCGAAGT	81374

RESULT 4  
AF315818  
LOCUS  
DEFINITION



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QY 550 ProProArgGluHisLeuValThrGluVal 559
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Db 1376 CCCCCAGGAAACACCTGCTCACCGAAGTG 1405

RESULT 5
AX352535
LOCUS AX352535 1341 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent WO0194390.
ACCESSION AX352535
VERSION AX352535.1 GI:18617765
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Curtis, R.A.
TITLE 52906, 33408, and 12189, potassium channel family members and uses
thereof
JOURNAL Patent: WO 0194390-A 7 13-DEC-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Source 1..1341
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LVCPKATFFKNWNILIDFVAILPYFVALGTRELARQGVGQOASLAILRVIRLVRVF
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BASE COUNT 190 a 443 c 411 g 297 t
ORIGIN

Alignment Scores:
Pred. No.: 1.14e-70 Length: 1341
Score: 2288.50 Matches: 443
Percent Similarity: 99.33% Conservative: 1
Best Local Similarity: 99.11% Mismatches: 2
Query Match: 78.43% Indels: 1
DB: 6 Gaps: 1

US-09-804-014A-8 (1-559) x AX352535 (1-1341)

QY 113 CysCysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThr 132
Db 1 TCGTCGGAGCGCTGGTGTCTAACGTGGCGCGGCTCGCGCTTCGAGACGGCGCGCAGC 60

QY 133 LeuGlyArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyAsp 152
Db 61 CTGGCGCGCTTCCGAGACTCTGTAGGGACCCAGCGCGCGCGCGCTTCTACGAC 120

QY 153 AspAlaArgGluThrPhePheAspArgHisArgProSerPheAspAlaValLeuTy 172
Db 121 GACGCGCGCGCGAGTATTTCTTCACCGCGCACCGCGCGCGCGCTTCGACGCTTCCTAC 180

QY 173 TyrTyrglnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeu 192
Db 181 TACTACAGTCGCGGGCGCTGGCGCGCGCGCGCGCGCTTCGACGCTTCCTCG 240

QY 193 GluGluValAlaPheTyrglyLeuGlyAlaAlaLeuAlaArgLeuArgGluAspGlu 212
Db 241 GAAGAGTGGCTTCTACGGCTGGCGCGCGCGCGCTGGCGCGCTGGCGCGGACGAG 300

QY 213 GlyCysProValProProGluArgProLeuProArgArgAlaPheAlaArgGlnLeuTrp 232
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RESULT 6

AF032099

LOCUS

AF032099

1599 bp

mRNA

linear

ROD 04-APR-1998

DEFINITION Mus musculus voltage-gated potassium channel Kv1.7 (Kcnc7) mRNA, complete cds.

ACCESSION AF032099

VERSION AF032099.1 GI:3004906

KEYWORDS

SOURCE Mus musculus.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1599)

AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.

TITLE Genomic organization, chromosomal localization, tissue distribution, and biophysical characterization of a novel mammalian Shaker-related voltage-gated potassium channel, Kv1.7

JOURNAL J. Biol. Chem. 273 (10), 5851-5857 (1998)

MEDLINE 98157988

PUBMED 9488722

REFERENCE 2 (bases 1 to 1599)

AUTHORS Kalman, K., Nguyen, A., Tseng-Crank, J., Dukes, I.D., Chandy, G., Hustad, C.M., Copeland, N.G., Jenkins, N.A., Mohrenweiser, H.M., Brandriff, B., Cahalan, M.D., Gutman, G.A. and Chandy, K.G.

TITLE Direct Submission

JOURNAL Submitted (30-OCT-1997) Physiology and Biophysics, University of California at Irvine, Irvine, CA 92697, USA

FEATURES

source 1..1599

gene /organism="Mus musculus"

CDS /db\_xref="taxon:10090"

1..1599

/gene="Kcnc7"

1..1599

/gene="Kcnc7"

/note="similar to Shaker"

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FLELGVLFSAAVFAEVDVDTHTSTPESFWAVTMTTVGMDAPVTGKIV  
GSLCAIAGVLTISLPVPVIVSNFSFYHRETEGEAGMISHVDTPCGTLEKANGGL  
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BASE COUNT 234 a 520 c 502 g 343 t

ORIGIN

Alignment Scores:

Pred. No.: 6,09e-68 Length: 1599

Score: 2210.50 Matches: 452

Percent Similarity: 84.77% Conservative: 10

Best Local Similarity: 82.94% Mismatches: 62

Query Match: 75.75% Indels: 21

DB: 10 Gaps: 9

US-09-804-014a-8 (1-559) x AF032099 (1-1599)

QY 21 ThrGlyLysAlaGlnSerArgArgGlyArgArgArgGlyArgAlaGlyArgAla 40

Db 7 ACAAGGAAAGCTCAAGAGATCCACGGA-----AAAGCGCGGGTGCAGTGTTCCACA 60

QY 41 SerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValPro 60

Db 61 GGTGTGGGAACGACGAGCGGCCCT-----AGCCCGCGGGGGTAAACACGCCGCC 111

QY 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAla----- 74

Db 112 CTTCCCGCGGCCCTCGGCCG-----ACTTTCATTTGGCGTGTCTCTTTCCACGCGAGCTAC 162

QY 75 ArgThrProAspThrGlyHisArgAlaGlyAlaValGlyAlaThrArgArgPheAla 94

Db 163 CGGACACCCGACATGGGGT-----GGTCGCGCGTCGGGGCCACACGTCCTCACC 213

QY 95 GlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysCys 114

Db 214 GGTGCGCGCGGCTGTGCGCCCATGAGCCACCGTTCGCGCGCGCCGCGC---CTGCGTGTGTC 270

QY 115 GluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGly 134

Db 271 GAGCGGTGTGTCTCAACGTGGCGGTTCGCTTCGAGACCCGCGCGCGCCTCGGC 330

QY 135 ArgPheProAspThrLeuLeuGlyAspProAlaAlaArgGlyArgPheTyrAspAla 154

Db 331 CGCTCCCGACACGCTGTGCGGGACCGCGTGGCGCGCAGCCGCTCTAGCAGCGCGC 390

QY 155 ArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 174

Db 391 CGGCGCGAGTATTCTTCGACCGACACCGCGCCAGCTTCGATGCGTGTCTACTACTAC 450

QY 175 GlnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlu 194

Db 451 CAGTCGGCGCGCGCTGAGACGCGCGCGCTGCGCTCGACGCTTCTTCCCTGGAGGAG 510

QY 195 ValAlaPheTyrGlyLeuGlyAlaAlaAlaAlaArgLeuArgGluAspGluGlyCys 214

Db 511 GTGCTCTTCTACGGGCTGGG---CGCGCGCTGGCGCGCTGCGGAGGAGGCTGC 567

QY 215 ProValProGluArgProLeuProArgAlaPheAlaArgGlnLeuTrpLeuLeu 234

Db 568 GCGGTC---GCCGAGCGCGCGCTGCC---CCGCGCTTTCGCGCTCAGCTCTGCTGCTC 621

QY 235 PheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuVal 254

Db 622 TTGGAATTCCTGAGAGCTCGCAGGCTGCGCGGTGCTCGCGGTGCTCCGTACTCGTC 681

QY 255 IleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspArg 274

Db 682 ATCTGCTCCATCCATCGTGGTCTTTGCTCGACACACTGCCAGACTTCCGCGAGCGCC 741

QY 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294

Db 742 GATGACCGCGGGTCCGCGCGGTAGCGGCTGCTACTGGCTCGTTCCTCGCGCGCTGAAT 801

QY 295 GlySerSerGlnMetProGlyAsnProArgLeuProPheAsnAspProPhePheVal 314

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QY 315 ValGluThrLeuCysIleCysTrpPheSerPheGluLeuValArgLeuValCys 334

Db 862 GTGAGACCCCTGTATCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921

QY 335 ProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeu 354

Db 922 CCTAGCAAGCTGTGTCTTCAAGAAATGTGATGAACCTAATGACTTCGTGGCCATCCTG 981

QY 355 ProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlnGlnAla 374

Db 982 CTTTACTTGTGCGCTTGGCGACGGAGTTAGCCCGCGCGGGGTGTGGCCAGCCGCT 1041

QY 375 MetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeu 394

Db 1042 ATGTCCTCGCCCATCTCAAGGGTCATCCGATTTGGTGGCTGCTCTCCGCATCTTCAAGCTC 1101

QY 395 SerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGlu 414

Db 1102 TCCAGCATTCGAAGGGTCTACAGATCTTGGGTGCAGACACTGCGGGCTTCCATGCGGTGAG 1161

QY 415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr 434

Db 1162 CTAGGTCTCTCATCT 1221

Qy 435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrpTrp 454  
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Qy 455 AlaValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 474  
Db 1282 GCAGTGGTTCACCATGACACCGGTTGGCTATGGGACATGGACCGCTCACGCTGGGTGGC 1341

Qy 475 LysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494  
Db 1342 AAGATCGTGGGCTCTCTGTGTGCCATTCAGGTGTGCTACCACTCTCTCCTGTGGCT 1401

Qy 495 ValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluAlaGly 514  
Db 1402 GTCATTGTCTCTAACTTTAGCTACTTTTACCACCGGGAGACAGAGGGCGAAGAGCAGGG 1461

Qy 515 MetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyGly 534  
Db 1462 ATGTACAGCCATGTGGACACACAGCCCTGCGGTACCCCTGGAGGCAAGGCTAATGGGGG 1521

Qy 535 LeuValAspGlyGluValProGluLeuProProProLeuTrpAlaProProArgGluHis 554  
Db 1522 CTGGTGGACTCTGAGTGCCTGAACCTCTCCACCATCTGCCCCCTGCAGGGAAACAC 1581

Qy 555 LeuValThrGluVal 559  
Db 1582 ATGGTGAAGTGGT 1596

RESULT 7  
I26643 LOCUS I26643 1599 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 9 from patent US 5559009.  
ACCESSION I26643  
VERSION I26643.1 GI:1606513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1599)  
AUTHORS Chandy, K.G., Kalman, K., Chandy, G. and Gutman, G.A.  
TITLE Voltage-gated potassium channel gene, Kv1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins  
JOURNAL Patent: US 5559009-A 9 24-SEP-1996;  
FEATURES Location/Qualifiers  
source 1. 1599  
BASE COUNT 233 a 521 c 502 g 343 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.le-67 Length: 1599  
Score: 2203.00 Matches: 452  
Percent Similarity: 84.93% Conservative: 10  
Best Local Similarity: 83.09% Mismatches: 61  
Query Match: 75.50% Indels: 22  
DB: 6 Gaps: 8

US-09-804-014A-8 (1-559) x I26643 (1-1599)

Qy 22 GlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgAlaGlyArgAlaSer 41  
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Qy 42 ArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValPro 61  
Db 71 CGGCAGAGGGG- - - - -CCCTAGC- - - - -CCCGGGGGTAAACCGGCCCT 114

Qy 62 ProSerArgProSerArgProAlaGlyLeuPheTyrAla- - - - -Arg 75  
Db 115 CCCCAGCCCTGGCGG- - - - -ACTTCCATGCTATTTTACCCGCCGACACCGG 165

Qy 76 ThrProAspThrGlyHisArgAlaGlyAlaAlaValGlyAlaThrArgArgPheAlaGly 95

Db 166 ACACCCGACTGGGT- - - - -GGCTGCGGCTCGGGGCCACACGTCCTCGTTACCGGT 216

Qy 96 ArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysCysGlu 115  
Db 217 CGCCGGGCTGTGCGCGCATGAGCCACGGTGCCTGGCGGCC- - -CTGCGCTGCTGCGAG 273

Qy 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135  
Db 274 CGGCTGGTCTCAACGCTGGCGGGTGGCTTCGAGACCCGCGGACGCTCGGCCG 333

Qy 136 PheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArg 155  
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Qy 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTrpGln 175  
Db 394 GCCGAGTATTTCTTCGACCGCACCCGGCCAGCTTCGATGCGGTGCTCTACTACTACCAG 453

Qy 176 SerGlyGlyArgArgProAlaHisValProLeuAspValPheLeuGluVal 195  
Db 454 TCGGCGCGGCTGAGACGGCGCGCACGTGCCCTCGACGCTCTCTGGAGGAGGTG 513

Qy 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlyCysPro 215  
Db 514 TCCTTCTACGGGCTGGG- - -CGCGGCTGCGCGGCTGCGGAGGACGAGGCTGCGCG 570

Qy 216 ValProProGluArgProLeuProArgArgAlaPheAlaArgGlnLeuTrpLeuPhe 235  
Db 571 GTC- - -GCCGAGCGCGCTGCC- - -CGCGCCTTTTGGCGCTCAGCTCTGGGTGCTTTC 624

Qy 236 GluPheProGluSerSerGlnAlaAlaArgValLeuAlaValValSerValLeuValIle 255  
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Qy 256 LeuValSerIleValIlePheCysLeuGluThrLeuProAspPheArgAspArgAsp 275  
Db 685 CTGGTCTCATCTGCTGCTTTTTCGTCGAGACACTGCCAGACTTCCGCGACACCGCAT 744

Qy 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295  
Db 745 GACCGGGGCTGCGCGCGTACGCGTCTCTGCTGCTGCTCTCTCGCTCAATGCG 804

Qy 296 SerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspPhePheValVal 315  
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Db 925 AGCAAGCTGTGTTCTTCAAGAATGTGATGAACCTTAATTTGCTGCGCCATCTCGCT 984

Qy 356 TyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnAlaLamet 375  
Db 985 TACTTGTGGGCTGGGCGAGGAGTTAGCCCGGACGCGGGTGGGCGCGCGCGCTATG 1044

Qy 376 SerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeuSer 395  
Db 1045 TCCCTGGCACTCAAGGTCATCCGATGTTGGTGGTGTCTTCCGATCTTCAAGCTCTCC 1104

Qy 396 ArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeu 415  
Db 1105 AGGCATTGGAAGGCTACAGATCTTGGGTACAGACTCGGGGCTTCCATGGGTGAGCTA 1164

Qy 416 GlyLeuLeuIlePhePheLeuIleGlyValValLeuPheSerSerAlaValTrpPhe 435  
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Qy 436 AlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrpAla 455  
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Db 1225 GCTGAAGTGGCGGTGGACACCCATTTCACCAGCATCCCGGAGTCCCTTTGGTGGGCA 1284
QY 456 ValValThrMetThrThrValGlyTyrGlyAspMetalapProValThrValGlyGlyLys 475
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QY 476 IleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValProVal 495
Db 1345 ATCGTGGGCTCTGTGTGCCATTTGACAGGTGTCTCACCATTCTCTGCTGTGCTGTGTC 1404
QY 496 IleValSerAsnPheserTyrPheTyrHisArgGluThrGluGlyGluAlaGlyMet 515
Db 1405 ATGTCTCTTAACCTTACCTTTTACCACCGGGAGACAGAGGGCGAAGAGCGGAGATG 1464
QY 516 PheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaGlyLeu 535
Db 1465 TACAGCCATGTGGACACACAGCCCTCGGTACCTGGAGGGCAAGCTAATGGGGGCTG 1524
QY 536 ValAspGlyGluValProGluLeuProProProLeuTriaAlaProProArgGluHisLeu 555
Db 1525 GTGGACTCTGTGGTGGCTGAACCTCTCCACCACCTGTGGCCCTCGCAGGAAACACATG 1584
QY 556 ValThrGluVal 559
Db 1585 GTGACTGAGGTG 1596

RESULT 8
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LOCUS
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pieces
AC073711
VERSION AC073711.2 GI:9256763
KEYWORDS HTG; HTGS-PHASE2; HTGS-DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus;
1. (bases 1 to 208632)
DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 208632)
AUTHORS DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810328.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1810994
Center clone name: RPCI-23_193A10
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Summary Statistics
Consensus quality: 204234 bases at least Q40
Consensus quality: 207322 bases at least Q30
Consensus quality: 207805 bases at least Q20
Estimated insert size: 221930; agarose-fp estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.34 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
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* the accession number will be preserved.
* 1 93558: contig of 93558 bp in length
* 93559 93658: gap of unknown length
* 93659 94751: contig of 1093 bp in length
* 94752 94851: gap of unknown length
* 94852 118285: contig of 23434 bp in length
* 118286 118385: gap of unknown length
* 118386 157043: contig of 38658 bp in length
* 157044 157143: gap of unknown length
* 157144 164561: contig of 7418 bp in length
* 164562 164661: gap of unknown length
* 164662 176791: contig of 12130 bp in length
* 176792 176891: gap of unknown length
* 176892 208632: contig of 31741 bp in length.
FEATURES
Location/Qualifiers
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/clone="RP23-193A10"
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ORIGIN
Alignment Scores:
Pred. No.: 1.15e-58 Length: 208632
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Best Local Similarity: 38.87% Mismatches: 59
Query Match: 68.28% Indels: 673
DB: 2 Gaps: 8
US-09-804-014A-8 (1-559) x AC073711 (1-208632)
QY 3 ArgArgArgThrGlySerArg-----ArgGlnLysAspGlyGluLysGlyAsp 18
Db 74941 AGGAGGATCAATAATCAAGGTCAGTTCAGCTACATAGACCTCGGTGTCATGAATCAAA 74882
QY 19 ProGlyThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgAlaGly 38
Db 74881 AGCCAAACAAATAAATAATAGTAGTACTACAAGGAAAGAACTCAAGAGATCCACGGAAAGCGC 74822
QY 39 ArgAlaSer-----ArgGlnAlaAlaArgGlyArgProValAla 51
Db 74821 CGGGTGGCAGTGTTCACAGGTGTGGGACGCGCAGGCGG-----CCC 74777
QY 52 LeuArgProAlaGlyValThrValProProProSerArgProSerArgProAlaGlyLeu 71
Db 74776 CTAGC-CCCGCGGGGTAAACACCGCCCTCCCGCGCGCTGGCGCG-----ACT 74727
QY 72 PheTyrAla-----ArgThrProAspThrGlyHisArgAlaGlyAla 85
Db 74726 TTCCATGCTATTTTACC CGCGCGACACCGCGGACACCGGACTGGGGT-----GGCTGC 74676
QY 86 AlaValGlyAlaThrArgArgPheAlaGlyArgGlyCysAlaArgHisGlyAlaAla 105
Db 74675 GCGTCGCGGCGCACACGCTCCGTCACCGGTGCGCGCGGTGTCGCGCCATGAGCCACG 74616
QY 106 ValProAlaAlaProCysGlyCysGlyArgLeuValLeuAsnValAlaGlyLeuArg 125
Db 74615 GTGCGCGCGG--CCCTGCGGCTGCTCGAGCGGCTGTCTCAACGTCGCGCGGTTCGCG 74558
QY 126 PheGluThrArgAlaThrLeuGlyArgPheProAspThrLeuLeuGlyAspProAla 145
Db 74557 TTCGAGACCGCGCGGCGACGCTCGCGCGCTTCCCGGACACGCTGTCTGGGGACCGCGTG 74498
QY 146 ArgArgGlyArgPheTyrAspAlaArgArgGlyTyrPhePheAspArgHisArgPro 165
Db 74497 CCGCGGACCGCGCTTCTACGACGCGCGCGCGCGAGTATTCTTCGACCGACACCGCGCC 74438
QY 166 SerPheAspAlaValLeuTyrTyrTyrGlnSerGlyArgLeuArgProAlaHis 185
Db 74437 AGCTTCGATGCGTCTCTACTTACCAGTCGGGCGCGCGGTGAGACGCGCGCGCGCAC 74378
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QY	186	ValProLeuAspValPheLeuGluValAlaPheTyrGlyLeuGlyAlaAlaLeu	205
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QY	206	AlaIqLeuArgGluAspGluGlyCysProValProGluArgProLeuProArgAtq	225
Db	74317	GGCGGCTCGGGAGACAGGGCTGCGGGGTGCGCGCGAGCGCGCTGCCCGCGC	74258
QY	226	AlaPheAlaArgGlnLeuTrpLeuLeuPheGluPheProGluSerSerGlnAlaAlaAtq	245
Db	74257	GCCTTTGGCGCTCAGCTCGCTGCTCTCGAATTTCTGAGAGCTCGCAGGCTGGCGC	74198
QY	246	ValLeuAlaValSerValLeuValIleLeuValSerIleValValPheCysLeuGlu	265
Db	74197	GTGCTCGCGGTGCTCTCCGACTCTGCTATCTGCTGCTCTCCATCGTCTTTTGCCTCGAG	74138
QY	266	ThrLeuProAspPheArgAspArgAspGlyThrGlyLeuAla---	284
Db	74137	ACACTGCCAGACTTCCGCGACGACCGCATGACCCGGGCTCGCGCCGTAGCGCTGCT	74078
QY	285	AlaGlyProVal-----	288
Db	74077	ACTGGCCCGTCTGAGGGCGGGGATTGGGGAGGTCCAGGGCGGGCTGGGAGACCTGG	74018
QY	288	-----	288
Db	74017	CCAGTCAGAAGGTGTGGCAAGGGCAGGAGGATGGAAGCCCTTTAAACAACAAAAA	73958
QY	288	-----	288
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Db	73897	CGAGATCTCTACAGGAGACAGACGATGGCCAGGGTTGAAGCCAGTGTGGGTACT	73838
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Db	73777	CCTGCCAGAGTTCTCTGTGAGGAGCTGGTCCCGGCTCAGTGTAGACCATCTGCAAT	73718
QY	288	-----	288
Db	73717	GCACTGCACAAAGTGACTTGGGGTTATGTGGCGAGTGGTAGAACTCCCTTACCACCT	73658
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
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QY	288	-----	288
Db	72397	TAGTTGTACAGACCTGTCTGCTCAGCTCCTGAGGGTGAATGACAGGCTCATGTCACT	72338
QY	288	-----	288
Db	72337	AGCCCCAGGAGACACACCTTTTCTGCCCTAGGTCTGAAGAACAGACATTCAGCTATCC	72278
QY	288	-----	288
Db	72277	AAAGGCAGTCGCTGGGCTTGTAGTTGTGTAGAGCAGTGAAGTCACCCCTCAGGAACACT	72218
QY	288	-----	288



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* 1740: contig of 1740 bp in length
* 1741: 1840: gap of unknown length
* 1841: 3040: contig of 1200 bp in length
* 3041: 3140: gap of unknown length
* 3141: 4347: contig of 1207 bp in length
* 4348: 4447: gap of unknown length
* 4448: 5658: contig of 1211 bp in length
* 5659: 5758: gap of unknown length
* 5759: 7065: contig of 1307 bp in length
* 7066: 7165: gap of unknown length
* 7166: 8912: contig of 1747 bp in length
* 8913: 9012: gap of unknown length
* 9013: 10121: contig of 1109 bp in length
* 10122: 10221: gap of unknown length
* 10223: 11495: contig of 1274 bp in length
* 11496: 11595: gap of unknown length
* 11596: 12895: contig of 1300 bp in length
* 12896: 12995: gap of unknown length
* 12996: 14935: contig of 1940 bp in length
* 14936: 15035: gap of unknown length
* 15036: 16336: contig of 1301 bp in length
* 16337: 16436: gap of unknown length
* 16437: 18286: contig of 1850 bp in length
* 18287: 18386: gap of unknown length
* 18388: 20381: contig of 1995 bp in length
* 20382: 20481: gap of unknown length
* 20483: 21823: contig of 1342 bp in length
* 21824: 21923: gap of unknown length
* 21924: 23103: contig of 1180 bp in length
* 23104: 23203: gap of unknown length
* 23204: 24238: contig of 1035 bp in length
* 24239: 24338: gap of unknown length
* 24340: 26241: contig of 1903 bp in length
* 26242: 26341: gap of unknown length
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* 29887: 29986: gap of unknown length
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* 33207: 35207: gap of unknown length
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* 38151: 38250: gap of unknown length
* 38251: 39679: contig of 1429 bp in length
* 39680: 39779: gap of unknown length
* 39780: 43111: contig of 3332 bp in length
* 43112: 43211: gap of unknown length
* 43212: 45028: contig of 1817 bp in length
* 45029: 45128: gap of unknown length
* 45129: 45530: contig of 1402 bp in length
* 45531: 46630: gap of unknown length
* 46631: 49509: contig of 2879 bp in length
* 49510: 49609: gap of unknown length
* 49610: 51389: contig of 1780 bp in length
* 51390: 51489: gap of unknown length
* 51490: 53715: contig of 2226 bp in length
* 53716: 53815: gap of unknown length
* 53816: 57135: contig of 3320 bp in length
* 57136: 57235: gap of unknown length
* 57236: 59889: contig of 2654 bp in length
* 59890: 59989: gap of unknown length
* 59990: 62234: contig of 2245 bp in length
* 62235: 62334: gap of unknown length
* 62335: 66086: contig of 3752 bp in length
* 66087: 66186: gap of unknown length
* 66187: 70673: contig of 4487 bp in length
* 70674: 70773: gap of unknown length
* 70774: 73088: contig of 2315 bp in length
* 73089: 73188: gap of unknown length
* 73189: 75049: contig of 1861 bp in length

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* 75050 75149: gap of unknown length
* 75150 78164: contig of 3015 bp in length
* 78165 78264: gap of unknown length
* 78265 81938: contig of 3674 bp in length
* 81939 82038: gap of unknown length
* 82039 85018: contig of 2980 bp in length
* 85019 85118: gap of unknown length
* 85119 89432: contig of 4314 bp in length
* 89433 89532: gap of unknown length
* 89533 93510: contig of 3978 bp in length
* 93511 93610: gap of unknown length
* 93611 97571: contig of 3961 bp in length
* 97572 97671: gap of unknown length
* 97672 102374: contig of 4603 bp in length
* 102375 102374: gap of unknown length
* 102375 105519: contig of 3145 bp in length
* 105520 105619: gap of unknown length
* 105620 108265: contig of 2646 bp in length
* 108266 108365: gap of unknown length
* 108366 113533: contig of 5168 bp in length
* 113534 113633: gap of unknown length
* 113634 117825: contig of 4192 bp in length
* 117826 117925: gap of unknown length
* 117926 124230: contig of 6305 bp in length
* 124231 124330: gap of unknown length
* 124331 129365: contig of 5035 bp in length
* 129366 129465: gap of unknown length
* 129466 136317: contig of 6852 bp in length
* 136318 136417: gap of unknown length
* 136418 144084: contig of 7667 bp in length
* 144085 144184: gap of unknown length
* 144185 151956: contig of 7772 bp in length
* 151957 152056: gap of unknown length
* 152057 159994: contig of 7938 bp in length
* 159995 160094: gap of unknown length
* 160095 172671: contig of 12577 bp in length.

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## Alignment Scores:

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Score:              1962.50           Matches:         462
Percent Similarity: 40.45%           Conservative:    10
Best Local Similarity: 39.59%         Mismatches:      51
Query Match:        67.25%           Indels:          6
DB:                  2                Gaps:             6

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US-09-804-014A-8 (1-559) x AC128792 (1-172671)

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QY 36 ArgAlaGlyArgAlaSerArgGlnArgAlaArgGly-----Arg 48
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Db 85761 AAACCTCGTGAAAGTGCGCCCACTGACCACTGGACATGGCGCAATGCGAAACTAAGA 85820

QY 49 ProValAlaLeuArgProAlaGlyValThrValProProSerArgProSerArgPro 68
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Db 85821 GAGGTGACACCCCGATCCCGCGGGGTAAACCCGCCCTTCCCGCGCGCTGGCGCGGACT 85880

QY 69 ---AlaGlyLeuPheTyrAlaArgThrProAspThr-GlyHisArgAlaGlyAlaVa 87
    :: ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85881 TTCCATGCTATATATACGCGGACACCGACACCGCGCTGG---GGTGGCTGGCGCGT 85937

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QY 147 gGlyArgPheTyrAspAlaArgArgGluTyrPhePheAspArgHisArgProSerPh 167  
Db 86116 | ||||| CACCCGCTCTACAGCGCGCGCGCGAGTATTTCTTCACCGACACCGCGCCAGCTT 86175  
QY 167 eAspAlaValLeuTyrTyrGlnSerGlyArgLeuArgArgProAlaHisValPr 187  
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QY 187 oLeuAspValPheLeuGluValAlaPheTyrGlyLeuGlyAlaAlaLeuAlaAr 207  
Db 86236 CCTCGACGCTCTCTCGAGGAGGTCTCTTCTACGGGCTGGGTGCGCGCGCTGCGCG 86295  
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QY 286 -GlyProValPhe----- 289  
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 Luneau,C.J.  
 Luneau,C.J.  
 Unpublished (1990)  
 2 (sites)  
 Swanson,R., Marshall,J., Smith,J., Williams,J., Boyle,M.B.,  
 Folander,K., Luneau,C.J., Antanavage,J., Oliva,C., Buhrow,S.A.,  
 Bennett,C., Stein,R.B. and Kaczmarek,L.M.  
 Cloning and expression of cDNA and genomic clones encoding three  
 delayed rectifier potassium channels in rat brain  
 Neuron 4 (6), 929-939 (1990)  
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 R.J. Swanson, 16-AUG-1989, for release after publication.  
 [1] Author Address  
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 West Point, PA 19486.  
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 Db 199 GGAGGAGGGAGG-----AGGAGCGGTCTGCACGCTGCAGCGGGCGCGCCACGCC 252  
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DEFINITION Sequence 1 from patent US 5827655.
ACCESSION AR050270
VERSION AR050270.1 GI:5972995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1994)
AUTHORS Chandy,K.G., Cahalan,M.D., Grissmer,S., Goldin,A.L., Dethlefs,B.A.,
Gutman,G.A. and Wasmuth,J.J.
TITLE Assay, methods and products based on n k.sup.+ channel expression
JOURNAL Patent: US 5827655-A 1 27-OCT-1998;
FEATURES
Location/Qualifiers
source 1..1994
/organism="unknown"
BASE COUNT 394 a 612 c 534 g 454 t
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Percent Similarity: 68.20% Conservative: 57
Best Local Similarity: 58.13% Mismatches: 118
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Job time : 4829 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	74	29.6	2064	4	US-09-178-109-3
5	74	29.6	2072	4	US-09-142-791A-3
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ALIGNMENTS

RESULT 1  
US-08-288-405A-9  
; Sequence 9, Application US/08288405A  
; Patent No. 5559009  
; GENERAL INFORMATION:  
; APPLICANT: Chandy, Kanianthara G.  
; APPLICANT: Kalman, Katalin  
; APPLICANT: Chandy, Grischa  
; APPLICANT: Gutman, George A.  
; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel  
; TITLE OF INVENTION: Gene  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert,  
; ADDRESSEE: Attn: Walter H. Dreger  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/288,405A  
; FILING DATE: 10-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,431  
; FILING DATE: 04-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-59844-1/WH0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1599 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1599  
US-08-288-405A-9

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Query Match      85.3%; Score 213.2; DB 1; Length 1599;
Best Local Similarity 90.8%; Pred. No. 7.6e-38;
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Db 513 GTCCTTCTAC 522

RESULT 2
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; Sequence 1, Application US/08527152
; Patent No. 5827655
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanlanthara G.
; APPLICANT: Cahalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.
; APPLICANT: Dethlefs, Brent A.
; APPLICANT: Gutman, George A.
; APPLICANT: Wasmuth, John J.
; TITLE OF INVENTION: Assay, Methods and Products Based On n
; TITLE OF INVENTION: K+ Channel Expression
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: W.H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/527,152
; FILING DATE: UNKNOWN
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/170,418
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/558,568
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Waller H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54444-2/WHID
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 150..1736
US-08-527-152-1

Query Match      54.6%; Score 136.4; DB 1; Length 1994;
Best Local Similarity 71.8%; Pred. No. 2e-21;
Matches 179; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1 GCGGCTGGTCTCAACGTGGCGGGCTGCGCTTCGAGACGGGGCGGCGGCGGCGGCGG 60
Db 320 GCGTGTGGTCTCAACATCTCCGGGCTGCGCTTCGAGACGAGCTCAAGACCTCTGCCA 379
QY 61 CTTCCCGGACACTGCTAGGGACCCAGCGCGGCGGCGGCTTCACGACGACGGCGG 120
Db 380 GTTCCCGGAGACACTGCTGGGCGACCCCAAGCGGCGCATGCGGTACTTTGACCCACTCCG 439
QY 121 CCGCGAGTATTCTTCGACCGGCGGCGGCGGCGGCGGCTTCGAGCGGCTGCTACTACTACCA 180
Db 440 CAATGAGTACTTCTTCGACCGCAACCGGCGGCGGCTTCGAGCGGCGGCGGCGGCGG 499
QY 181 GTCGGTGGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCTTCGCGCTCGACGCTCTTCTGGAAGAGGT 240
Db 500 GTCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 559
QY 241 GGCCTTCTAC 250
Db 560 CCGCTTCTAC 569

RESULT 3
US-09-336-643A-9
; Sequence 9, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2195)
; OTHER INFORMATION: K+hov12
US-09-336-643A-9

Query Match      31.2%; Score 78; DB 4; Length 3424;
Best Local Similarity 63.0%; Pred. No. 5.9e-09;
Matches 155; Conservative 0; Mismatches 85; Indels 6; Gaps 2;

QY 5 CTGCTGCTCAACGTGGCGGGCTGCGCTTCGAGACGGGGCGGCGGCGGCGGCGGCGGCTTC 64
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Db 380 CTGGTGGTGAACGCTGACGGACCGCGCTTTTGAGACTTGAAGAATACGCTGACCGCTAC 439  
QY 65 CCGGACACTCTGCTAGGGACACGACGCGCCGCGCTTCTAGACGACGCGCGCGCG 124  
Db 440 CCAGACACCTTCTGGGACGCTGGAGAG---GAACTTCTTACGATGCTACTCAGCG 496  
QY 125 GAGTATTTCTCGACGGGACCGGCGCCAGCTTTCGACGCGCTCTCTACTACTACAGTCC 184  
Db 497 GAGTACTTCTTCGATCGGACGACCTGACATGTTCCGGCATGTGCTGAACCTTCTACCGAAC- 555  
QY 185 GGTGGCGGCTCGGCGGCGCGGCGGACGCTGCGCTCGAGCTCTTCTGGAAGAGTGGCC 244  
Db 556 --GGGCGGCTGCAFTTGCCACGCGAGGAGTGCATCCAGGCGCTTCGACGAAGAGTGGCT 613  
QY 245 TTCTAC 250  
Db 614 TTCTAC 619

RESULT 4  
US-09-178-109-3  
; Sequence 3, Application US/09178109  
; Patent No. 6395477  
; GENERAL INFORMATION:  
; APPLICANT: Cockett, Mark I.  
; APPLICANT: Dिल्s, Daniel W.  
; APPLICANT: Chang Ling, Huai-Ping  
; APPLICANT: Sokol, Patricia T.  
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
; TITLE OF INVENTION: Polypeptides and Uses Therefor  
; FILE REFERENCE: ahp-98089  
; CURRENT APPLICATION NUMBER: US/09/178,109  
; CURRENT FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2064  
; TYPE: DNA  
; ORGANISM: human  
US-09-178-109-3

Query Match 29.6%; Score 74; DB 4; Length 2064;  
Best Local Similarity 61.6%; Pred. No. 4.3e-08;  
Matches 154; Conservative 0; Mismatches 90; Indels 6; Gaps 2;

QY 1 GCGGCTGGTGTCAAGTGGCGGCTGGCTTTCGAGACGCGGCGCGACGCTGGCGG 60  
Db 192 GCTGATTGCTTCAAGCTAGTGGCGGAGGTTCAGACCTGGAGACCCACGCTGGAGCG 251  
QY 61 CTTCGCGGACACTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGCGCG 120  
Db 252 CTACCCGGACACCTGCTGGGACGACGAGAGAGGATTCTTCTCAACGAGGACAC--- 308  
QY 121 CCGGAGTATTTCTCGACCGGACGCGGCGCCAGCTTTCGACGCGGCTCTACTACTACCA 180  
Db 309 CAAGAGTACTTCTTCGACCGGACCCGAGGTGTTCCGCTGCGTCTCAACTTCTACC- 367  
QY 181 GTCCGGTGGCGGCTGCGGCGCGGCGGACGCTGCGCTCGACGCTTCTCTGGAAGAGT 240  
Db 368 --GCACGGGAGCTGCATACCCGGCTACGAGTGCATCTCTGCTTACGACGAGCT 425  
QY 241 GGCCTTCTAC 250  
Db 426 GGCCTTCTAC 435

RESULT 5  
US-09-142-791A-3  
; Sequence 3, Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Brill  
; APPLICANT: Thierry Paul Gerard Calmels

; APPLICANT: Jean-Francois Simon Pierre Faivre  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142,791A  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2072  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-142-791A-3

Query Match 29.6%; Score 74; DB 4; Length 2072;  
Best Local Similarity 61.6%; Pred. No. 4.3e-08;  
Matches 154; Conservative 0; Mismatches 90; Indels 6; Gaps 2;

QY 1 GCGGCTGGTGTCAAGTGGCGGCTGGCTTTCGAGACGCGGCGCGACGCTGGCGG 60  
Db 120 GCTGATTGCTTCAAGCTAGTGGCGGAGGTTCAGACCTGGAGACCCACGCTGGAGCG 179  
QY 61 CTTCGCGGACACTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGACGCGCG 120  
Db 180 CTACCCGGACACCTGCTGCGGACGACGAGAGAGGATTCTTCTCAACGAGGACAC--- 236  
QY 121 CCGGAGTATTTCTTCGACCGGACCGGCGCCAGCTTTCGACGCGGCTCTACTACTACCA 180  
Db 237 CAAGAGTACTTCTTCGACCGGACCCGAGGTGTTCCGCTGCGTCTCAACTTCTACC- 295  
QY 181 GTCCGGTGGCGGCTGCGGCGCGGCGGACGCTGCGCTCGAGCTTCTCTGGAAGAGT 240  
Db 296 --GCACGGGAGCTGCATACCCGGCTACGAGTGCATCTCTGCTTACGACGAGCT 353  
QY 241 GGCCTTCTAC 250  
Db 354 GGCCTTCTAC 363

RESULT 6  
US-09-142-791A-1  
; Sequence 1, Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Brill  
; APPLICANT: Thierry Paul Gerard Calmels  
; APPLICANT: Jean-Francois Simon Pierre Faivre  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142,791A  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1

QY 241 GGCCCTTCTAC 250

; CURRENT FILING DATE: 1999-06-18

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1805 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-955-916-6

Query Match . 23.8%; Score 59.4; DB 1; Length 1805;
Best Local Similarity 55.3%; Pred. No. 5.6e-05;
Matches 142; Conservative 0; Mismatches 106; Indels 9; Gaps 1

QY 1 GCGGGTGTGTCTCAACGTGGCGGGCTGCGCTTCGAGA-----CGCGGGGGCGGCAC 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 GCGCATCGTGTATCAACGTGGCGGCACGCGGCCACACAGACGTACGGCTCGACGCTGGCGCAC 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 52 GCTGGCGCGCTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGA 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 GCTGCCGCGCAGCGCGCTTGCTGGCTGGCAGAGCGGACGCCACACAGCCATTCGACTA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 CGACGGCGCGCCGCGAGTATTTCTTTCGACGGCAGCCGCGCAGCTTCGACGCGGTGCTTA 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 TGACCCCGGTGGCAGCAGGTTCTTTCTTGACGGCCACCCGGGGCTCTTCGCTCACATCCT 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 172 CTACTACCAAGTCCGCTGGCGGCTGCGGCGCGCGCGCGCACGTGCCGCTTCCTCTTCT 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 GAACATATTACCCACACCGCAAGCTTACTGCCGCGCGCAGCTGTGTGGGCGCGCTCTACGA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 232 GGAAGAGGTGGCTTCT 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 GGAGGAGTGGCTTCT 416
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RESULT 11
US-08-403-852D-2
; Sequence 2, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1268
; US-08-403-852D-2

Query Match          16.7%; Score 41.8; DB 2; Length 1268;
Best Local Similarity 51.3%; Pred. No. 0.33;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 44 GCGCGCACGCTGGCGCGCTTCCCGGACACTCTGCTAGGGAGCCAGCGCGCGCGCGC 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 574 GCGCGCGCGCGCGCGCGCGCGCTCATCATCCAGCGCGCGCTCTCGCGGTGGGACGC 633

QY 104 TTCTAGACAGCGCGCGCGCGAGTAGTTTCTTCGACGGGACCGCGCCAGCTTCGAGCGC 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 GAGTTGCGCGCGCGCGCGCGAGTCTTCCACCGGCACACCGCGTCTCCGAGCGC 693

QY 164 GTGCTCTACTACTACAGTCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 CAGGACTTCTACGGGACCTCAAGGACGCGTCCGCGCGCGCGCGCGCGCGCGAGAG 753

QY 224 GTCTTCTGT 232
   ||| ||| |||
Db 754 GTCCTCGTG 762

RESULT 12
US-08-510-646B-2
; Sequence 2, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1268
; US-08-510-646B-2

Query Match          16.7%; Score 41.8; DB 3; Length 1268;
Best Local Similarity 51.3%; Pred. No. 0.33;
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 44 GCGCGCACGCTGGCGCGCTTCCCGGACACTCTGCTAGGGAGCCAGCGCGCGCGCGC 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 574 GCGCGCGCGCGCGCGCGCGCGCTCATCATCCAGCGCGCGCTCTCGCGGTGGGACGC 633

QY 104 TTCTAGACAGCGCGCGCGCGAGTAGTTTCTTCGACGGGACCGCGCCAGCTTCGAGCGC 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 GAGTTGCGCGCGCGCGCGAGTCTTCCACCGGCACACCGCGTCTCCGAGCGC 693

QY 164 GTGCTCTACTACTACAGTCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 CAGGACTTCTACGGGACCTCAAGGACGCGTCCGCGCGCGCGCGCGCGCGAGAG 753

QY 224 GTCTTCTGT 232
   ||| ||| |||
Db 754 GTCCTCGTG 762

RESULT 13
US-09-231-818-2
; Sequence 2, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
```

APPLICANT: Debussche, Laurent  
APPLICANT: De Crecy-Lagard, Valerie  
TITLE OF INVENTION: Polypeptides Involved In The  
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/231,818  
FILING DATE: 10-MAY-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,852  
FILING DATE: 25-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03806.0054-00000  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: S.pristinaespiralis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1268  
US-09-231-818-2

Query Match 16.7%; Score 41.8; DB 4; Length 1268;  
Best Local Similarity 51.3%; Pred. No. 0.33;  
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;  
QY 44 GCGCGCAGCGCTGGCGCGCTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCG 103  
Db 574 GCGCGCGCGCGCGCGCGCGCGCGCGCTCCATCCAGCGCGCTCTCCGCGTGGGACGC 633  
QY 104 TTCTAGCAGCAGCGCGCGCGCGAGTATTTCTTCGACCGGCACCGCGCGCGCTCGACGCG 163  
Db 634 GAGTTCCGCGCGCGCGCGCGCGAGTCTATTCACCGCGCACACCGGCTCTCCGACGCG 693  
QY 164 GTGCTCTACTACTACAGTCCGGTGGCGGCTGCGCGCGCGCGCGCGCTGCGCTCGAC 223  
Db 694 CAGGACTTCTAGGGGACCTCAAGGCACGCGTCCGCGCGCGCGCGCGCGCGAGAG 753  
QY 224 GTCTTCTG 232  
Db 754 GTCTCTGTG 762

RESULT 14  
US-08-403-852D-1  
Sequence 1, Application US/08403852D  
Patent No. 5951695  
GENERAL INFORMATION:  
APPLICANT: Blanc, Veronique  
APPLICANT: Blanche, Francis  
APPLICANT: Crouzet, Joel  
APPLICANT: Jacques, Nathalie  
APPLICANT: Lacroix, Patricia  
APPLICANT: Thibaut, Denis  
APPLICANT: Zagorec, Monique  
APPLICANT: Debussche, Laurent  
APPLICANT: De Crecy-Lagard, Valerie  
TITLE OF INVENTION: Polypeptides Involved In The  
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,852D  
FILING DATE: 10-MAY-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 93/00923  
FILING DATE: 25-SEP-1993  
APPLICATION NUMBER: FR 92/11441  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03806.0054-00000  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5392 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: S.pristinaespiralis  
US-08-403-852D-1

Query Match 16.7%; Score 41.8; DB 2; Length 5392;  
Best Local Similarity 51.3%; Pred. No. 0.32;  
Matches 97; Conservative 0; Mismatches 92; Indels 0; Gaps 0;  
QY 44 GCGCGCAGCGCTGGCGCGCTCCCGGACACTCTGCTAGGGACCCAGCGCGCGCGCGCG 103  
Db 621 GCGCGCGCGCGCGCGCGCGCGCGCTATCCAGCGCGCGCTCTCCGCGTGGGACGC 680  
QY 104 TTCTAGCAGCAGCGCGCGCGAGTATTTCTTCGACCGGCACCGCGCGCGCTCGACGCG 163  
Db 681 GAGTTCCGCGCGCGCGCGCGAGTCTATTCACCGCGCACCGGCTCTCCGACGCG 740  
QY 164 GTGCTCTACTACTACAGTCCGGTGGCGCGCTGCGCGCGCGCGCGCGCTCGAC 223



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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 23:59:06 ; Search time 59.8275 Seconds  
(without alignments)  
9410.374 Million cell updates/sec

Title: US-09-804-014A-7\_COPY\_382\_631

Perfect score: 250

Sequence: 1 gcggctggtgctcaacgtgg.....tggaagaggtgcctcttac 250

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*
- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
- 10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*
- 11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*
- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*
- 13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*
- 14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*
- 15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*
- 16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*
- 17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*
- 18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*
- 19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*
- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	250	100.0	1341	ABL57038	Human potassium ch
2	250	100.0	1686	AAS78540	DNA encoding novel
3	250	100.0	1747	AAS13338	Human cDNA encodin
4	250	100.0	1792	AAD37899	Human ion channel
5	213.2	85.3	1598	AAT04953	Mouse Kv1.7 voltag
6	175.4	70.2	994	ABQ19702	Oligonucleotide fo
7	175.4	70.2	994	ABQ19703	Oligonucleotide fo
8	168.4	67.4	994	ABQ19704	Oligonucleotide fo
9	168.4	67.4	994	ABQ19705	Oligonucleotide fo

10	133.4	53.4	2867	24	ABN95856	Gene #2354 used to
11	133.4	53.4	2867	24	ABL65917	Lung cancer relate
12	125.2	50.1	3147	24	AB199654	Mouse ischaemic co
13	119	47.6	1836	22	AAH21452	Human Kv1.5 DNA..
c 14	100.2	40.1	1521	24	ABQ49288	Oligonucleotide fo
15	100.2	40.1	1521	24	ABQ49289	Oligonucleotide fo
c 16	100.2	40.1	1521	24	ABL33117	Human immune syste
c 17	92.2	36.9	7488	24	ABL33113	Human immune syste
c 18	91.8	36.7	701	24	ABQ16958	Oligonucleotide fo
c 19	91.8	36.7	701	24	ABQ16959	Oligonucleotide fo
c 20	91.8	36.7	8758	24	ABL33119	Human immune syste
21	81.4	32.6	2237	23	ABL13285	Drosophila melanog
22	78	31.2	2033	22	AAH21248	Human KCND1 exon1
23	78	31.2	2578	22	AAH99538	Human protein enco
24	78	31.2	2711	22	AAH21246	Human Kv4.1 cDNA..
25	78	31.2	3424	20	AAZ11901	Human potassium ch
26	74	29.6	2064	24	ABN84401	Human Kv4.3 potass
27	74	29.6	2072	19	AAV61572	Human Kv potassium
28	74	29.6	2104	19	AAV61571	Human Kv potassium
29	74	29.6	2121	24	ABN84400	Human Kv4.3 potass
30	72.4	29.0	2104	19	AAV61573	Human Kv potassium
31	71.4	28.6	1521	24	ABQ49286	Oligonucleotide fo
c 32	71.4	28.6	1521	24	ABQ49287	Oligonucleotide fo
33	71.4	28.6	7642	24	ABL33116	Human immune syste
34	69.2	27.7	7488	24	ABL33112	Human immune syste
35	67.4	27.0	1716	23	ABL29811	Drosophila melanog
36	66.8	26.7	701	24	ABQ16960	Oligonucleotide fo
c 37	66.8	26.7	701	24	ABQ16961	Oligonucleotide fo
38	66.8	26.7	8758	24	ABL33118	Human immune syste
c 39	66.2	26.5	18028	23	ABL13284	Drosophila melanog
40	65.6	26.2	1927	20	AAZ11898	Human potassium ch
41	62.4	25.0	3174	23	AAS64788	DNA encoding novel
42	54.2	21.7	612	22	ABA76453	Human foetal liver
43	54.2	21.7	612	22	ABA40984	Probe #19450 for g
44	54.2	21.7	612	22	AAK25090	Human brain expres
45	54.2	21.7	612	22	AAK51097	Human bone marrow

ALIGNMENTS

RESULT 1  
ABL57038  
ID ABL57038 standard; cDNA; 1341 BP.

XX ABL57038;

XX 22-JUL-2002 (first entry)

XX Human potassium channel 12189 partial cDNA.

DE Potassium channel; ion transport; 12189; nootropic; anticonvulsant;  
KW neuroprotective; antiparkinsonian; hypotensive; neuroleptic;  
KW antidepressant; antimanic; tranquilizer; anorectic; antimigraine;  
KW antiarteriosclerotic; vasotropic; vulnerary; antiarrhythmic;  
KW cardiant; antinflammatory; cytostatic; osteopathic; hepatotropic;  
KW antidiabetic; immunosuppressive; antiarthritic; antirheumatic;  
KW antipsoriatic; antithyroid; antitumor; dermatological; antianaemic;  
KW antiasthmatic; antiallergic; ophthalmological; immunomodulator;  
KW analgesic; virucide; human; gene therapy; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1341

FT /tag= a

FT /product= "12189"

FT /partial

XX /note= "The CDS does not include a start codon"

XX WO200194390-A2.

XX 13-DEC-2001.

XX PF 06-JUN-2001; 2001WO-US18340.  
XX PR 06-JUN-2000; 2000US-209845P.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Curtis RAJ;  
XX DR WPI; 2002-401589/43.  
XX DR P-PSDB; ABB76166.  
XX PT New potassium channel family member polypeptide and polynucleotide,  
XX PT useful for diagnosing, treating viral diseases, neurological, cardiac,  
XX PT cellular proliferative or differentiative, bone, immune, liver and  
XX PT metabolic disorders -  
XX PS Claim 1; Page 135-136; 158pp; English.  
XX CC The present sequence is that of a partial cDNA for human 12189  
XX CC (see ABB76166), a novel potassium channel family member. 12189  
XX CC contains a potassium channel tetramerisation domain, an ion  
XX CC transport protein domain and a core membrane region including 6  
XX CC transmembrane domains. The invention provides human potassium  
XX CC channel 52906, 33408 and 12189 nucleic acids and proteins, as well  
XX CC as antisense nucleic acid molecules, recombinant expression vectors,  
XX CC host cells, transgenic animals, fusion proteins, antigenic peptides  
XX CC and antibodies. Also claimed are: a method for detecting the  
XX CC presence of a 52906, 33408 or 12189 nucleic acid; a method for  
XX CC modulating the activity of a 52906, 33408 or 12189 polypeptide using  
XX CC a compound that binds the polypeptide; a method for identifying a  
XX CC compound which modulates the activity of the polypeptide; a method  
XX CC of treating or preventing an ion flux-related disorder using an  
XX CC agent that modulates the activity or expression of a 52906 or  
XX CC 12189 polypeptide or nucleic acid, especially a peptide,  
XX CC phosphopeptide, small molecule, antibody, antisense molecule,  
XX CC ribozyme, a triple helix molecule, or a 52906 or 12189 nucleic  
XX CC acid. The ion flux-related disorders include: potassium channel  
XX CC associated disorders, such as neurological disorders and central  
XX CC nervous system disorders such as cognitive and neurodegenerative  
XX CC disorders e.g. Alzheimer's disease, Parkinson's disease, senile  
XX CC dementia, Huntington's disease, Gilles de la Tourette's syndrome,  
XX CC multiple sclerosis, progressive supranuclear palsy, epilepsy,  
XX CC Jacob-Creutzfeldt disease, autonomic function disorders such as  
XX CC hypertension and sleep disorders, neuropsychiatric disorders such  
XX CC as depression, schizophrenia, mania, anxiety disorders or phobic  
XX CC disorders, learning or memory disorders, amnesia or age-related  
XX CC memory loss, attention deficit disorder, obsessive-compulsive  
XX CC disorder, migraine or obesity; cardiac-related disorders such as  
XX CC arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial  
XX CC inflammation, tachycardia, congestive heart failure, myocardial  
XX CC infarction and arrhythmia. The polypeptides and nucleic acids are  
XX CC also useful as diagnostic targets and therapeutic agents for:  
XX CC controlling cellular proliferative and/or differentiative disorders  
XX CC e.g. haematopoietic neoplastic disorders, carcinoma and sarcoma;  
XX CC disorders associated with bone metabolism such as osteoporosis;  
XX CC rickets, osteopenia, cirrhosis, hyperparathyroidism, idiopathic  
XX CC hypercalcaemia; immune disorders such as autoimmune disorders,  
XX CC diabetes mellitus, arthritis, including rheumatoid arthritis,  
XX CC osteoarthritis and psoriatic arthritis, multiple sclerosis,  
XX CC myasthenia gravis, autoimmune thyroiditis, ulcerative colitis,  
XX CC psoriasis, Sjogren's syndrome, dermatitis, Crohn's disease, asthma,  
XX CC allergic asthma, conjunctivitis, aplastic anaemia, Grave's disease,  
XX CC chronic active hepatitis, autoimmune uveitis, scleroderma; liver  
XX CC disorders including storage disorders such as Gaucher's disease,  
XX CC glycogen storage disease, haemochromatosis and peroxisomal  
XX CC disorders; viral diseases; pain; or metabolic disorders such as  
XX CC obesity, anorexia nervosa, cachexia, lipid disorders and diabetes.  
XX SQ Sequence 1341 BP; 190 A; 443 C; 411 G; 297 T; 0 other;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGGCTGGTGTCAAGTGGCGGCTTCGAGACGCGGCGGCGGCGGCGGCGG 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 9 GCGGCTGGTGTCAAGTGGCGGCTTCGAGACGCGGCGGCGGCGGCGGCGGCGG 68  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 61 CTTCCGGGACACTCTGCTAGGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 69 CTTCCGGGACACTCTGCTAGGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 128  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 121 CCGCGAGTATTTCTTCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 129 CCGCGAGTATTTCTTCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 188  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 181 GTCGGTGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 189 GTCGGTGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 248  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 241 GGCCTTCTAC 250  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 249 GGCCTTCTAC 258  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
RESULT 2  
AAS78540  
ID AAS78540 standard; cDNA; 1686 BP.  
XX AC AAS78540;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #14344.  
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR P-PSDB; ABG14353.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity -  
XX PS Claim 1; SEQ ID NO 14344; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX CC polynucleotides are also used in diagnostics as expressed sequence tags  
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques  
XX CC to restore normal activity of (II) or to treat disease states involving  
XX CC (II). (II) is useful for generating antibodies against it, detecting or  
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as  
XX CC a food supplement. (II) and its binding partners are useful in medical  
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating  
XX CC disorders involving aberrant protein expression or biological activity.



CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 1686 BP; 236 A; 545 C; 562 G; 343 T; 0 other;

Query Match 100.0%; Score 250; DB 23; Length 1686;  
Best Local Similarity 100.0%; Pred. No. 3.3e-45;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTGTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 60  
DB 417 GCGGCTGGTGTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 476  
QY 61 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTAGAGAGCGCGG 120  
DB 477 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTAGAGAGCGCGG 536  
QY 121 CGCGAGATTTCTTCGACCGGCGCGCGCGCGCGCGCGCGCGCTTCTACTACTACCA 180  
DB 537 CGCGAGATTTCTTCGACCGGCGCGCGCGCGCGCGCGCGCGCTTCTACTACTACCA 596  
QY 181 GTCGGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGT 240  
DB 597 GTCGGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGT 656  
QY 241 GGCCTTCTAC 250  
DB 657 GGCCTTCTAC 666

RESULT 3  
AAS13338  
ID AAS13338 standard; cDNA; 1747 BP.

AC AAS13338;

XX 18-DEC-2001 (first entry)

DE Human cDNA encoding NOV4 protein.

XX Human; NOV4; ss; cytostatic; nontropic; neuroprotective; vulnery;  
KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;  
KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;  
KW antiatherosclerotic; dermatological; cancer; neurological disorder;  
KW parkinson's disease; diabetes mellitus; asthma; enamel defect;  
KW immune disorder; autoimmune disease; respiratory disorder;  
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;  
KW cell growth regulation disorder; lesional psoriatic skin;  
KW atherosclerosis; abdominal aortic aneurysm.

OS Homo sapiens.

XX Location/Qualifiers

FT 5'UTR 1..37

FT /\*tag= a

FT CDS 38..1717

FT /\*tag= b

FT /\*product= "NOV4"

FT 1718..1747

FT /\*tag= c

XX WO200168851-A2.

XX 20-SEP-2001.

XX 12-MAR-2001; 2001WO-US07735.

XX 10-MAR-2000; 2000US-0188277.  
PR 10-MAR-2000; 2000US-0188316.  
PR 14-MAR-2000; 2000US-0189139.  
PR 14-MAR-2000; 2000US-0189140.  
PR 17-MAR-2000; 2000US-0190231.  
PR 17-MAR-2000; 2000US-0190401.  
XX (CURA-) CURAGEN CORP.  
XX Padigar M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;  
PI Majumder K, Li L;  
XX WPI; 2001-570869/64.  
DR P-PSDB; AAU08660.  
XX Novel polypeptides and nucleic acids homologous to members of collagen,  
PT potassium channel, tuftelin family of proteins for diagnosing, treating  
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders  
PT  
XX Claim 9; Page 15-16; 128pp; English.

CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and  
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides  
CC and anti-NOVX antibodies are useful for treating or preventing a  
CC pathology associated with NOVX polypeptide in humans and for treating a  
CC syndrome associated with human disease e.g. disorders characterised by  
CC altered cell motility, proliferation and migration e.g. cancer, e.g.  
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.  
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's  
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,  
CC asthma, hypertension and seizure (NOV4), enamel defects, such as  
CC amelogenesis imperfecta and disorders involving enamel defects,  
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic  
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem  
CC encephalitis occurring during testicular cancer, diabetes, reproductive  
CC health, metabolic and endocrine disorders, gastrointestinal disorders,  
CC immune disorders and autoimmune diseases, respiratory disorders, bone  
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell  
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and  
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders  
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that  
CC binds to it and a cell expressing NOVX polypeptide is useful for  
CC identifying a therapeutic agent for use in treatment of a NOVX related  
CC pathology. The antibodies and a polypeptide having 95% sequence identity  
CC to NOVX polypeptide are useful for treating a pathological state in a  
CC mammal. The present sequence encodes NOV4, a possible voltage gated  
CC potassium channel.

SQ Sequence 1747 BP; 255 A; 582 C; 575 G; 335 T; 0 other;

Query Match 100.0%; Score 250; DB 22; Length 1747;  
Best Local Similarity 100.0%; Pred. No. 3.3e-45;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTGTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 60  
DB 382 GCGGCTGGTGTCAACGTGGCGGGCTGGCTTCGAGAGCGGGCGCGACGCTGGCGG 441  
QY 61 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTAGAGAGCGCGG 120  
DB 442 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTAGAGAGCGCGG 501  
QY 121 CGCGAGATTTCTTCGACCGGCGCGCGCGCGCGCGCGCGCTTCTACTACTACCA 180  
DB 502 CGCGAGATTTCTTCGACCGGCGCGCGCGCGCGCGCGCGCTTCTACTACTACCA 561  
QY 181 GTCGGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGT 240  
DB 562 GTCGGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCGCTTCTCTGGAAGAGT 621  
QY 241 GGCCTTCTAC 250

Db 622 GGCCCTTCTAC 631  
|||||

## RESULT 4

AAD37899

ID AAD37899 standard; cDNA; 1792 BP.

XX

AC AAD37899;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human ion channel protein encoding cDNA.

XX

KW Human; novel human protein; NHP; ion channel protein; forensic biology;  
KW pharmacogenomic; drug screening; mental disorder; biological disorder;  
KW symptomatic manifestation; phenotypic manifestation; medical disorder;  
KW gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 93..1463

FT CDS

FT /tag= a

FT /product= "Human ion channel protein"

FT /note= "This region is specifically claimed as

FT SEQ ID NO: 1 in claim 1 of the specification"

FT

PN WO200231150-A2.

XX

PD 18-APR-2002.

XX

PF 10-OCT-2001; 2001WO-US31900.

XX

PR 10-OCT-2000; 2000US-239623P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E, Gerhardt B, Turner CA;

XX

DR WPI: 2002-452348/48.

XX

DR P-PSDB; AAE23655.

XX

XX Novel human ion channel polynucleotide encoding protein sharing  
PT structural similarity with mammalian ion channel proteins, e.g.  
PT potassium channels useful in therapeutic, diagnostic and  
PT pharmacogenomic applications

XX

PS Disclosure; Page 36; 36pp; English.  
XX

CC The present invention relates to novel human proteins (NHPs), human ion  
CC channel proteins and polynucleotides encoding such proteins. Sequences of  
CC the invention are useful in therapeutic, diagnostic and pharmacogenomic  
CC applications. They are useful for the identification of protein coding  
CC sequences, for mapping a unique gene to a particular chromosome, as  
CC additional DNA markers for restriction fragment length polymorphism  
CC (RFLP) analysis and in forensic biology, for screening libraries,  
CC isolating clones, preparing templates for cloning and sequencing, as  
CC hybridisation probes, in microarrays or other assay formats, to screen  
CC collections of genetic material from patients who have a particular  
CC medical condition, to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay. NHPs are useful  
CC for the detection of mutant human proteins or inappropriately expressed  
CC proteins for the diagnosis of disease, for the generation of antibodies,  
CC for screening for drugs effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of the  
CC protein in the body, for identification of other cellular gene products  
CC related to the protein and as reagents in assays for screening for  
CC compounds that can be used as pharmaceutical agents in the therapeutic  
CC treatment of mental, biological or medical disorders and diseases. The  
CC present sequence is a cDNA encoding human ion channel protein.

XX Sequence 1792 BP; 265 A; 534 C; 592 G; 399 T; 2 other;

Query Match 100.0%; Score 250; DB 24; Length 1792;

Best Local Similarity 100.0%; Pred. No. 3 3e-45;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGGTGCTCAAGCTGGCGGGCTTTCGAGACGCGGGCGGCGACGCTGGGCGG 60

Db 131 GCGGCTGGTGCTCAAGCTGGCGGGCTTTCGAGACGCGGGCGGCGACGCTGGGCGG 190

QY 61 CTTCCCGGACACTCTCTAGGAGACCCAGCGCGCGCGCGCGCTTCTACGACGCGGCG 120

Db 191 CTTCCCGGACACTCTCTAGGAGACCCAGCGCGCGCGCGCTTCTACGACGCGGCG 250

QY 121 CCGCGAGTATTTCTCGACCGCACCGCGCCAGCTTCGACGCGCGTCTTACTACTACCA 180

Db 251 CCGCGAGTATTTCTCGACCGCACCGCGCCAGCTTCGACGCGCGTCTTACTACTACCA 310

QY 181 GTCGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCTTCGACGCTTCCTGGAAGAGGT 240

Db 311 GTCGGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCTTCGACGCTTCCTGGAAGAGGT 370

QY 241 GGCTTCTAC 250

Db 371 GGCTTCTAC 380

RESULT: 5

AAT04953

ID AAT04953 standard; cDNA; 1598 BP.

XX AC AAT04953;

XX

DT 11-APR-1996. (first entry)

DE Mouse Kv1.7 voltage-gated potassium channel coding sequence.

XX

KW Mouse Kv1.7 voltage-gated potassium channel;

KW insulin antagonist drug screening; insulin agonist drug screening;

KW non-insulin-dependent diabetes mellitus; ds.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT 1..1598

FT CDS

FT /\*tag= a

FT /note= "specification states sequence is 1599.

FT Incomplete stop codon given"

FT

XX

PN WO9523858-A1.

XX

PD 08-SEP-1995.

XX

PF 23-FEB-1995; 95WO-US02221.

XX

PR 10-AUG-1994; 94US-0288405.

XX

PR 04-MAR-1994; 94US-0207401.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Chandy G, Chandy KG, Gutman GA, Kalman K;

XX

XX WPI: 1995-320573/41.

XX

DR P-PSDB; AAR82937.

XX

XX New voltage-gated potassium channel gene - used to identify

XX material(s) which can increase insulin release e.g. for treating

XX non-insulin dependent diabetes mellitus.

XX

XX Claim 1; Page 22-23; 38pp; English.

XX

XX The DNA encodes a mouse Kv1.7, which is a Shaker-related voltage-

XX gated potassium channel. It may be used in drug screening for

XX identification of therapeutics which modulate the channel and,

CC

CC therefore, modulate insulin secretion. Selective antagonists  
CC increase insulin release and thereby reduce hyperglycaemia  
CC associated with non-insulin-dependent diabetes mellitus.  
XX  
SQ Sequence 1598 BP; 232 A; 521 C; 502 G; 343 T; 0 other;  
0;  
Query Match 85.3%; Score 213.2; DB 16; Length 1598;  
Best Local Similarity 90.8%; Pred. No. 2.7e-37;  
Matches 227; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 1 GGGGCTGGTGCACAGTGGCGGCTGCGCTTCGAGACGGCGGCGCACGCTGGGCG 60  
DB 273 GCGGCTGGTGCACAGTGGCGGCTGCGCTTCGAGACGGCGGCGCACGCTGGGCG 332  
QY 61 CTTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGG 120  
DB 333 CTTCCCGGACACTCTGCTAGGGGACCCGCTGCGCGCGCGCGCTTCTACGACGCGG 392  
QY 121 CCAGAGTATTTCTTCGACCGGACCGGCGCCAGCTTCGAGCGCGTCTACTACTACCA 180  
DB 393 CGCGAGTATTTCTTCGACCGGACCGGCGCCAGCTTCGATGCGGTGCTCTACTACTACCA 452  
QY 181 GTCGGTGGCGGCTGCGCGCGCGCGCGCACGCTGCGGCTTCGAGAGGT 240  
DB 453 GTCGGGCGCGGCTGAGACGGCGCGCGCACGCTGCGGCTTCGAGAGGT 512  
QY 241 GGCCTTCTAC 250  
DB 513 GTCCTTCTAC 522  
RESULT 6  
ABQ19702/c  
ID ABQ19702 standard; DNA; 994 BP.  
XX  
AC ABQ19702;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6293.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP10074.  
XX  
PR 01-SEP-2000; 2000DE-1043826.  
PR 05-SEP-2000; 2000DE-1044543.  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue  
CC types and for investigating cell differentiation. The method allows the  
CC methylation status of many C residues to be determined simultaneously.  
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
CC method for determining the degree of cytosine methylation described in  
CC the disclosure of the invention.  
XX  
SQ Sequence 994 BP; 129 A; 152 C; 354 G; 359 T; 0 other;  
0;  
Query Match 70.2%; Score 175.4; DB 24; Length 994;  
Best Local Similarity 81.5%; Pred. No. 3.7e-29;  
Matches 203; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
QY 2 CGGCTGGTGTCAACGTGGCGGCTGCGCTTCGAGACGGCGGCGCGCTTCTACGACGCGCGC 61  
DB 534 CGACTAATACTCAACGTAACCGAACTACGCTTCGAAACGCGAACGCGCTTAAACCGC 475  
QY 62 TTCCCGGACACTCTGCTAGGGGACCCAGCGCGCGCGCGCTTCTACGACGACGCGCGC 121  
DB 474 TTCCCGAACACTCTACTAAAAACCCAGCGCGCGCGCGCTTCTACGACGACGCGCGC 415  
QY 122 CGCGAGTATTTCTTCGACCGGACCGCGCCAGCTTCGACGCGCTGCTCTACTACTACCA 181  
DB 414 CGCGAATATTTCTTCGACCGGACCGCGCCAGCTTTCGACGCGCTTCTACTACTACCA 355  
QY 182 TCCGTTGGCGGCTGCGCGCGCGCGCGCACGCTGCGGCTTCTCTCTTCTTGAAGAGGTG 241  
DB 354 TCCGATAAACGACTACGACGACGCGCGCGCGCTACCGCTTCGCTTCTTCTTAAAAATA 295  
QY 242 GCTTCTAC 250  
DB 294 ACCTTCTAC 286  
RESULT 7  
ABQ19703  
ID ABQ19703 standard; DNA; 994 BP.  
XX  
AC ABQ19703;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 6294.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP10074.  
PR 01-SEP-2000; 2000DE-1043826.  
PR 05-SEP-2000; 2000DE-1044543.  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.  
XX  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue  
CC types and for investigating cell differentiation. The method allows the  
CC methylation status of many C residues to be determined simultaneously.  
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
CC method for determining the degree of cytosine methylation described in  
CC the disclosure of the invention.  
XX  
XX Sequence 994 BP; 359 A; 354 C; 152 G; 129 T; 0 other;  
SQ  
Query Match 70.2%; Score 175.4; DB 24; Length 994;  
Best Local Similarity 81.5%; Pred. No. 3.7e-29;  
Matches 203; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
QY 2 CGCGTGGTCTCAACGTGGCGGGTGGCGTTCGAGACGGCGCGCAGCGTGGGCGCG 61  
Db 461 CGACTAATATCTCAACGTAAACCACTACGCTTCGAACCGCAACCGCGCTAAACCGC 520  
QY 62 TTCGCGGACACTCTGCTAGGGGACCCAGCGCGCGCGGCTTCACGACGACGCGCGC 121  
Db 521 TTCGCGGACACTCTACTAAAAACCCACGCGCGCGCGCTTCACGACGACGCGCGC 580  
QY 122 CGCGAGTATTTCTTCGACCGCCACCGCCAGCTTCGACCGCGTCTACTACTACCAG 181  
Db 581 CGCGAATATTTCTTCGACCGCACACCGACCACTTCGACCGCTACTCTACTACCAA 640  
QY 182 TCGGTTGGCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241  
Db 641 TCGGATAAACGACTACGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 700  
QY 242 GCCTTCTAC 250  
Db 701 ACCTTCTAC 709  
RESULT 8  
ABQ19704  
ID ABQ19704 standard; DNA; 994 BP.  
XX  
XX  
AC ABQ19704;  
XX  
XX  
DT 12-JUL-2002 (first entry)  
XX  
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 6295.  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
XX Homo sapiens.  
OS

XX WO200218632-A2.  
XX  
XX  
PD 07-MAR-2002.  
XX  
XX  
PF 01-SEP-2001; 2001WO-EP10074.  
XX  
XX  
PR 01-SEP-2000; 2000DE-1043826.  
PR 05-SEP-2000; 2000DE-1044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
XX WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue  
CC types and for investigating cell differentiation. The method allows the  
CC methylation status of many C residues to be determined simultaneously.  
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
CC method for determining the degree of cytosine methylation described in  
CC the disclosure of the invention.  
XX  
XX Sequence 994 BP; 131 A; 152 C; 380 G; 331 T; 0 other;  
SQ  
Query Match 67.4%; Score 168.4; DB 24; Length 994;  
Best Local Similarity 79.6%; Pred. No. 1.2e-27;  
Matches 199; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 1 GCGGCTGGTCTCAACGTGGCGGGTGGCGTTCGAGACGGCGCGCGCGCGCGCGCG 60  
Db 460 GCGGTTGGTCTTAAACGTGGTGGTGGTTCGAGACGGCGCGCGCGCGCGCGCG 519  
QY 61 CTTCGCGGACACTCTCTAGGGGACCCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
Db 520 TTTTTCGAGATATTTTGTAGGGGATTTAGCGCGCTTCGCGCGCGCGCGCGCGCG 579  
QY 121 CCGCGAGTATTTCTTCGACCGCGCACCGCCAGCTTCGACCGCGCTCTACTACTACCA 180  
Db 580 TCGCGAGTATTTTTCGATCCGATATCGTTCGATTCGATTCGATTCGATTCGATTCGAT 639  
QY 181 GTCCCGTGGCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 640 GTTCGCGTGGCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 699  
QY 241 GCCTTCTAC 250  
Db 700 GGTTCCTAC 709  
RESULT 9  
ABQ19705/c  
ID ABQ19705 standard; DNA; 994 BP.



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QY 72 CTCTGCTAGGGGACCCAGCCGCGCGCGCTTCTACGACGACGGCGCGCGCGAGTATT 131
Db 659 CACTCTGGGGACCCGCGCAAGCGCTGCGCTACTTCGACCCCTCAGGAAGCGAGTACT 718
QY 132 TCTTCGACGGGACCCGCGCGCGCTTCTACGACGCGTCTCTACTACTACCGTGGGCG 191
Db 719 TCTTCGACCGCAACCGCGCGCGCTTCTACTACTCTCTACTACTACCGTGGGCGG 778
QY 192 GGCTGGGCGCGCGCGCGCGCTCGCGCTCGACGCTTCTCTGGAAGAGGTGGCTTCTAC 250
Db 779 GCCTGGGAGCGCGGTCAAGCTCTCCCTGGACGTGTTCGGCGGAGAGATACGCTTCTAC 837

RESULT 11
ABL65917
ID ABL65917 standard; DNA; 2867 BP.
XX
AC ABL65917;
XX
DT 15-MAY-2002 (first entry)
DE
DE Lung cancer related gene sequence SEQ ID NO:4254.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-233133P.
XX 18-SEP-2000; 2000US-233617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 22-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.
XX 25-SEP-2000; 2000US-234567P.
XX 25-SEP-2000; 2000US-234923P.
XX 25-SEP-2000; 2000US-234924P.
XX 25-SEP-2000; 2000US-235077P.
XX 25-SEP-2000; 2000US-235082P.
XX 25-SEP-2000; 2000US-235134P.
XX 25-SEP-2000; 2000US-235280P.
XX 26-SEP-2000; 2000US-235637P.
XX 26-SEP-2000; 2000US-235638P.
XX 27-SEP-2000; 2000US-235711P.
XX 27-SEP-2000; 2000US-235720P.
XX 27-SEP-2000; 2000US-235840P.
XX 28-SEP-2000; 2000US-236028P.
XX 28-SEP-2000; 2000US-236032P.
XX 28-SEP-2000; 2000US-236033P.
XX 28-SEP-2000; 2000US-236034P.
XX 28-SEP-2000; 2000US-236109P.
XX 28-SEP-2000; 2000US-236111P.
XX 29-SEP-2000; 2000US-236842P.
XX 29-SEP-2000; 2000US-236891P.
XX 02-OCT-2000; 2000US-237172P.
XX 02-OCT-2000; 2000US-237173P.
XX 02-OCT-2000; 2000US-237278P.
XX 02-OCT-2000; 2000US-237294P.
XX 02-OCT-2000; 2000US-237295P.
XX 02-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237425P.
XX 03-OCT-2000; 2000US-237598P.
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PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
XX Claim 1; SEQ ID 4254; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
XX anti-neoplastic agent. The method involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening
XX an anti-neoplastic agent, and can be used for producing a product which
XX is the data collected with respect to the anti-neoplastic agent as a
XX result of M1, and the data is sufficient to convey the chemical
XX structure and/or properties of the agent. M1 can be used in the
XX treatment of cancer such as colon, breast, stomach, lung, thyroid,
XX oesophageal, ovarian, kidney, prostate or pancreatic cancer,
XX adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
XX infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
XX carcinoma, papillary carcinoma and Wilms' tumour.
XX
XX Sequence 2867 BP; 565 A; 839 C; 845 G; 618 T; 0 other;

Query Match 53.4%; Score 133.4; DB 24; Length 2867;
Best Local Similarity 72.4%; Pred. No. 3.8e-20;
Matches 173; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 12 TCAACGTGGCGCGCGCTTCGACGACGGCGCGCGCGCTGGCGCGCTTCCCGGACA 71
Db 599 TCAACATCTCCGCGCTTTCGAGCGAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGG 658
QY 72 CTCTGCTAGGGGACCCAGCGCGCGCGCTTCTACGACGACGGCGCGCGGAGTATT 131
Db 659 CACTCTGGGGACCCGCGCGCGCTGCGCTACTTCGACCGCGCTGAGGAGGAGTACT 718
QY 132 TCTTCGACCGGACCGCGCGCGCTTCGACGCGCTCTCTACTACTACCGTGGGCGG 191
Db 719 TCTTCGACCGCAACCGCGCGCGCTTCTACTACTACTACTACCGTGGGCGGCGG 778
QY 192 GGCTGGGCGCGCGCGCGCGCTCGCGCTCGACGCTTCTCTGGAAGAGGTGGCGTTC 250
Db 779 GCCTGGGAGCGCGGTCAAGCTCTCCCTGGACGTGTTCGGCGGAGAGATACGCTTCTAC 837

RESULT 12
ABI99654
ID ABI99654 standard; cDNA; 3147 BP.
XX
XX ABI99654;
XX
XX 07-MAR-2002 (first entry)
XX
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:683.
XX
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
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OS Mus musculus.  
XX WO20018188-A2.  
XX 22-NOV-2001.  
XX 18-MAY-2001; 2001WO-JP04192.  
XX 18-MAY-2000; 2000JP-0145977.  
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX WPI; 2002-034733/04.  
XX P-PSDB; ABB57250.  
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
XX Claim 2; Page 1705-1709; 2690pp; English.  
XX The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
XX Sequence 3147 BP; 704 A; 859 C; 887 G; 697 T; 0 other;  
SQ  
Query Match 50.1%; Score 125.2; DB 24; Length 3147;  
Best Local Similarity 68.8%; Pred. No. 2.2e-18;  
Matches 172; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
QY 1 GCGGCTGGTCTCAACGTGCGCGGCTGCGCTTCGAGACGCGGCGCGACGCTGGCGG 60  
DB 1567 GCGGCTAGTANTCAACATCTCGGGCTGCGCTTCGAAACGCGAGCTCAAGACTCTGCGACA 1626  
QY 61 CTTCCCGGACACTGCTAGGGGACCCAGCGCGCGCGCGCGCTTCTACGACGACGCGG 120  
DB 1627 GTTCCCCCAACACGCTGCTGGGCAACCCGAAGAAACGATGCGCTACTTTTGACCCCTGAG 1686  
QY 121 CCGCGAGTATTTCTTGACGCGGACCGCGCCAGCTTCGAGCGCGTCTACTACTACCA 180  
DB 1687 GAACGAGTACTTTTGAACCGCAACCGCGCCAGCTTCGATGCCATCTTTATTACTACCA 1746  
QY 181 GTCCGGTGGCGGCTGCGGCGCGCGCGCACGTCGCGCTCGAGCTCTTCTTGAAGAGT 240  
DB 1747 GTCCGGGGCGCGCTGCGGAGCGCGGTCAACGTGCCCTTGACATGTTCTCCGAGGAGAT 1806  
QY 241 GGCCTTCTAC 250  
DB 1807 TAAATTTTAC 1816  
RESULT 13  
AAH21452  
ID AAH21452 standard; DNA; 1836 BP.  
XX  
XX AAH21452;  
XX 18-SEP-2001 (first entry)  
DT

XX Human Kv1.5 DNA.  
XX Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;  
KW activator; ds.  
XX Homo sapiens.  
XX WO200151519-A2.  
XX 19-JUL-2001.  
XX 05-JAN-2001; 2001WO-EP00055.  
XX 11-JAN-2000; 2000DE-1000651.  
XX (AVET) AVENTIS PHARMA DEUT GMBH.  
XX Leberer E, Leeuw T, Ritscher A;  
XX WPI; 2001-442137/47.  
XX Identifying inhibitors and activators of eukaryotic potassium channels,  
PT for use as pharmaceuticals, comprises using yeast cells that express  
PT heterologous, but no endogenous, potassium channels -  
XX Disclosure; Page 45-46; 78pp; German.  
XX This sequence represents a novel method for identifying inhibitors or  
CC activators (A) of a eukaryotic potassium channel (KC) by applying a test  
CC compound to a mutant *Saccharomyces cerevisiae* cell in which: (i) the  
CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a  
CC eukaryotic KC is expressed heterologously, where the effect of the  
CC compound on the eukaryotic KC is then determined. The method is used to  
CC identify inhibitors or activators (A) of a eukaryotic potassium channel.  
CC (A) are potentially useful as pharmaceuticals. The method is easily  
CC automated for parallel processing of many samples, using either different  
CC concentrations of test compounds and/or different levels of heterologous  
CC gene expression. It allows identification of compounds that inhibit human  
CC KC selectively. This sequence represents the human Kv1.5 encoding DNA  
CC described in the method of the invention.  
XX  
XX Sequence 1836 BP; 323 A; 614 C; 580 G; 319 T; 0 other;  
SQ  
Query Match 47.6%; Score 119; DB 22; Length 1836;  
Best Local Similarity 71.5%; Pred. No. 4.8e-17;  
Matches 171; Conservative 0; Mismatches 65; Indels 3; Gaps 1;  
QY 12 TCAACGTGCGCGGCTGCGCTTCGAGACGCGGCGCGCGCTGCGGCGGCTTCCCGACA 71  
DB 368 TCAACATCTCCGGCTGCGCTTTGAGACGCGAGCTGGGCGAGCTTCCCAACA 427  
QY 72 CTCTGCTAGGGACCCAGCGCGCGCGCTTCTACGACGCGCGCGAGTATT 131  
DB 428 CACTCTGGGGGACCCCGCAAGCGCTGCGCTACTTCGACCCCTGAGGAACGAGTACT 487  
QY 132 TCTTCCACCGGACCGCGCGCGCTTCGACGCGCTGCTACTACTACAGTCCGGTGGC 191  
DB 488 TCTTCCACCGACCGCGCGCGCTTCGACGCTATCTCTACTACTACAGTCCGGGCGC 547  
QY 192 GGTGCGGCGCGCGCGCGAGCTGCGCTCGACGCTTCTCTGGAAGAGGTGCGCTTCTAC 250  
DB 548 GCCTGCGAGG---GGTCAACGCTCTCCCTGGACGCTGTTCGCGGAGAGATACGCTTCTAC 603  
RESULT 14  
ABO49288/c  
ID ABO49288 standard; DNA; 1521 BP.  
XX  
XX ABO49288;  
XX 12-JUL-2002 (first entry)  
DT

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35879.  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200218632-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 01-SEP-2001; 2001WO-EP10074.  
XX  
XX 01-SEP-2000; 2000DE-1043826.  
PR  
XX 05-SEP-2000; 2000DE-1044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
PI WPI; 2002-371829/40.  
DR  
XX Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue  
CC types and for investigating cell differentiation. The method allows the  
CC methylation status of many C residues to be determined simultaneously.  
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
CC method for determining the degree of cytosine methylation described in  
CC the disclosure of the invention.  
XX  
XX Sequence 1521 BP; 220 A; 179 C; 533 G; 589 T; 0 other;  
SQ  
Query Match 40.1%; Score 100.2; DB 24; Length 1521;  
Best Local Similarity 62.7%; Pred. No. 5.3e-13;  
Matches 156; Conservative 0; Mismatches 93; Indels 0; Gaps 0;  
QY 2 CGGCTGGTGTCAACGTGGCGGCGTTCGAGACGCGGCGCGCGCGTGGCGCGC 61  
DB 700 CGGCTAATCATCAACATCTCCGAACTACGCTTCGAACGCACTAAACCCCTTTACCAA 641  
QY 62 TTCCCGGACACTCTGTAGGGGACCCAGCGCGCGCGCGCGCTTCACGACGCGCGC 121  
DB 640 TTCCCGGAAACGCTACTAAACGACCCCAACGACGATAAATACCTTCGACCGCTCCGC 581  
QY 122 CGCGAGTATTCTTCGACGGGACCGCGCGCTTCGACCGCTCTACTACTACCAG 181  
DB 580 AAGCAATACTTCTTCGACGCAACCCGACCACTTCGAGCCACTCTCTACTATCA 521  
QY 182 TCCGGTGGGCGGCTGGCGGCGCGCGCGCTTCGACGCTCTCTCTGGAAGAGGTG 241  
DB 520 TCCGAAACCGCATCCGCGGACCGGATCAAGGTACCATCGACATTTCTCCGAAATATC 461

QY 242 GCCTTCTAC 250  
DB 460 CGCTTCTAC 452  
RESULT 15  
ABQ49289  
ID ABQ49289 standard; DNA; 1521 BP.  
XX  
XX ABQ49289;  
XX  
XX 12-JUL-2002 (first entry)  
XX  
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 35880.  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200218632-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 01-SEP-2001; 2001WO-EP10074.  
XX  
XX 01-SEP-2000; 2000DE-1043826.  
PR  
XX 05-SEP-2000; 2000DE-1044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
PI WPI; 2002-371829/40.  
DR  
XX Determining the degree of cytosine methylation in genomic DNA, useful  
PT for diagnosis and prognosis, comprises selective hybridization of  
PT amplicons from chemically treated DNA -  
XX  
XX Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one  
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
CC and the degree of hybridisation to both classes is determined from the  
CC label on the amplicon. From the ratio of labels hybridised to the two  
CC classes of oligomers, the degree of methylation is calculated. The method  
CC is used: (i) for diagnosis and/or prognosis of side effects of  
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CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
CC systems etc., particularly by detecting mutations or single nucleotide  
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Best Local Similarity 62.7%; Pred. No. 5.3e-13;  
Matches 156; Conservative 0; Mismatches 93; Indels 0; Gaps 0;  
QY 2 CGGCTGGTGTCAACGTGGCGGCGTTCGAGACGCGGCGCGCGCTGGCGCGC 61  
DB 822 CGGCTAATCATCAACATCTCCGAACTACGCTTCGAACGCACTAAACCCCTTTACCAA 881





